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- (71) Applicant: SENOMYX, INC. [US/US]; Suite 160, 11099 N. Torrey Pines Road, La Jolla, CA 92037 (US).
- (72) Inventor: ZOZULYA, Sergey; 3950 Mahaila Avenue #B22, San Diego, CA 92122 (US).
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(54) Title: HUMAN OLFACTORY RECEPTORS AND GENES ENCODING SAME

(57) Abstract: Newly identified Olfactory G protein-coupled receptors (ORs), and the genes and cDNA encoding said receptors are described. Specifically, G protein-coupled receptors active in olfactory signaling, and the genes and cDNA encoding the same, are described, along with methods for isolating such genes and for isolating and expressing such receptors. Methods for representing olfactory perception of a particular odorant in a mammal are also described, as are methods for generating novel molecules or combinations of molecules that elicit a predetermined odor perception in a mammal, and methods for simulating one or more odors. Further, methods for stimulating or blocking odor perception in a mammal are also disclosed.

## HUMAN OLFACTORY RECEPTORS AND GENES ENCODING SAME

### Cross Reference to Related Applications

This application claims priority to the following provisional applications: U.S. Ser. No. 60/188,914, filed March 13, 2000, entitled, "NOVEL OLFACTORY RECEPTORS AND GENES ENCODING SAME," to Zozulya; U.S. Ser. No. 60/192,033, filed March 24, 2000, entitled, "NOVEL OLFACTORY RECEPTORS AND GENES ENCODING SAME," to Zozulya; U.S. Ser. No. 60/198,474, filed April 12, 2000, entitled, "NOVEL OLFACTORY RECEPTORS AND GENE ENCODING THE SAME" to Zozulya; U.S. Ser. No. 60/199,335, filed April 24, 2000, "HUMAN OLFACTORY RECEPTORS AND GENES ENCODING THE SAME", to Zozulya; U.S. Ser. No. 60/207,702, filed May 26, 2000, entitled, "HUMAN OLFACTORY RECEPTORS AND GENES ENCODING THE SAME", to Zozulya; U.S. Ser. No. 60/213,849, filed June 23, 2000, entitled, "HUMAN OLFACTORY RECEPTORS AND GENES ENCODING THE SAME", to Zozulya; U.S. Ser. No. 60/226,534, filed August 16, 2000, "HUMAN OLFACTORY RECEPTORS AND GENES ENCODING THE SAME", to Zozulya; U.S. Ser. No. 60/230,732, filed September 7, 2000, "HUMAN OLFACTORY RECEPTORS AND GENES ENCODING THE SAME", to Zozulya; and U.S. Ser. No. 60/266,862, filed February 7, 2001, "HUMAN OLFACTORY RECEPTORS AND GENES ENCODING THE SAME", to Zozulya. All of these applications are herein incorporated by reference in their entireties.

### Field of the Invention

The invention relates to newly identified mammalian chemosensory G protein-coupled receptors, particularly olfactory receptors, fragments thereof, classes of such receptors, genes and cDNAs encoding said receptors, vectors including said receptors, and cells that express said receptors. The invention also relates to methods of using such receptors, fragments, genes, cDNAs, vectors, and cells to identify molecules involved in olfactory perception. The invention therefore has application in the selection and design of odorant compositions, as well as malodor blockers (olfactory receptor antagonists), particularly perfumes and fragrance compositions and components of deodorants and other malodor blocking compositions.

Description of the Related Art

The olfactory system provides sensory information about the chemical composition of the external world. Olfactory sensation is thought to involve distinct  
5 signaling pathways. These pathways are believed to be mediated by olfactory receptors (ORs). Cells which express olfactory receptors, when exposed to certain chemical stimuli, elicit olfactory sensation by depolarizing to generate an action potential, which is believed to trigger the sensation.

As such, olfactory receptors specifically recognize molecules that elicit  
10 specific olfactory sensation. These molecules are also referred to herein as "odorants." Olfactory receptors belong to the 7-transmembrane receptor superfamily (Buck *et al.*, *Cell* 65:175-87 (1991)), which are also known as G protein-coupled receptors (GPCRs). G protein-coupled receptors control many physiological functions, such as endocrine function, exocrine function, heart rate, lipolysis,  
15 carbohydrate metabolism, and transmembrane signaling. The biochemical analysis and molecular cloning of a number of such receptors has revealed many basic principles regarding the function of these receptors.

For example, U. S. Patent No. 5,691,188 describes how upon a ligand binding to a GPCR, the receptor presumably undergoes a conformational change leading to  
20 activation of the G protein. G proteins are comprised of three subunits: a guanyl nucleotide binding  $\alpha$  subunit, a  $\beta$  subunit, and a  $\gamma$  subunit. G proteins cycle between two forms, depending on whether GDP or GTP is bound to the  $\alpha$  subunit. When GDP is bound, the G protein exists as a heterotrimer: the  $G\alpha\beta\gamma$  complex. When GTP is bound, the  $\alpha$  subunit dissociates from the heterotrimer, leaving a  $G\beta\gamma$  complex. When  
25 a  $G\alpha\beta\gamma$  complex operatively associates with an activated G protein-coupled receptor in a cell membrane, the rate of exchange of GTP for bound GDP is increased and the rate of dissociation of the bound  $G\alpha$  subunit from the  $G\alpha\beta\gamma$  complex increases. The free  $G\alpha$  subunit and  $G\beta\gamma$  complex are thus capable of transmitting a signal to downstream elements of a variety of signal transduction pathways. These events form  
30 the basis for a multiplicity of different cell signaling phenomena, including for example the signaling phenomena that are identified as neurological sensory perceptions such as taste and/or smell.

Genes encoding the olfactory receptors are active primarily in olfactory neurons (Axel, *Sci. Amer.*, 273:154-59 (1995)). Individual olfactory receptor types are expressed in subsets of cells distributed in distinct zones of the olfactory epithelium (Breer, *Semin. Cell Biol.*, 5:25-32 (1994)). The human genome contains approximately one thousand genes that encode a diverse repertoire of olfactory receptors (Rouquier, *Nat. Genet.*, 18:243-50 (1998); Trask, *Hum. Mol. Genet.*, 7:2007-20 (1998)). It has been demonstrated that members of the OR gene family are distributed on all but a few human chromosomes. Through fluorescence *in situ* hybridization analysis, Rouquier showed that OR sequences reside at more than 25 locations in the human genome. Rouquier also determined that the human genome has accumulated a striking number of dysfunctional OR copies: 72% of the analyzed sequences were found to be pseudogenes. An understanding of an animal's ability to detect and discriminate among the thousands of distinct odorants or tastants, and more particularly to distinguish, for example beneficial tastants or odorants from toxic tastants or odorants, is complicated by the fact that chemosensory receptors belong to a multigene family with over a thousand members. For instance, there are up to 1,000 odorant receptors in mammals.

Moreover, each chemosensory receptor neuron may express only one or a few of these receptors. With respect to odorant receptors, any given olfactory neuron can respond to a small set of odorant ligands. In addition, odorant discrimination for a given neuron may depend on the ligand specificity of the one or few receptors it expresses. To analyze odorant-receptor interactions and their effects on olfactory cells, specific ligands and the olfactory receptors to which they bind are identified. This analysis requires isolation and expression of olfactory polypeptides, followed by binding assays.

Some studies suggest that OR genes can be expressed in tissues other than the olfactory epithelium, indicating potential alternative biological roles for this class of chemosensory receptors. Expression of various ORs has been reported in human and murine erythroid cells (Feingold 1999), developing rat heart (Drutel, *Receptor Channels*, 3(1):33-40 (1995)), avian notochord (Nef, *PNAS*, 94(9):4766-71 (1997)) and lingual epithelium (Abe, *FES Lett.*, 316(3):253-56 (1993)). One experimentally documented case also established the existence of a large subset of mammalian ORs transcribed in testes and expressed on the surface of mature spermatozoa, thereby



suggesting a possible role of ORs in sperm chemotaxis (Parmenthler, *Nature*, 355:453-55 (1992); Walensky, *Mol. Med.*, 1(2):130-41 (1998); Branscomb, *Genetics*, 156(2):785-97 (2000)). It was also hypothesized that olfactory receptors might provide molecular codes for highly specific cell-cell recognition functions in development and embryogenesis (Dreyer, *PNAS*, 95(11):9072-77 (1998)).

Complete or partial sequences of numerous human and other eukaryotic chemosensory receptors are currently known. See, e.g., Pilpel, Y. and Lancet, D., *Protein Science*, 8:969-77 (1999); Mombaerts, P., *Annu. Rev. Neurosci.*, 22:487-50 (1999); see also, EP0867508A2, US 5874243, WO 92/17585, WO 95/18140, WO 97/17444, WO 99/67282. Due to the complexity of ligand-receptor interactions, and more particularly odorant-receptor interactions, information about ligand-receptor recognition is lacking. In part, the present invention addresses the need for better understanding of these interactions. The present invention also provides, among other things, novel chemosensory receptors, and methods for utilizing such novel chemosensory receptors and the genes and cDNAs encoding such receptors, especially for identifying compounds that can be used to module chemosensory transduction, such as olfaction.

#### Summary of the Invention

Toward that end, it is an object of the invention to provide a new family of G protein-coupled receptors comprising over two hundred fifty olfactory G protein-coupled receptors (OR) active in olfactory perception. It is another object of the invention to provide fragments and variants of such ORs which retain odorant-binding activity.

It is yet another object of the invention to provide nucleic acid sequences or molecules that encode such ORs, fragments, or allelic variants.

It is still another object of the invention to provide expression vectors which include nucleic acid sequences that encode such ORs, or fragments, or variants thereof, which are operably linked to at least one regulatory sequence such as a promoter, enhancer, or other sequences involved in positive or negative gene transcription and/or translation.

It is still another object of the invention to provide human or non-human cells that functionally express at least one of such ORs, or fragments, or variants thereof.

It is still another object of the invention to provide OR fusion proteins or polypeptides which include at least a fragment of at least one of such ORs.

It is another object of the invention to provide an isolated nucleic acid molecule encoding an OR comprising a nucleic acid sequence that is at least 30%,  
5 more preferably at least 50%, still more preferably at least 60-70%, and still more preferably 75%, preferably 85%, 90%, 95%, 96%, 97%, 98%, or 99% identical to a nucleic acid sequence selected from the group consisting of: SEQ. ID. NO. 2, SEQ. ID. NO. 4, SEQ. ID. NO. 6, SEQ. ID. NO. 8, SEQ. ID. NO. 10, SEQ. ID. NO. 12, SEQ. ID. NO. 14, SEQ. ID. NO. 16, SEQ. ID. NO. 18, SEQ. ID. NO. 20, SEQ. ID. NO. 22, SEQ. ID. NO. 24, SEQ. ID. NO. 26, SEQ. ID. NO. 28, SEQ. ID. NO. 30, SEQ. ID. NO. 32, SEQ. ID. NO. 34, SEQ. ID. NO. 36, SEQ. ID. NO. 38, SEQ. ID. NO. 40, SEQ. ID. NO. 42, SEQ. ID. NO. 44, SEQ. ID. NO. 46, SEQ. ID. NO. 48, SEQ. ID. NO. 50, SEQ. ID. NO. 52, SEQ. ID. NO. 54, SEQ. ID. NO. 56, SEQ. ID. NO. 58, SEQ. ID. NO. 60, SEQ. ID. NO. 62, SEQ. ID. NO. 64, SEQ. ID. NO. 66, SEQ. ID. NO. 68, SEQ. ID. NO. 70, SEQ. ID. NO. 72, SEQ. ID. NO. 74, SEQ. ID. NO. 76, SEQ. ID. NO. 78, SEQ. ID. NO. 80, SEQ. ID. NO. 82, SEQ. ID. NO. 84, SEQ. ID. NO. 86, SEQ. ID. NO. 88, SEQ. ID. NO. 90, SEQ. ID. NO. 92, SEQ. ID. NO. 94, SEQ. ID. NO. 96, SEQ. ID. NO. 98, SEQ. ID. NO. 100, SEQ. ID. NO. 102, SEQ. ID. NO. 104, SEQ. ID. NO. 106, SEQ. ID. NO. 108, SEQ. ID. NO. 110, SEQ. ID. NO. 112, SEQ. ID. NO. 114, SEQ. ID. NO. 116, SEQ. ID. NO. 118, SEQ. ID. NO. 120, SEQ. ID. NO. 122, SEQ. ID. NO. 124, SEQ. ID. NO. 126, SEQ. ID. NO. 128, SEQ. ID. NO. 130, SEQ. ID. NO. 132, SEQ. ID. NO. 134, SEQ. ID. NO. 136, SEQ. ID. NO. 138, SEQ. ID. NO. 140, SEQ. ID. NO. 142, SEQ. ID. NO. 144, SEQ. ID. NO. 146, SEQ. ID. NO. 148, SEQ. ID. NO. 150, SEQ. ID. NO. 152, SEQ. ID. NO. 154, SEQ. ID. NO. 156, SEQ. ID. NO. 158, SEQ. ID. NO. 160, SEQ. ID. NO. 162, SEQ. ID. NO. 164, SEQ. ID. NO. 166, SEQ. ID. NO. 168, SEQ. ID. NO. 170, SEQ. ID. NO. 172, SEQ. ID. NO. 174, SEQ. ID. NO. 176, SEQ. ID. NO. 178, SEQ. ID. NO. 180, SEQ. ID. NO. 182, SEQ. ID. NO. 184, SEQ. ID. NO. 186, SEQ. ID. NO. 188, SEQ. ID. NO. 190, SEQ. ID. NO. 192, SEQ. ID. NO. 194, SEQ. ID. NO. 196, SEQ. ID. NO. 198, SEQ. ID. NO. 200, SEQ. ID. NO. 202, SEQ. ID. NO. 204, SEQ. ID. NO. 206, SEQ. ID. NO. 208, SEQ. ID. NO. 210, SEQ. ID. NO. 212, SEQ. ID. NO. 214, SEQ. ID. NO. 216, SEQ. ID. NO. 218, SEQ. ID. NO. 220, SEQ. ID. NO. 222, SEQ. ID.

NO. 224, SEQ. ID. NO. 226, SEQ. ID. NO. 228, SEQ. ID. NO. 230; SEQ. ID.  
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NO. 274, SEQ ID NO: 276, SEQ ID NO: 278, SEQ ID NO: 280, SEQ ID NO: 282,  
SEQ ID NO: 284, SEQ ID NO: 286, SEQ ID NO: 288, SEQ ID NO: 290, SEQ ID  
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10 SEQ ID NO: 302, SEQ ID NO: 304, SEQ ID NO: 306, SEQ ID NO: 308, SEQ ID  
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SEQ ID NO: 410, SEQ ID NO: 412, SEQ ID NO: 414, SEQ ID NO: 416, SEQ ID  
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SEQ ID NO: 428, SEQ ID NO: 430, SEQ ID NO: 432, SEQ ID NO: 434, SEQ ID  
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SEQ ID NO: 500, SEQ ID NO: 502, SEQ ID NO: 504, SEQ ID NO: 506, SEQ ID  
NO: 508, SEQ ID NO: 510 and SEQ ID NO: 512.

It is a further object of the invention to provide an isolated nucleic acid molecule comprising a nucleic acid sequence that encodes a polypeptide having an amino acid sequence which is at least 40%, more preferably at least 50%, still more preferably at least 60-70%, and still more preferably 75%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identical to an amino acid sequence selected from the group consisting of: SEQ. ID. NO. 1, SEQ. ID. NO. 3, SEQ. ID. NO. 5, SEQ. ID. NO. 7, SEQ. ID. NO. 9, SEQ. ID. NO. 11, SEQ. ID. NO. 13, SEQ. ID. NO. 15, SEQ. ID. NO. 17, SEQ. ID. NO. 19, SEQ. ID. NO. 21, SEQ. ID. NO. 23, SEQ. ID. NO. 25, SEQ. ID. NO. 27, SEQ. ID. NO. 29, SEQ. ID. NO. 31, SEQ. ID. NO. 33, SEQ. ID. NO. 35, SEQ. ID. NO. 37, SEQ. ID. NO. 39, SEQ. ID. NO. 41, SEQ. ID. NO. 43, SEQ. ID. NO. 45, SEQ. ID. NO. 47, SEQ. ID. NO. 49, SEQ. ID. NO. 51, SEQ. ID. NO. 53, SEQ. ID. NO. 55, SEQ. ID. NO. 57, SEQ. ID. NO. 59, SEQ. ID. NO. 61, SEQ. ID. NO. 63, SEQ. ID. NO. 65, SEQ. ID. NO. 67, SEQ. ID. NO. 69, SEQ. ID. NO. 71, SEQ. ID. NO. 73, SEQ. ID. NO. 75, SEQ. ID. NO. 77, SEQ. ID. NO. 79, SEQ. ID. NO. 81, SEQ. ID. NO. 83, SEQ. ID. NO. 85, SEQ. ID. NO. 87, SEQ. ID. NO. 89, SEQ. ID. NO. 91, SEQ. ID. NO. 93, SEQ. ID. NO. 95, SEQ. ID. NO. 97, SEQ. ID. NO. 99, SEQ. ID. NO. 101, SEQ. ID. NO. 103, SEQ. ID. NO. 105, SEQ. ID. NO. 107, SEQ. ID. NO. 109, SEQ. ID. NO. 111, SEQ. ID. NO. 113, SEQ. ID. NO. 115, SEQ. ID. NO. 117, SEQ. ID. NO. 119, SEQ. ID. NO. 121, SEQ. ID. NO. 123, SEQ. ID. NO. 125, SEQ. ID. NO. 127, SEQ. ID. NO. 129, SEQ. ID. NO. 131, SEQ. ID. NO. 133, SEQ. ID. NO. 135, SEQ. ID. NO. 137, SEQ. ID. NO. 139, SEQ. ID. NO. 141, SEQ. ID. NO. 143, SEQ. ID. NO. 145, SEQ. ID. NO. 147, SEQ. ID. NO. 149, SEQ. ID. NO. 151, SEQ. ID. NO. 153, SEQ. ID. NO. 155, SEQ. ID. NO. 157, SEQ. ID. NO. 159, SEQ. ID. NO. 161, SEQ. ID. NO. 163, SEQ. ID. NO. 165, SEQ. ID. NO. 167, SEQ. ID. NO. 169, SEQ. ID. NO. 171, SEQ. ID. NO. 173, SEQ. ID. NO. 175, SEQ. ID. NO. 177, SEQ. ID. NO. 179, SEQ. ID. NO. 181, SEQ. ID. NO. 183, SEQ. ID. NO. 185, SEQ. ID. NO. 187, SEQ. ID. NO. 189, SEQ. ID. NO. 191, SEQ. ID. NO. 193, SEQ. ID. NO. 195, SEQ. ID. NO. 197, SEQ. ID. NO. 199, SEQ. ID. NO. 201, SEQ. ID. NO. 203, SEQ. ID. NO. 205, SEQ. ID. NO. 207, SEQ. ID. NO. 209, SEQ. ID. NO. 211, SEQ. ID. NO. 213, SEQ. ID. NO. 215, SEQ. ID. NO. 217, SEQ. ID. NO. 219, SEQ. ID. NO. 221, SEQ. ID. NO. 223, SEQ. ID. NO. 225, SEQ. ID. NO. 227, SEQ. ID. NO. 229, SEQ. ID. NO. 231, SEQ. ID. NO. 233, SEQ. ID.

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It is still a further object of the invention to provide an isolated nucleic acid molecule comprising a nucleic acid sequence that encodes a fragment of a polypeptide having an amino acid sequence selected from the group consisting of: SEQ. ID. NO. 1, SEQ. ID. NO. 3, SEQ. ID. NO. 5, SEQ. ID. NO. 7, SEQ. ID. NO. 9, SEQ. ID. NO. 11, SEQ. ID. NO. 13, SEQ. ID. NO. 15, SEQ. ID. NO. 17, SEQ. ID. NO. 19, SEQ. ID. NO. 21, SEQ. ID. NO. 23, SEQ. ID. NO. 25, SEQ. ID. NO. 27, SEQ. ID. NO. 29, SEQ. ID. NO. 31, SEQ. ID. NO. 33, SEQ. ID. NO. 35, SEQ. ID. NO. 37, SEQ. ID. NO. 39, SEQ. ID. NO. 41, SEQ. ID. NO. 43, SEQ. ID. NO. 45, SEQ. ID. NO. 47, SEQ. ID. NO. 49, SEQ. ID. NO. 51, SEQ. ID. NO. 53, SEQ. ID. NO. 55, SEQ. ID. NO. 57, SEQ. ID. NO. 59, SEQ. ID. NO. 61, SEQ. ID. NO. 63, SEQ. ID. NO. 65, SEQ. ID. NO. 67, SEQ. ID. NO. 69, SEQ. ID. NO. 71, SEQ. ID. NO. 73, SEQ. ID. NO. 75, SEQ. ID. NO. 77, SEQ. ID. NO. 79, SEQ. ID. NO. 81, SEQ. ID. NO. 83, SEQ. ID. NO. 85, SEQ. ID. NO. 87, SEQ. ID. NO. 89, SEQ. ID. NO. 91, SEQ. ID. NO. 93, SEQ. ID. NO. 95, SEQ. ID. NO. 97, SEQ. ID. NO. 99, SEQ. ID. NO. 101, SEQ. ID. NO. 103, SEQ. ID. NO. 105, SEQ. ID. NO. 107, SEQ. ID. NO. 109, SEQ. ID. NO. 111, SEQ. ID. NO. 113, SEQ. ID. NO. 115, SEQ. ID. NO. 117, SEQ. ID. NO. 119, SEQ. ID. NO. 121, SEQ. ID. NO. 123, SEQ. ID. NO. 125, SEQ. ID. NO. 127, SEQ. ID. NO. 129, SEQ. ID. NO. 131, SEQ. ID. NO. 133, SEQ. ID. NO. 135, SEQ. ID. NO. 137, SEQ. ID. NO. 139, SEQ. ID. NO. 141, SEQ. ID. NO. 143, SEQ. ID. NO. 145, SEQ. ID. NO. 147, SEQ. ID. NO. 149, SEQ. ID. NO. 151, SEQ. ID. NO. 153, SEQ. ID. NO. 155, SEQ. ID. NO. 157, SEQ. ID. NO. 159, SEQ. ID. NO. 161, SEQ. ID. NO. 163, SEQ. ID. NO. 165, SEQ. ID. NO. 167, SEQ. ID. NO. 169, SEQ. ID. NO. 171, SEQ. ID. NO. 173, SEQ. ID. NO. 175, SEQ. ID. NO. 177, SEQ. ID. NO. 179, SEQ. ID. NO. 181, SEQ. ID. NO. 183, SEQ. ID. NO. 185, SEQ. ID. NO. 187, SEQ. ID. NO. 189, SEQ. ID. NO. 191, SEQ. ID. NO. 193, SEQ. ID. NO. 195, SEQ. ID. NO. 197, SEQ. ID. NO. 199, SEQ. ID. NO. 201, SEQ. ID. NO. 203, SEQ. ID. NO. 205, SEQ. ID. NO. 207, SEQ. ID. NO. 209, SEQ. ID. NO. 211, SEQ. ID. NO. 213, SEQ. ID. NO. 215, SEQ. ID. NO. 217, SEQ. ID. NO. 219, SEQ. ID. NO. 221, SEQ. ID. NO. 223, SEQ. ID. NO. 225, SEQ. ID. NO. 227, SEQ. ID. NO. 229, SEQ. ID. NO. 231, SEQ. ID. NO. 233, SEQ. ID. NO. 235, SEQ. ID. NO. 237, SEQ. ID. NO. 239, SEQ. ID. NO. 241, SEQ. ID. NO. 243, SEQ. ID. NO. 245, SEQ. ID. NO. 247, SEQ. ID. NO. 249, SEQ. ID. NO. 251, SEQ. ID. NO. 253,

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ID. NO. 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID NO:  
30 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and  
SEQ ID NO: 511, wherein the fragment is at least 10, preferably 20, 30, 50, 70, 100,  
or 150 amino acids in length.

It is still a further object of the invention to provide an isolated nucleic acid molecule comprising a nucleic acid sequence that encodes a variant of said fragment, wherein there is a variation in at most 10, preferably 5, 4, 3, 2, or 1 amino acid residues.

- 5 It is still another object of the invention to provide an isolated polypeptide comprising an amino acid sequence that is at least 40%, 50%, 60%, 70%, 80%, 90%, 95%, 96%, 97%, 98%, or 99% identical to an amino acid sequence selected from the group consisting of: SEQ. ID. NO. 1, SEQ. ID. NO. 3, SEQ. ID. NO. 5, SEQ. ID. NO. 7, SEQ. ID. NO. 9, SEQ. ID. NO. 11, SEQ. ID. NO. 13, SEQ. ID. NO. 15, SEQ. ID. NO. 17, SEQ. ID. NO. 19, SEQ. ID. NO. 21, SEQ. ID. NO. 23, SEQ. ID. NO. 25, SEQ. ID. NO. 27, SEQ. ID. NO. 29, SEQ. ID. NO. 31, SEQ. ID. NO. 33, SEQ. ID. NO. 35, SEQ. ID. NO. 37, SEQ. ID. NO. 39, SEQ. ID. NO. 41, SEQ. ID. NO. 43, SEQ. ID. NO. 45, SEQ. ID. NO. 47, SEQ. ID. NO. 49, SEQ. ID. NO. 51, SEQ. ID. NO. 53, SEQ. ID. NO. 55, SEQ. ID. NO. 57, SEQ. ID. NO. 59, SEQ. ID. NO. 61, SEQ. ID. NO. 63, SEQ. ID. NO. 65, SEQ. ID. NO. 67, SEQ. ID. NO. 69, SEQ. ID. NO. 71, SEQ. ID. NO. 73, SEQ. ID. NO. 75, SEQ. ID. NO. 77, SEQ. ID. NO. 79, SEQ. ID. NO. 81, SEQ. ID. NO. 83, SEQ. ID. NO. 85, SEQ. ID. NO. 87, SEQ. ID. NO. 89, SEQ. ID. NO. 91, SEQ. ID. NO. 93, SEQ. ID. NO. 95, SEQ. ID. NO. 97, SEQ. ID. NO. 99, SEQ. ID. NO. 101, SEQ. ID. NO. 103, SEQ. ID. NO. 105, SEQ. ID. NO. 107, SEQ. ID. NO. 109, SEQ. ID. NO. 111, SEQ. ID. NO. 113, SEQ. ID. NO. 115, SEQ. ID. NO. 117, SEQ. ID. NO. 119, SEQ. ID. NO. 121, SEQ. ID. NO. 123, SEQ. ID. NO. 125, SEQ. ID. NO. 127, SEQ. ID. NO. 129, SEQ. ID. NO. 131, SEQ. ID. NO. 133, SEQ. ID. NO. 135, SEQ. ID. NO. 137, SEQ. ID. NO. 139, SEQ. ID. NO. 141, SEQ. ID. NO. 143, SEQ. ID. NO. 145, SEQ. ID. NO. 147, SEQ. ID. NO. 149, SEQ. ID. NO. 151, SEQ. ID. NO. 153, SEQ. ID. NO. 155, SEQ. ID. NO. 157, SEQ. ID. NO. 159, SEQ. ID. NO. 161, SEQ. ID. NO. 163, SEQ. ID. NO. 165, SEQ. ID. NO. 167, SEQ. ID. NO. 169, SEQ. ID. NO. 171, SEQ. ID. NO. 173, SEQ. ID. NO. 175, SEQ. ID. NO. 177, SEQ. ID. NO. 179, SEQ. ID. NO. 181, SEQ. ID. NO. 183, SEQ. ID. NO. 185, SEQ. ID. NO. 187, SEQ. ID. NO. 189, SEQ. ID. NO. 191, SEQ. ID. NO. 193, SEQ. ID. NO. 195, SEQ. ID. NO. 197, SEQ. ID. NO. 199, SEQ. ID. NO. 201, SEQ. ID. NO. 203, SEQ. ID. NO. 205, SEQ. ID. NO. 207, SEQ. ID. NO. 209, SEQ. ID. NO. 211, SEQ. ID. NO. 213, SEQ. ID. NO. 215, SEQ. ID. NO. 217, SEQ. ID.



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 ID. NO. 491, SEQ. ID. NO. 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO:

499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511.

It is still a further object of the invention to provide an isolated polypeptide comprising a fragment of a polypeptide having an amino acid sequence selected from the group consisting of: SEQ. ID. NO. 1, SEQ. ID. NO. 3, SEQ. ID. NO. 5, SEQ. ID. NO. 7, SEQ. ID. NO. 9, SEQ. ID. NO. 11, SEQ. ID. NO. 13, SEQ. ID. NO. 15, SEQ. ID. NO. 17, SEQ. ID. NO. 19, SEQ. ID. NO. 21, SEQ. ID. NO. 23, SEQ. ID. NO. 25, SEQ. ID. NO. 27, SEQ. ID. NO. 29, SEQ. ID. NO. 31, SEQ. ID. NO. 33, SEQ. ID. NO. 35, SEQ. ID. NO. 37, SEQ. ID. NO. 39, SEQ. ID. NO. 41, SEQ. ID. NO. 43, SEQ. ID. NO. 45, SEQ. ID. NO. 47, SEQ. ID. NO. 49, SEQ. ID. NO. 51, SEQ. ID. NO. 53, SEQ. ID. NO. 55, SEQ. ID. NO. 57, SEQ. ID. NO. 59, SEQ. ID. NO. 61, SEQ. ID. NO. 63, SEQ. ID. NO. 65, SEQ. ID. NO. 67, SEQ. ID. NO. 69, SEQ. ID. NO. 71, SEQ. ID. NO. 73, SEQ. ID. NO. 75, SEQ. ID. NO. 77, SEQ. ID. NO. 79, SEQ. ID. NO. 81, SEQ. ID. NO. 83, SEQ. ID. NO. 85, SEQ. ID. NO. 87, SEQ. ID. NO. 89, SEQ. ID. NO. 91, SEQ. ID. NO. 93, SEQ. ID. NO. 95, SEQ. ID. NO. 97, SEQ. ID. NO. 99, SEQ. ID. NO. 101, SEQ. ID. NO. 103, SEQ. ID. NO. 105, SEQ. ID. NO. 107, SEQ. ID. NO. 109, SEQ. ID. NO. 111, SEQ. ID. NO. 113, SEQ. ID. NO. 115, SEQ. ID. NO. 117, SEQ. ID. NO. 119, SEQ. ID. NO. 121, SEQ. ID. NO. 123, SEQ. ID. NO. 125, SEQ. ID. NO. 127, SEQ. ID. NO. 129, SEQ. ID. NO. 131, SEQ. ID. NO. 133, SEQ. ID. NO. 135, SEQ. ID. NO. 137, SEQ. ID. NO. 139, SEQ. ID. NO. 141, SEQ. ID. NO. 143, SEQ. ID. NO. 145, SEQ. ID. NO. 147, SEQ. ID. NO. 149, SEQ. ID. NO. 151, SEQ. ID. NO. 153, SEQ. ID. NO. 155, SEQ. ID. NO. 157, SEQ. ID. NO. 159, SEQ. ID. NO. 161, SEQ. ID. NO. 163, SEQ. ID. NO. 165, SEQ. ID. NO. 167, SEQ. ID. NO. 169, SEQ. ID. NO. 171, SEQ. ID. NO. 173, SEQ. ID. NO. 175, SEQ. ID. NO. 177, SEQ. ID. NO. 179, SEQ. ID. NO. 181, SEQ. ID. NO. 183, SEQ. ID. NO. 185, SEQ. ID. NO. 187, SEQ. ID. NO. 189, SEQ. ID. NO. 191, SEQ. ID. NO. 193, SEQ. ID. NO. 195, SEQ. ID. NO. 197, SEQ. ID. NO. 199, SEQ. ID. NO. 201, SEQ. ID. NO. 203, SEQ. ID. NO. 205, SEQ. ID. NO. 207, SEQ. ID. NO. 209, SEQ. ID. NO. 211, SEQ. ID. NO. 213, SEQ. ID. NO. 215, SEQ. ID. NO. 217, SEQ. ID. NO. 219, SEQ. ID. NO. 221, SEQ. ID. NO. 223, SEQ. ID. NO. 225, SEQ. ID. NO. 227, SEQ. ID. NO. 229, SEQ. ID. NO. 231, SEQ. ID. NO. 233, SEQ. ID. NO. 235, SEQ. ID. NO. 237, SEQ. ID. NO. 239, SEQ. ID. NO. 241, SEQ. ID. NO.

243, SEQ. ID. NO. 245, SEQ. ID. NO. 247, SEQ. ID. NO. 249, SEQ. ID. NO. 251, SEQ. ID. NO. 253, SEQ. ID. NO. 255, SEQ. ID. NO. 257, SEQ. ID. NO. 259, SEQ. ID. NO. 261, SEQ. ID. NO., 263, SEQ. ID. NO., 265, SEQ. ID. NO. 267, SEQ. ID. NO. 269, SEQ. ID. NO. 271, SEQ. ID. NO. 273, SEQ. ID. NO. 275, SEQ. ID. NO. 277, SEQ. ID. NO. 279, SEQ. ID. NO. 281, SEQ. ID. NO. 283, SEQ. ID. NO. 285, SEQ. ID. NO. 287, SEQ. ID. NO. 289, SEQ. ID. NO. 291, SEQ. ID. NO. 293, SEQ. ID. NO. 295, SEQ. ID. NO. 297, SEQ. ID. NO. 299, SEQ. ID. NO. 301, SEQ. ID. NO. 303, SEQ. ID. NO. 305, SEQ. ID. NO. 307, SEQ. ID. NO. 309, SEQ. ID. NO. 311, SEQ. ID. NO. 313, SEQ. ID. NO. 315, SEQ. ID. NO. 317, SEQ. ID. NO. 319, SEQ. ID. NO. 321, SEQ. ID. NO. 323, SEQ. ID. NO. 325, SEQ. ID. NO. 327, SEQ. ID. NO. 329, SEQ. ID. NO. 331, SEQ. ID. NO. 333, SEQ. ID. NO. 335, SEQ. ID. NO. 337, SEQ. ID. NO. 339, SEQ. ID. NO. 341, SEQ. ID. NO. 343, SEQ. ID. NO. 345, SEQ. ID. NO. 347, SEQ. ID. NO. 349, SEQ. ID. NO. 351, SEQ. ID. NO. 353, SEQ. ID. NO. 355, SEQ. ID. NO. 357, SEQ. ID. NO. 359, SEQ. ID. NO. 361, SEQ. ID. NO. 363, SEQ. ID. NO. 365, SEQ. ID. NO. 367, SEQ. ID. NO. 369, SEQ ID NO: 371, SEQ. ID. NO. 373, SEQ. ID. NO. 375, SEQ. ID. NO. 377, SEQ. ID. NO. 379, SEQ. ID. NO. 381, SEQ. ID. NO. 383, SEQ. ID. NO. 385, SEQ. ID. NO. 387, SEQ. ID. NO. 389, SEQ. ID. NO. 391, SEQ. ID. NO. 393, SEQ. ID. NO. 395, SEQ. ID. NO. 397, SEQ. ID. NO. 399, SEQ. ID. NO. 401, SEQ. ID. NO. 403, SEQ. ID. NO. 405, SEQ. ID. NO. 407, SEQ. ID. NO. 409, SEQ. ID. NO. 411, SEQ. ID. NO. 413, SEQ. ID. NO. 415, SEQ. ID. NO. 417, SEQ. ID. NO. 419, SEQ. ID. NO. 421, SEQ. ID. NO. 423, SEQ. ID. NO. 425, SEQ. ID. NO. 427, SEQ. ID. NO. 429, SEQ. ID. NO. 431, SEQ. ID. NO. 433, SEQ. ID. NO. 435, SEQ. ID. NO. 437, SEQ. ID. NO. 439, SEQ. ID. NO. 441, SEQ. ID. NO. 443, SEQ. ID. NO. 445, SEQ. ID. NO. 447, SEQ. ID. NO. 449, SEQ. ID. NO. 451, SEQ. ID. NO. 453, SEQ. ID. NO. 455, SEQ. ID. NO. 457, SEQ. ID. NO. 459, SEQ. ID. NO. 461, SEQ. ID. NO. 463, SEQ. ID. NO. 465, SEQ. ID. NO. 467, SEQ. ID. NO. 469, SEQ. ID. NO. 471, SEQ. ID. NO. 473, SEQ. ID. NO. 475, SEQ. ID. NO. 477, SEQ. ID. NO. 479, SEQ. ID. NO. 481, SEQ. ID. NO. 483, SEQ. ID. NO. 485, SEQ. ID. NO. 487, SEQ. ID. NO. 489, SEQ. ID. NO. 491, SEQ. ID. NO. 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511, wherein the fragment is at least 40, preferably 60, 80, 100, 150, 200, or 250 amino acids in length.

It is still a further object of the invention to provide an isolated polypeptide comprising a variant of said fragment, especially naturally occurring allelic variants, the expression of which may be significant in the manner by which different persons in the human population perceive odors differently, both on a qualitative and quantitative level, wherein there is a variation in at most 10, preferably 5, 4, 3, 2, or 1 amino acid residues.

It is still another object of the invention to provide agonists, including inverse agonists, or antagonists of such ORs, or fragments or variants thereof.

It is yet another object of the invention to provide methods for representing the perception of odor and/or for predicting the perception of odor in a mammal, including in a human. Preferably, such methods may be performed by using the ORs, or fragments or variants thereof, and genes encoding such ORs, or fragments or variants thereof, disclosed herein.

It is yet another object of the invention to provide novel molecules or combinations of molecules which elicit a predetermined olfactory perception in a mammal. Such molecules or compositions can be generated by determining a value of olfactory perception in a mammal for a known molecule or combinations of molecules; determining a value of olfactory perception in a mammal for one or more unknown molecules or combinations of molecules; comparing the value of olfactory perception in a mammal for one or more unknown compositions to the value of olfactory perception in a mammal for one or more known compositions; selecting a molecule or combination of molecules that elicits a predetermined olfactory perception in a mammal; and combining two or more unknown molecules or combinations of molecules to form a molecule or combination of molecules that elicits a predetermined olfactory perception in a mammal. The combining step yields a single molecule or a combination of molecules that elicits a predetermined olfactory perception in a mammal.

It is still a further object of the invention to provide a method of screening one or more compounds for the presence of an odor detectable by a mammal, comprising: a step of contacting said one or more compounds with the disclosed ORs, fragments or variants thereof, preferably wherein the mammal is a human.

It is another object of the invention to provide a method for simulating a fragrance, comprising: for each of a plurality of ORs, or fragments of variants thereof

disclosed herein, preferably human ORs, ascertaining the extent to which the OR interacts with the fragrance; and combining a plurality of compounds, each having a previously ascertained interaction with one or more of the ORs, in amounts that together provide a receptor-stimulation profile that mimics the profile for the fragrance. Interaction of a fragrance with an OR can be determined using any of the binding or reporter assays described herein. The plurality of compounds may then be combined to form a mixture. If desired, one or more of the plurality of the compounds can be combined covalently. The combined compounds substantially stimulate at least 50%, 60%, 70%, 75%, 80% or 90% or all of the receptors that are substantially stimulated by the fragrance.

In yet another aspect of the invention, a method is provided wherein a plurality of standard compounds are tested against a plurality of ORs, or fragments or variants thereof, to ascertain the extent to which the ORs each interact with each standard compound, thereby generating a receptor stimulation profile for each standard compound. These receptor stimulation profiles may then be stored in a relational database on a data storage medium. The method may further comprise providing a desired receptor-stimulation profile for a scent; comparing the desired receptor stimulation profile to the relational database; and ascertaining one or more combinations of standard compounds that most closely match the desired receptor-stimulation profile. The method may further comprise combining standard compounds in one or more of the ascertained combinations to simulate the scent.

It is a further object of the invention to provide a method for representing olfactory perception of a particular smell in a mammal, comprising: providing values  $X_1$  to  $X_n$  representative of the quantitative stimulation of each of  $n$  ORs of said vertebrate, where  $n$  is greater than or equal to 4,  $n$  is greater than or equal to 12;  $n$  is greater than or equal to 24,  $n$  is greater than or equal to 48;  $n$  is greater than or equal to 72;  $n$  is greater than or equal to 96;  $n$  is greater than or equal to 120;  $n$  is greater than or equal to 144;  $n$  is greater than or equal to 168;  $n$  is greater than or equal to 192;  $n$  is greater than or equal to 216, or  $n$  is greater than or equal to 256; and generating from said values a quantitative representation of olfactory perception. The ORs may be an olfactory receptor disclosed herein, or fragments or variants thereof, the representation may constitute a point or a volume in  $n$ -dimensional space, may constitute a graph or a spectrum, and may constitute a matrix of quantitative representations. Also, the

providing step may comprise contacting a plurality of recombinantly produced ORs, or fragments or variants thereof, with a test composition and quantitatively measuring the interaction of said composition with said receptors.

It is yet another object of the invention to provide a method for predicting the  
5 olfactory perception in a mammal generated by one or more molecules or combinations of molecules yielding unknown olfactory perception in a mammal, comprising: providing values  $X_1$  to  $X_n$  representative of the quantitative stimulation of each of  $n$  ORs of said vertebrate, where  $n$  is greater than or equal to 4  $n$  is greater than or equal to 12;  $n$  is greater than or equal to 24,  $n$  is greater than or equal to 48;  $n$  is  
10 greater than or equal to 72;  $n$  is greater than or equal to 96;  $n$  is greater than or equal to 120;  $n$  is greater than or equal to 144;  $n$  is greater than or equal to 168;  $n$  is greater than or equal to 192;  $n$  is greater than or equal to 216, or  $n$  is greater than or equal to 256; for one or more molecules or combinations of molecules yielding known olfactory perception in a mammal; and generating from said values a quantitative  
15 representation of olfactory perception in a mammal for the one or more molecules or combinations of molecules yielding known olfactory perception in a mammal, providing values  $X_1$  to  $X_n$  representative of the quantitative stimulation of each of  $n$  ORs of said vertebrate, where  $n$  is greater than or equal to 4,  $n$  is greater than or equal to 12;  $n$  is greater than or equal to 24,  $n$  is greater than or equal to 48;  $n$  is greater than  
20 or equal to 72;  $n$  is greater than or equal to 96;  $n$  is greater than or equal to 120;  $n$  is greater than or equal to 144;  $n$  is greater than or equal to 168;  $n$  is greater than or equal to 192;  $n$  is greater than or equal to 216, or  $n$  is greater than or equal to 273; for one or more molecules or combinations of molecules yielding unknown olfactory perception in a mammal; and generating from said values a quantitative representation of  
25 olfactory perception in a mammal for the one or more molecules or combinations of molecules yielding unknown olfactory perception in a mammal, and predicting the olfactory perception in a mammal generated by one or more molecules or combinations of molecules yielding unknown olfactory perception in a mammal by comparing the quantitative representation of olfactory perception in a mammal for the  
30 one or more molecules or combinations of molecules yielding unknown olfactory perception in a mammal to the quantitative representation of olfactory perception in a mammal for the one or more molecules or combinations of molecules yielding known

olfactory perception in a mammal. The ORs used in this method may include an olfactory receptor, or fragment or variant thereof, disclosed herein.

#### Brief Description of the Drawings

5           Figure 1 illustrates the multiple sequence alignment derived for fifty novel ORs, indicating areas of homology and presence of sequence motifs characteristic for olfactory receptors. The fifty novel human olfactory receptors (hOR) proteins described herein are designated AOLFR1 through AOLFR52. The alignment protocol used the Clustal method with PAM250 residue weight table. Amino acid sequences  
10 AOLFR2 through AOLFR52 were analyzed for alignment with the AOLFR1 amino acid sequence.

          Figure 2 illustrates the multiple sequence alignment derived for fifty novel ORs, indicating areas of homology and presence of sequence motifs characteristic for olfactory receptors. The fifty novel human olfactory receptors (hOR) proteins  
15 described herein are designated AOLFR54 through AOLFR109. The alignment protocol used the Clustal method with PAM250 residue weight table. Amino acid sequences AOLFR55 through AOLFR109 were analyzed for alignment with the AOLFR54 amino acid sequence.

          Figure 3 illustrates the multiple sequence alignment derived for fifty novel  
20 ORs, indicating areas of homology and presence of sequence motifs characteristic for olfactory receptors. The fifty novel human olfactory receptors (hOR) proteins described herein are designated AOLFR110 through AOLFR163. The alignment protocol used the Clustal method with PAM250 residue weight table. Amino acid sequences AOLFR111 through AOLFR163 were analyzed for alignment with the  
25 AOLFR110 amino acid sequence.

          Figure 4 illustrates the multiple sequence alignment derived for fifty-four novel ORs, indicating areas of homology and presence of sequence motifs characteristic for olfactory receptors. The fifty-four novel human olfactory receptors (hOR) proteins described herein are designated AOLFR165 through AOLFR217. The  
30 alignment protocol used the Clustal method with PAM250 residue weight table. Amino acid sequences AOLFR166 through AOLFR217 were analyzed for alignment with the AOLFR165 amino acid sequence.

Figure 5 illustrates the multiple sequence alignment derived for fifty-two novel ORs, indicating areas of homology and presence of sequence motifs characteristic for olfactory receptors. The fifty-two novel human olfactory receptors (hOR) proteins described herein, which are designated AOLFR218 through AOLFR328. The alignment protocol used the Clustal method with PAM250 residue weight table. Amino acid sequences AOLFR219 through AOLFR328 were analyzed for alignment with the AOLFR218 amino acid sequence.

#### Detailed Description of the Invention

The invention thus provides isolated nucleic acid molecules encoding olfactory-cell-specific G protein-coupled receptors ("GPCRs"), and the polypeptides they encode. These nucleic acid molecules and the polypeptides that they encode are members of the olfactory receptor family. Other members of the olfactory receptor family are disclosed in Krautwurst, *et al.*, *Cell*, 95:917-26 (1998), and WO 0035274, the contents of which are herein incorporated by reference in their entireties.

According to one aspect of the invention, genes encoding over two hundred fifty distinct, novel human olfactory (odorant) receptors (also herein referred to ORs) have been identified in genome sequence databases. All of these receptor genes have been initially detected by computer DNA sequence analysis of genomic clones (unfinished High Throughput Genomic Sequence database accession numbers AB045359, AP002532, AP002533, AL365440, AC073487, AL359636, AL359955, AP002535, AB045365, AL359218, AC002555, AB045361, AL359512, AC023255, AL358773, AL357767, AL358874, AC068380, AC025283, AP002407, AC018700, AC022289, AC006313, AC002556, AC011571, AL121944, AC007194, AP001112, AC021660, AP000723, AC016856, AC018700, AP000818, AC00596, AP000916, AC011517, AP001112, AP000916, AC021427, AC021427, AC020884, AC019108, AL135841, AL133410, AF186996, AL138834, AC009237, AC025249, AC010930, AC009758, AC009642, AC009758, AC025249, AF101706, AC009642, AC025249, AC021660, AC011647, AC011711, AC09642, AC020597, AC011711, AC019088, AC022882, AC011571, AL121944, AP000435, AC012616, AC010332, AC010766, AP000743, AC021809, AC011879, AC021304, AC023226, AL160314, AC021304, AC020380, AC011904, AC004977, AC021304, AP000868, AP000825, AC023080, AC022207, AC121986, AC010814, AC018700, AC021304, AC008620, AC011537,



AC010760, AC027641, AC017103, AC024729, AC024257, AC025115, AP001524, AP000916, AC010814, AL162254, AC025234, AP001521, AC026090, AC019088, AC016856, AC016787, AC009594, AC026038, AQ628489, AC025942, AL163152, AC026975, AC024654, AP001803, AP001804, AL353767, AP001884, AC026083, 5 AC018793, AP000818, AL353894, AL049734, AL355366, AC011464, AC037472, AC036111, AC019093, AC027239, AC027522, AC009545, AC021333, AC036216, AC021935, AC022762, AL356019, AC055861, AC018375, AC072059, AC068339, AC022891, AL357039, AP002345, AC044810, AC073113, AC024399, AC023564, AL390860, AC074365, AP002826, AL359636, AL391534, AC055731, AC076959, 10 AP002826, AC019088, AC009779, AL445307, AP002512, AP000818, AC079190) by virtue of their sequence homology to some of the known human and other mammalian olfactory receptor genes.

Alternatively, nucleic acids encoding the olfactory receptors (ORs) and polypeptides of the invention can be isolated from a variety of sources, genetically 15 engineered, amplified, synthesized, and/or expressed recombinantly according to the methods disclosed in WO 0035374, which is herein incorporated by reference in its entirety.

These nucleic acids provide valuable probes for the identification of olfactory cells, as the nucleic acids are specifically expressed in olfactory cells. They can also 20 serve as tools for the generation of sensory topographical maps that elucidate the relationship between olfactory cells and olfactory sensory neurons leading to olfactory centers in the brain. Furthermore, the nucleic acids and the polypeptides they encode can be used as probes to elucidate olfactory-induced behaviors.

The invention also provides methods of screening for modulators, *e.g.*, 25 activators, inhibitors, stimulators, enhancers, agonists, inverse agonists and antagonists, of the ORs, or fragments or variants thereof, of the invention. Such modulators of olfactory transduction are useful for pharmacological and genetic modulation of olfactory signaling pathways. These methods of screening can be used to identify high affinity agonists and antagonists of olfactory cell activity. These 30 modulator compounds can then be used in the food, pharmaceutical, and cosmetic industries to customize odors and fragrances.

Thus, the invention provides assays for olfactory modulation, where the ORs, or fragments or variants thereof, of the invention act as direct or indirect reporter

molecules for the effect of modulators on olfactory transduction. The ORs, or fragments or variants thereof, can be used in assays, *e.g.*, to measure changes in ion concentration, membrane potential, current flow, ion flux, transcription, signal transduction, receptor-ligand interaction, second messenger concentrations, *in vitro*, *in vivo* and *ex vivo*. In one embodiment, the ORs, or fragments or variants thereof, can be used as an indirect reporters via attachment to second reporter molecules, such as green fluorescent protein (*see, e.g.,* Mistili *et al.*, *Nature Biotech.*, 15:961-64 (1997)). In another embodiment, the ORs, or fragments or variants thereof, can be expressed in host cells, and modulation of olfactory transduction via OR activity can be assayed by measuring changes in  $\text{Ca}^{2+}$  levels.

Methods of assaying for modulators of olfactory transduction include *in vitro* ligand binding assays using the ORs of the invention, or fragments or variants thereof. More particularly, such assays can use the ORs; portions thereof such as the extracellular or transmembrane domains; chimeric proteins comprising one or more of such domains; oocyte receptor expression; tissue culture cell receptor expression; transcriptional activation of the receptor; G protein binding to the receptor; ligand binding assays; voltage, membrane potential and conductance changes; ion flux assays; changes in intracellular second messengers such as cAMP and inositol triphosphate; changes in intracellular  $\text{Ca}^{2+}$  levels; and neurotransmitter release.

The invention also provides for methods of detecting olfactory nucleic acid and protein expression, allowing for the investigation of olfactory transduction regulation and specific identification of olfactory receptor cells. The ORs, fragments, and variants of the invention can also be used to generate monoclonal and polyclonal antibodies useful for identifying olfactory receptor cells. Olfactory receptor cells can be identified using techniques such as reverse transcription and amplification of mRNA, isolation of total RNA or poly A<sup>+</sup> RNA, northern blotting, dot blotting, *in situ* hybridization, RNase protection, S1 digestion, probing DNA microchip arrays, western blots, and the like.

#### A. Identification and Characterization of Olfactory Receptors

The amino acid sequences of the ORs and polypeptides of the invention can be identified by putative translation of the coding nucleic acid sequences. These various

amino acid sequences and the coding nucleic acid sequences may be compared to one another or to other sequences according to a number of methods.

For example, in sequence comparison, typically one sequence acts as a reference sequence, to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are entered into a computer, subsequence coordinates are designated, if necessary, and sequence algorithm program parameters are designated. Default program parameters can be used, as described below for the BLASTN and BLASTP programs, or alternative parameters can be designated. The sequence comparison algorithm then calculates the percent sequence identities for the test sequences relative to the reference sequence, based on the program parameters.

A "comparison window," as used herein, includes reference to a segment of any one of the number of contiguous positions selected from the group consisting of: from 20 to 600, usually about 50 to about 200, more usually about 100 to about 150 in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned. Methods of alignment of sequences for comparison are well known in the art. Optimal alignment of sequences for comparison can be conducted, *e.g.*, by the local homology algorithm of Smith & Waterman, *Adv. Appl. Math.* 2:482 (1981), by the homology alignment algorithm of Needleman & Wunsch, *J Mol. Biol.* 48:443 (1970), by the search for similarity method of Pearson & Lipman, *PNAS*, 85:2444 (1988), by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Dr., Madison, WI), or by manual alignment and visual inspection (*see, e.g., Current Protocols in Molecular Biology* (Ausubel *et al.*, eds. 1995 supplement)).

A preferred example of an algorithm that is suitable for determining percent sequence identity and sequence similarity are the BLAST and BLAST 2.0 algorithms, which are described in Altschul *et al.*, *Nuc. Acids Res.* 25:3389-3402 (1977) and Altschul *et al.*, *J Mol. Biol.* 215:403-410 (1990), respectively. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (<http://www.ncbi.nlm.nih.gov/>). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued

threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul *et al.*, Altschul *et al.*, *Nuc. Acids Res.* 25:3389-3402 (1977) and Altschul *et al.*, *J Mol. Biol.* 215:403-410 (1990)). These initial neighborhood word hits act as seeds for initiating  
5 searches to find longer HSPs containing them. The word hits are extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a  
10 scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and  
15 X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) or 10, M=5, N=-4 and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength of 3, and expectation (E) of 10, and the BLOSUM62 scoring matrix (*see* Henikoff & Henikoff, *PNAS*, 89:10915 (1989))  
20 alignments (B) of 50, expectation (E) of 10, M=5, N=-4, and a comparison of both strands.

Another example of a useful algorithm is PILEUP. PILEUP creates a multiple sequence alignment from a group of related sequences using progressive, pairwise alignments to show relationship and percent sequence identity. It also plots a so-  
25 called "tree" or "dendogram" showing the clustering relationships used to create the alignment (*see, e.g.*, Figure 2). PILEUP uses a simplification of the progressive alignment method of Feng & Doolittle, *J Mol. Evol.* 35:351-60 (1987). The method used is similar to the method described by Higgins & Sharp, *CABIOS* 5:151-153 (1989). The program can align up to 300 sequences, each of a maximum length of  
30 5,000 nucleotides or amino acids. The multiple alignment procedure begins with the pairwise alignment of the two most similar sequences, producing a cluster of two aligned sequences. This cluster is then aligned to the next most related sequence or cluster of aligned sequences. Two clusters of sequences are aligned by a simple

extension of the pairwise alignment of two individual sequences. The final alignment is achieved by a series of progressive, pairwise alignments. The program is run by designating specific sequences and their amino acid or nucleotide coordinates for regions of sequence comparison and by designating the program parameters. Using

5 PILEUP, a reference sequence is compared to other test sequences to determine the percent sequence identity relationship using the following parameters: default gap weight (3.00), default gap length weight (0.10), and weighted end gaps. PILEUP can be obtained from the GCG sequence analysis software package, *e.g.*, version 7. 0 (Devereaux *et al.*, *Nuc. Acids Res.* 12:387-395 (1984) encoded by the genes were

10 derived by conceptual translation of the corresponding open reading frames. Comparison of these protein sequences to all known proteins in the public sequence databases using BLASTP algorithm revealed their strong homology to the members of the mammalian olfactory receptor family, each of the odorant receptor sequences having at least 50%, and preferably at least 55%, at least 60%, at least 65%, and most

15 preferably at least 70%, amino acid identity to at least one known member of the family.

The nucleic acid molecules of the present invention are typically intronless and encode putative OR proteins generally having lengths of approximately 290 to approximately 400 amino acid residues that contain seven transmembrane domains, as

20 predicted by hydrophobicity plotting analysis, indicating that they belong to the G protein-coupled receptor 7-transmembrane (7TM) superfamily, which includes the subset of taste and olfactory receptors. In addition to the overall structural similarity, each of the ORs identified herein has a characteristic sequence signature of an olfactory receptor. In particular, all the identified sequences contain very close

25 matches to the following consensus amino acid motifs (Mombaerts, 1999, Pilpel 1999): EFILL (SEQ ID NO: 513) before transmembrane domain 1, LHTPMY (SEQ ID No: 514) in intracellular loop 1, MAYDRYVAIC (SEQ ID NO: 510) at the end of transmembrane domain 3 and the beginning of intracellular loop 2, SY at the end of transmembrane domain 5, FSTCSSH (SEQ ID NO: 516) in the beginning of

30 transmembrane domain 6, and PMLNPF (SEQ ID NO: 517) in transmembrane domain 7. Combination of all the above-mentioned structural features of the identified genes and encoded proteins strongly suggests that they represent novel members of the human olfactory receptor family.

As noted above, complete or partial sequences of numerous human and other eukaryotic olfactory receptors are currently known. The novel human receptors have amino acid sequences distinctly different from the previously known human olfactory receptors, which suggests their different specificity in odorant recognition. Therefore, these novel receptors and their genes can be used, alone or in combination with known olfactory receptors, in developing detection systems and assays for chemically distinct types of odorants not recognized by the known receptors, as well as for diagnostic and research purposes.

## B. Definitions

As used herein, the following terms have the meanings ascribed to them unless specified otherwise.

“OR” refers to one or more members of a family of G protein-coupled receptors that are expressed in olfactory cells. Olfactory receptor cells can also be identified on the basis of morphology (*see, e.g., Roper, supra*), or by the expression of proteins specifically expressed in olfactory cells. OR family members may have the ability to act as receptors for olfactory transduction.

“OR” nucleic acids encode a family of GPCRs with seven transmembrane regions that have “G protein-coupled receptor activity,” *e.g.*, they may bind to G proteins in response to extracellular stimuli and promote production of second messengers such as IP<sub>3</sub>, cAMP, cGMP, and Ca<sup>2+</sup> via stimulation of enzymes such as phospholipase C and adenylate cyclase (for a description of the structure and function of GPCRs, *see, e.g., Fong, supra*, and Baldwin, *supra*). A single olfactory cell may contain many distinct OR polypeptides.

Topologically, certain chemosensory GPCRs have an “N-terminal domain;” “extracellular domains;” “transmembrane domains” comprising seven transmembrane regions, and corresponding cytoplasmic, and extracellular loops; “cytoplasmic domains,” and a “C-terminal domain” (*see, e.g., Hoon et al., Cell*, 96:541-51 (1999); Buck & Axel, *Cell*, 65:175-87 (1991)). These domains can be structurally identified using methods known to those of skill in the art, such as sequence analysis programs that identify hydrophobic and hydrophilic domains (*see, e.g., Stryer, Biochemistry*, (3rd ed. 1988); *see also* any of a number of Internet based sequence analysis programs, such as those found at dot.imgen.bcm.tmc.edu). Such domains are useful

for making chimeric proteins and for in vitro assays of the invention, *e.g.*, ligand binding assays.

“Extracellular domains” therefore refers to the domains of OR polypeptides that protrude from the cellular membrane and are exposed to the extracellular face of the cell. Such domains generally include the “N terminal domain” that is exposed to the extracellular face of the cell, and optionally can include portions of the extracellular loops of the transmembrane domain that are exposed to the extracellular face of the cell, *i.e.*, the loops between transmembrane regions 2 and 3, between transmembrane regions 4 and 5, and between transmembrane regions 6 and 7.

The “N terminal domain” region starts at the N-terminus and extends to a region close to the start of the transmembrane domain. “Transmembrane domain,” which comprises the seven “transmembrane regions,” refers to the domain of OR polypeptides that lies within the plasma membrane, and may also include the corresponding cytoplasmic (intracellular) and extracellular loops. The seven transmembrane regions and extracellular and cytoplasmic loops can be identified using standard methods, as described in Kyte & Doolittle, *J. Mol. Biol.*, 157:105-32 (1982)), or in Stryer, *supra*. The general secondary and tertiary structure of transmembrane domains, in particular the seven transmembrane domains of 7-transmembrane receptors such as olfactory receptors, are well known in the art. Thus, primary structure sequence can be designed or predicted based on known transmembrane domain sequences, as described in detail below. These transmembrane domains are useful for *in vitro* ligand-binding assays, both soluble and solid phase.

“Cytoplasmic domains” refers to the domains of OR polypeptides that face the inside of the cell, *e.g.*, the “C terminal domain” and the intracellular loops of the transmembrane domain, *e.g.*, the intracellular loop between transmembrane regions 1 and 2, the intracellular loop between transmembrane regions 3 and 4, and the intracellular loop between transmembrane regions 5 and 6. “C terminal domain” refers to the region that spans the end of the last transmembrane domain and the C-terminus of the protein, and which is normally located within the cytoplasm.

The term “ligand-binding region” or “ligand-binding domain” refers to sequences derived from a chemosensory receptor, particularly an olfactory receptor,

that substantially incorporates at least transmembrane domains II to VII. The ligand-binding region may be capable of binding a ligand, and more particularly, an odorant.

The phrase "functional effects" in the context of assays for testing compounds that modulate OR family member mediated olfactory transduction includes the determination of any parameter that is indirectly or directly under the influence of the receptor, *e.g.*, functional, physical and chemical effects. It includes ligand binding, changes in ion flux, membrane potential, current flow, transcription, G protein binding, GPCR phosphorylation or dephosphorylation, signal transduction, receptor-ligand interactions, second messenger concentrations (*e.g.*, cAMP, cGMP, IP3, or intracellular  $\text{Ca}^{2+}$ ), *in vitro*, *in vivo*, and *ex vivo* and also includes other physiologic effects such increases or decreases of neurotransmitter or hormone release.

By "determining the functional effect" in the context of assays is meant assays for a compound that increases or decreases a parameter that is indirectly or directly under the influence of an OR family member, *e.g.*, functional, physical and chemical effects. Such functional effects can be measured by any means known to those skilled in the art, *e.g.*, changes in spectroscopic characteristics (*e.g.*, fluorescence, absorbance, refractive index), hydrodynamic (*e.g.*, shape), chromatographic, or solubility properties, patch clamping, voltage-sensitive dyes, whole cell currents, radioisotope efflux, inducible markers, oocyte OR gene expression; tissue culture cell OR expression; transcriptional activation of OR genes; ligand-binding assays; voltage, membrane potential and conductance changes; ion flux assays; changes in intracellular second messengers such as cAMP, cGMP, and inositol triphosphate (IP3); changes in intracellular calcium levels; neurotransmitter release, and the like.

"Inhibitors," "activators," and "modulators" of OR genes or proteins are used interchangeably to refer to inhibitory, activating, or modulating molecules identified using *in vitro* and *in vivo* assays for olfactory transduction, *e.g.*, ligands, agonists, antagonists, and their homologs and mimetics. Inhibitors are compounds that, *e.g.*, bind to, partially or totally block stimulation, decrease, prevent, delay activation, inactivate, desensitize, or down regulate olfactory transduction, *e.g.*, antagonists. Activators are compounds that, *e.g.*, bind to, stimulate, increase, open, activate, facilitate, enhance activation, sensitize, or up regulate olfactory transduction, *e.g.*, agonists. Modulators include compounds that, *e.g.*, alter the interaction of a receptor



with: extracellular proteins that bind activators or inhibitor (*e.g.*, ebnerin and other members of the hydrophobic carrier family); G proteins; kinases (*e.g.*, homologs of rhodopsin kinase and beta adrenergic receptor kinases that are involved in deactivation and desensitization of a receptor); and arrestins, which also deactivate and desensitize receptors. Modulators can include genetically modified versions of OR family members, *e.g.*, with altered activity, as well as naturally occurring and synthetic ligands, antagonists, agonists, small chemical molecules and the like. Such assays for inhibitors and activators include, *e.g.*, expressing OR family members in cells or cell membranes, applying putative modulator compounds, in the presence or absence of tastants, *e.g.*, sweet tastants, and then determining the functional effects on olfactory transduction, as described above. Samples or assays comprising OR family members that are treated with a potential activator, inhibitor, or modulator are compared to control samples without the inhibitor, activator, or modulator to examine the extent of modulation. Control samples (untreated with modulators) are assigned a relative OR activity value of 100%. Inhibition of a OR is achieved when the OR activity value relative to the control is about 80%, optionally 50% or 25-0%. Activation of an OR is achieved when the OR activity value relative to the control is 110%, optionally 150%, optionally 200-500%, or 1000-3000% higher.

The terms "purified," "substantially purified," and "isolated" as used herein refer to the state of being free of other, dissimilar compounds with which the compound of the invention is normally associated in its natural state, so that the "purified," "substantially purified," and "isolated" subject comprises at least 0.5%, 1%, 5%, 10%, or 20%, and most preferably at least 50% or 75% of the mass, by weight, of a given sample. In one preferred embodiment, these terms refer to the compound of the invention comprising at least 95% of the mass, by weight, of a given sample. As used herein, the terms "purified," "substantially purified," and "isolated" "isolated," when referring to a nucleic acid or protein, of nucleic acids or proteins, also refers to a state of purification or concentration different than that which occurs naturally in the mammalian, especially human, body. Any degree of purification or concentration greater than that which occurs naturally in the mammalian, especially human, body, including (1) the purification from other associated structures or compounds or (2) the association with structures or compounds to which it is not normally associated in the mammalian, especially human, body, are within the

meaning of "isolated." The nucleic acid or protein or classes of nucleic acids or proteins, described herein, may be isolated, or otherwise associated with structures or compounds to which they are not normally associated in nature, according to a variety of methods and processes known to those of skill in the art.

5           As used herein, the term "isolated," when referring to a nucleic acid or polypeptide refers to a state of purification or concentration different than that which occurs naturally in the mammalian, especially human, body. Any degree of purification or concentration greater than that which occurs naturally in the body, including (1) the purification from other naturally-occurring associated structures or  
10       compounds, or (2) the association with structures or compounds to which it is not normally associated in the body are within the meaning of "isolated" as used herein. The nucleic acids or polypeptides described herein may be isolated or otherwise associated with structures or compounds to which they are not normally associated in nature, according to a variety of methods and processes known to those of skill in the  
15       art.

          As used herein, the terms "amplifying" and "amplification" refer to the use of any suitable amplification methodology for generating or detecting recombinant or naturally expressed nucleic acid, as described in detail, below. For example, the invention provides methods and reagents (*e.g.*, specific degenerate oligonucleotide  
20       primer pairs) for amplifying (*e.g.*, by polymerase chain reaction, PCR) naturally expressed (*e.g.*, genomic or mRNA) or recombinant (*e.g.*, cDNA) nucleic acids of the invention (*e.g.*, tastant-binding sequences of the invention) *in vivo* or *in vitro*.

          The term "7- transmembrane receptor" means a polypeptide belonging to a superfamily of transmembrane proteins that have seven domains that span the plasma  
25       membrane seven times (thus, the seven domains are called "transmembrane" or "TM" domains TM I to TM VII). The families of olfactory and certain taste receptors each belong to this super-family. 7-transmembrane receptor polypeptides have similar and characteristic primary, secondary and tertiary structures, as discussed in further detail below.

30           The term "library" means a preparation that is a mixture of different nucleic acid or polypeptide molecules, such as the library of recombinantly generated chemosensory, particularly olfactory receptor ligand-binding domains generated by amplification of nucleic acid with degenerate primer pairs, or an isolated collection of

vectors that incorporate the amplified ligand-binding domains, or a mixture of cells each randomly transfected with at least one vector encoding an olfactory receptor.

The term "nucleic acid" or "nucleic acid sequence" refers to a deoxy-ribonucleotide or ribonucleotide oligonucleotide in either single- or double-stranded form. The term encompasses nucleic acids, i.e., oligonucleotides, containing known  
5 analogs of natural nucleotides. The term also encompasses nucleic-acid-like structures with synthetic backbones (*see e.g., Oligonucleotides and Analogues, a Practical Approach*, ed. F. Eckstein, Oxford Univ. Press (1991); *Antisense Strategies, Annals of the N.Y. Acad. of Sci.*, Vol. 600, Eds. Baserga *et al.* (NYAS 1992); Milligan  
10 *J. Med. Chem.* 36:1923-1937 (1993); *Antisense Research and Applications* (1993, CRC Press), WO 97/03211; WO 96/39154; Mata; *Toxicol. Appl. Pharmacol.* 144:189-197 (1997); Strauss-Soukup, *Biochemistry* 36:8692-8698 (1997); Samstag, *Antisense Nucleic Acid Drug Dev*, 6:153-156 (1996)).

Unless otherwise indicated, a particular nucleic acid sequence also implicitly  
15 encompasses conservatively modified variants thereof (*e.g.*, degenerate codon substitutions) and complementary sequences, as well as the sequence explicitly indicated. Specifically, degenerate codon substitutions may be achieved by generating, *e.g.*, sequences in which the third position of one or more selected codons is substituted with mixed-base and/or deoxyinosine residues (Batzer *et al.*, *Nucleic  
20 Acid Res.*, 19:5081 (1991); Ohtsuka *et al.*, *J. Biol. Chem.*, 260:2605-08 (1985); Rossolini *et al.*, *Mol. Cell. Probes*, 8:91-98 (1994)). The term nucleic acid is used interchangeably with gene, cDNA, mRNA, oligonucleotide, and polynucleotide.

The terms "polypeptide," "peptide" and "protein" are used interchangeably herein to refer to a polymer of amino acid residues. The terms apply to amino acid  
25 polymers in which one or more amino acid residue is an artificial chemical mimetic of a corresponding naturally occurring amino acid, as well as to naturally occurring amino acid polymers and non-naturally occurring amino acid polymer.

The term "plasma membrane translocation domain" or simply "translocation domain" means a polypeptide domain that, when incorporated into the amino terminus  
30 of a polypeptide coding sequence, can with great efficiency "chaperone" or "translocate" the hybrid ("fusion") protein to the cell plasma membrane. For instance, a "translocation domain" may be derived from the amino terminus of the bovine rhodopsin receptor polypeptide. In one embodiment, the translocation domain may be

functionally equivalent to an exemplary translocation domain (5'-MNGTEGPNFYVPFSNKTGVV; SEQ ID NO: 518). However, rhodopsin from any mammal may be used, as can other translocation facilitating sequences. Thus, the translocation domain is particularly efficient in translocating 7-transmembrane fusion proteins to the plasma membrane, and a protein (e.g., an olfactory receptor polypeptide) comprising an amino terminal translocating domain will be transported to the plasma membrane more efficiently than without the domain. However, if the N-terminal domain of the polypeptide is active in binding, the use of other translocation domains may be preferred.

“Functional equivalency” means the domain’s ability and efficiency in translocating newly translated proteins to the plasma membrane as efficiently as exemplary SEQ ID NO: 518 under similar conditions; relative efficiencies can be measured (in quantitative terms) and compared, as described herein. Domains falling within the scope of the invention can be determined by routine screening for their efficiency in translocating newly synthesized polypeptides to the plasma membrane in a cell (mammalian, *Xenopus*, and the like) with the same efficiency as the twenty amino acid long translocation domain SEQ ID NO: 518, as described in detail below.

The “translocation domain,” “ligand-binding domain”, and chimeric receptors compositions described herein also include “analogs,” or “conservative variants” and “mimetics” (“peptidomimetics”) with structures and activity that substantially correspond to the exemplary sequences. Thus, the terms “conservative variant” or “analog” or “mimetic” refer to a polypeptide which has a modified amino acid sequence, such that the change(s) do not substantially alter the polypeptide’s (the conservative variant’s) structure and/or activity, as defined herein. These include conservatively modified variations of an amino acid sequence, *i.e.*, amino acid substitutions, additions or deletions of those residues that are not critical for protein activity, or substitution of amino acids with residues having similar properties (e.g., acidic, basic, positively or negatively charged, polar or non-polar, *etc.*) such that the substitutions of even critical amino acids does not substantially alter structure and/or activity. Conservative substitution tables providing functionally similar amino acids are well known in the art.

More particularly, “conservatively modified variants” applies to both amino acid and nucleic acid sequences. With respect to particular nucleic acid sequences,

conservatively modified variants refers to those nucleic acids which encode identical or essentially identical amino acid sequences, or where the nucleic acid does not encode an amino acid sequence, to essentially identical sequences. Because of the degeneracy of the genetic code, a large number of functionally identical nucleic acids  
5 encode any given protein.

For instance, the codons GCA, GCC, GCG and GCU all encode the amino acid alanine. Thus, at every position where an alanine is specified by a codon, the codon can be altered to any of the corresponding codons described without altering the encoded polypeptide.

10 Such nucleic acid variations are "silent variations," which are one species of conservatively modified variations. Every nucleic acid sequence herein which encodes a polypeptide also describes every possible silent variation of the nucleic acid. One of skill will recognize that each codon in a nucleic acid (except AUG, which is ordinarily the only codon for methionine, and TGG, which is ordinarily the only  
15 codon for tryptophan) can be modified to yield a functionally identical molecule. Accordingly, each silent variation of a nucleic acid which encodes a polypeptide is implicit in each described sequence.

Conservative substitution tables providing functionally similar amino acids are well known in the art. For example, one exemplary guideline to select conservative  
20 substitutions includes (original residue followed by exemplary substitution): ala/gly or ser; arg/lys; asn/gln or his; asp/glu; cys/ser; gln/asn; gly/asp; gly/ala or pro; his/asn or gln; ile/leu or val; leu/ile or val; lys/arg or gln or glu; met/leu or tyr or ile; phe/met or leu or tyr; ser/thr; thr/ser; trp/tyr; tyr/trp or phe; val/ile or leu. An alternative exemplary guideline uses the following six groups, each containing amino acids that  
25 are conservative substitutions for one another: 1) Alanine (A), Serine (S), Threonine (T); 2) Aspartic acid (D), Glutamic acid (E); 3) Asparagine (N), Glutamine (Q); 4) Arginine (R), Lysine (I); 5) Isoleucine (I), Leucine (L), Methionine (M), Valine (V); and 6) Phenylalanine (F), Tyrosine (Y), Tryptophan (W); (*see also, e.g.,* Creighton, *Proteins*, W.H. Freeman and Company (1984); Schultz and Schimer, *Principles of*  
30 *Protein Structure*, Springer-Verlag (1979)). One of skill in the art will appreciate that the above-identified substitutions are not the only possible conservative substitutions. For example, for some purposes, one may regard all charged amino acids as conservative substitutions for each other whether they are positive or negative. In

addition, individual substitutions, deletions or additions that alter, add or delete a single amino acid or a small percentage of amino acids in an encoded sequence can also be considered "conservatively modified variations."

The terms "mimetic" and "peptidomimetic" refer to a synthetic chemical compound that has substantially the same structural and/or functional characteristics of the polypeptides, *e.g.*, translocation domains, ligand-binding domains, or chimeric receptors of the invention. The mimetic can be either entirely composed of synthetic, non-natural analogs of amino acids, or may be a chimeric molecule of partly natural peptide amino acids and partly non-natural analogs of amino acids. The mimetic can also incorporate any amount of natural amino acid conservative substitutions as long as such substitutions also do not substantially alter the mimetic's structure and/or activity.

As with polypeptides of the invention which are conservative variants, routine experimentation will determine whether a mimetic is within the scope of the invention, *i.e.*, that its structure and/or function is not substantially altered. Polypeptide mimetic compositions can contain any combination of non-natural structural components, which are typically from three structural groups: a) residue linkage groups other than the natural amide bond ("peptide bond") linkages; b) non-natural residues in place of naturally occurring amino acid residues; or c) residues which induce secondary structural mimicry, *i.e.*, to induce or stabilize a secondary structure, *e.g.*, a beta turn, gamma turn, beta sheet, alpha helix conformation, and the like. A polypeptide can be characterized as a mimetic when all or some of its residues are joined by chemical means other than natural peptide bonds. Individual peptidomimetic residues can be joined by peptide bonds, other chemical bonds or coupling means, such as, *e.g.*, glutaraldehyde, N-hydroxysuccinimide esters, bifunctional maleimides, N,N'-dicyclohexylcarbodiimide (DCC) or N,N'-diisopropylcarbodiimide (DIC). Linking groups that can be an alternative to the traditional amide bond ("peptide bond") linkages include, *e.g.*, ketomethylene (*e.g.*, -C(=O)-CH<sub>2</sub>- for -C(=O)-NH-), aminomethylene (CH<sub>2</sub>-NH), ethylene, olefin (CH=CH), ether (CH<sub>2</sub>-O), thioether (CH<sub>2</sub>-S), tetrazole (CN<sub>4</sub>), thiazole, retroamide, thioamide, or ester (*see, e.g.*, Spatola, *Chemistry and Biochemistry of Amino Acids, Peptides and Proteins*, 7:267-357, "Peptide Backbone Modifications," Marcell Dekker, NY (1983)). A polypeptide can also be characterized as a mimetic by

containing all or some non-natural residues in place of naturally occurring amino acid residues; non-natural residues are well described in the scientific and patent literature.

A “label” or a “detectable moiety” is a composition detectable by spectroscopic, photochemical, biochemical, immunochemical, or chemical means. For  
5 example, useful labels include  $^{32}\text{P}$ , fluorescent dyes, electron-dense reagents, enzymes (*e.g.*, as commonly used in an ELISA), biotin, digoxigenin, or haptens and proteins which can be made detectable, *e.g.*, by incorporating a radiolabel into the peptide or used to detect antibodies specifically reactive with the peptide.

A “labeled nucleic acid probe or oligonucleotide” is one that is bound, either  
10 covalently, through a linker or a chemical bond, or noncovalently, through ionic, van der Waals, electrostatic, or hydrogen bonds to a label such that the presence of the probe may be detected by detecting the presence of the label bound to the probe.

As used herein a “nucleic acid probe or oligonucleotide” is defined as a nucleic acid capable of binding to a target nucleic acid of complementary sequence  
15 through one or more types of chemical bonds, usually through complementary base pairing, usually through hydrogen bond formation. As used herein, a probe may include natural (*i.e.*, A, G, C, or T) or modified bases (7-deazaguanosine, inosine, *etc.*). In addition, the bases in a probe may be joined by a linkage other than a phosphodiester bond, so long as it does not interfere with hybridization. Thus, for  
20 example, probes may be peptide nucleic acids in which the constituent bases are joined by peptide bonds rather than phosphodiester linkages. It will be understood by one of skill in the art that probes may bind target sequences lacking complete complementarity with the probe sequence depending upon the stringency of the hybridization conditions. The probes are optionally directly labeled as with isotopes,  
25 chromophores, lumiphores, chromogens, or indirectly labeled such as with biotin to which a streptavidin complex may later bind. By assaying for the presence or absence of the probe, one can detect the presence or absence of the select sequence or subsequence.

The term “heterologous” when used with reference to portions of a nucleic  
30 acid indicates that the nucleic acid comprises two or more subsequences that are not found in the same relationship to each other in nature. For instance, the nucleic acid is typically recombinantly produced, having two or more sequences from unrelated genes arranged to make a new functional nucleic acid, *e.g.*, a promoter from one

source and a coding region from another source. Similarly, a heterologous protein indicates that the protein comprises two or more subsequences that are not found in the same relationship to each other in nature (*e.g.*, a fusion protein).

5 A "promoter" is defined as an array of nucleic acid sequences that direct transcription of a nucleic acid. As used herein, a promoter includes necessary nucleic acid sequences near the start site of transcription, such as, in the case of a polymerase II type promoter, a TATA element. A promoter also optionally includes distal enhancer or repressor elements, which can be located as much as several thousand base pairs from the start site of transcription. A "constitutive" promoter is a promoter  
10 that is active under most environmental and developmental conditions. An "inducible" promoter is a promoter that is active under environmental or developmental regulation. The term "operably linked" refers to a functional linkage between a nucleic acid expression control sequence (such as a promoter, or array of transcription factor binding sites) and a second nucleic acid sequence, wherein the  
15 expression control sequence directs transcription of the nucleic acid corresponding to the second sequence.

As used herein, "recombinant" refers to a polynucleotide synthesized or otherwise manipulated *in vitro* (*e.g.*, "recombinant polynucleotide"), to methods of using recombinant polynucleotides to produce gene products in cells or other  
20 biological systems, or to a polypeptide ("recombinant protein") encoded by a recombinant polynucleotide. "Recombinant means" also encompass the ligation of nucleic acids having various coding regions or domains or promoter sequences from different sources into an expression cassette or vector for expression of, *e.g.*, inducible or constitutive expression of a fusion protein comprising a translocation domain of the  
25 invention and a nucleic acid sequence amplified using a primer of the invention.

The phrase "selectively (or specifically) hybridizes to" refers to the binding, duplexing, or hybridizing of a molecule only to a particular nucleotide sequence under stringent hybridization conditions when that sequence is present in a complex mixture (*e.g.*, total cellular or library DNA or RNA).

30 The phrase "stringent hybridization conditions" refers to conditions under which a probe will hybridize to its target subsequence, typically in a complex mixture of nucleic acid, but to no other sequences. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer



sequences hybridize specifically at higher temperatures. An extensive guide to the hybridization of nucleic acids is found in Tijssen, *Techniques in Biochemistry and Molecular Biology - Hybridisation with Nucleic Probes*, "Overview of principles of hybridization and the strategy of nucleic acid assays" (1993). Generally, stringent

5 conditions are selected to be about 5-10° C lower than the thermal melting point ( $T_m$ ) for the specific sequence at a defined ionic strength pH. The  $T_m$  is the temperature (under defined ionic strength, pH, and nucleic concentration) at which 50% of the probes complementary to the target hybridize to the target sequence at equilibrium (as the target sequences are present in excess, at  $T_m$ , 50% of the probes are occupied at

10 equilibrium). Stringent conditions will be those in which the salt concentration is less than about 1.0 M sodium ion, typically about 0.01 to 1.0 M sodium ion concentration (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30° C for short probes (e.g., 10 to 50 nucleotides) and at least about 60° C for long probes (e.g., greater than 50 nucleotides). Stringent conditions may also be achieved with the

15 addition of destabilizing agents such as formamide. For selective or specific hybridization, a positive signal is at least two times background, optionally 10 times background hybridization. Exemplary stringent hybridization conditions can be as following: 50% formamide, 5x SSC, and 1% SDS, incubating at 42°C, or, 5x SSC, 1% SDS, incubating at 65°C, with wash in 0.2x SSC, and 0.1 % SDS at 65°C. Such

20 hybridizations and wash steps can be carried out for, e.g., 1, 2, 5, 10, 15, 30, 60; or more minutes.

Nucleic acids that do not hybridize to each other under stringent conditions are still substantially related if the polypeptides that they encode are substantially related. This occurs, for example, when a copy of a nucleic acid is created using the maximum

25 codon degeneracy permitted by the genetic code. In such cases, the nucleic acids typically hybridize under moderately stringent hybridization conditions. Exemplary "moderately stringent hybridization conditions" include a hybridization in a buffer of 40% formamide, 1 M NaCl, 1% SDS at 37°C, and a wash in 1x SSC at 45°C. Such hybridizations and wash steps can be carried out for, e.g., 1, 2, 5, 10, 15, 30, 60, or

30 more minutes. A positive hybridization is at least twice background. Those of ordinary skill will readily recognize that alternative hybridization and wash conditions can be utilized to provide conditions of similar stringency.

“Antibody” refers to a polypeptide comprising a framework region from an immunoglobulin gene or fragments thereof that specifically binds and recognizes an antigen. The recognized immunoglobulin genes include the kappa, lambda, alpha, gamma, delta, epsilon, and mu constant region genes, as well as the myriad  
5 immunoglobulin variable region genes. Light chains are classified as either kappa or lambda. Heavy chains are classified as gamma, mu, alpha, delta, or epsilon, which in turn define the immunoglobulin classes, IgG, IgM, IgA, IgD and IgE, respectively.

An exemplary immunoglobulin (antibody) structural unit comprises a tetramer. Each tetramer is composed of two identical pairs of polypeptide chains, each pair  
10 having one “light” (about 25 kDa) and one “heavy” chain (about 50-70 kDa). The N-terminus of each chain defines a variable region of about 100 to 110 or more amino acids primarily responsible for antigen recognition. The terms variable light chain (VL) and variable heavy chain (VH) refer to these light and heavy chains respectively.

A “chimeric antibody” is an antibody molecule in which (a) the constant  
15 region, or a portion thereof, is altered, replaced or exchanged so that the antigen binding site (variable region) is linked to a constant region of a different or altered class, effector function and/or species, or an entirely different molecule which confers new properties to the chimeric antibody, *e.g.*, an enzyme, toxin, hormone, growth factor, drug, *etc.*; or (b) the variable region, or a portion thereof, is altered, replaced or  
20 exchanged with a variable region having a different or altered antigen specificity.

An “anti-OR” antibody is an antibody or antibody fragment that specifically binds a polypeptide encoded by a OR gene, cDNA, or a subsequence thereof.

The term “immunoassay” is an assay that uses an antibody to specifically bind an antigen. The immunoassay is characterized by the use of specific binding  
25 properties of a particular antibody to isolate, target, and/or quantify the antigen.

The phrase “specifically (or selectively) binds” to an antibody or, “specifically (or selectively) immunoreactive with,” when referring to a protein or peptide, refers to a binding reaction that is determinative of the presence of the protein in a heterogeneous population of proteins and other biologics. Thus, under designated  
30 immunoassay conditions, the specified antibodies bind to a particular protein at least two times the background and do not substantially bind in a significant amount to other proteins present in the sample. Specific binding to an antibody under such conditions may require an antibody that is selected for its specificity for a particular

protein. For example, polyclonal antibodies raised to an OR family member from specific species such as rat, mouse, or human can be selected to obtain only those polyclonal antibodies that are specifically immunoreactive with the OR polypeptide or an immunogenic portion thereof and not with other proteins, except for orthologs or polymorphic variants and alleles of the OR polypeptide. This selection may be achieved by subtracting out antibodies that cross-react with OR molecules from other species or other OR molecules. Antibodies can also be selected that recognize only OR GPCR family members but not GPCRs from other families. A variety of immunoassay formats may be used to select antibodies specifically immunoreactive with a particular protein. For example, solid-phase ELISA immunoassays are routinely used to select antibodies specifically immunoreactive with a protein (*see, e.g., Harlow & Lane, Antibodies, A Laboratory Manual, (1988), for a description of immunoassay formats and conditions that can be used to determine specific immunoreactivity*). Typically a specific or selective reaction will be at least twice background signal or noise and more typically more than 10 to 100 times background.

The phrase "selectively associates with" refers to the ability of a nucleic acid to "selectively hybridize" with another as defined above, or the ability of an antibody to "selectively (or specifically) bind to a protein, as defined above.

The term "expression vector" refers to any recombinant expression system for the purpose of expressing a nucleic acid sequence of the invention *in vitro* or *in vivo*, constitutively or inducibly, in any cell, including prokaryotic, yeast, fungal, plant, insect or mammalian cell. The term includes linear or circular expression systems. The term includes expression systems that remain episomal or integrate into the host cell genome. The expression systems can have the ability to self-replicate or not, i.e., drive only transient expression in a cell. The term includes recombinant expression "cassettes which contain only the minimum elements needed for transcription of the recombinant nucleic acid.

By "host cell" is meant a cell that contains an expression vector and supports the replication or expression of the expression vector. Host cells may be prokaryotic cells such as *E. coli*, or eukaryotic cells such as yeast, insect, amphibian, or mammalian cells such as CHO, HeLa, HEK-293, and the like, *e.g.,* cultured cells, explants, and cells *in vivo*.

### C. Isolation and Expression of Olfactory Receptors

Isolation and expression of the ORs, or fragments or variants thereof, of the invention can be performed as described below. PCR primers can be used for the amplification of nucleic acids encoding olfactory receptor ligand-binding regions and libraries of these nucleic acids can thereby be generated. Libraries of expression vectors can then be used to infect or transfect host cells for the functional expression of these libraries. These genes and vectors can be made and expressed *in vitro* or *in vivo*. One of skill will recognize that desired phenotypes for altering and controlling nucleic acid expression can be obtained by modulating the expression or activity of the genes and nucleic acids (*e.g.*, promoters, enhancers and the like) within the vectors of the invention. Any of the known methods described for increasing or decreasing expression or activity can be used. The invention can be practiced in conjunction with any method or protocol known in the art, which are well described in the scientific and patent literature.

The nucleic acid sequences of the invention and other nucleic acids used to practice this invention, whether RNA, cDNA, genomic DNA, vectors, viruses or hybrids thereof, may be isolated from a variety of sources, genetically engineered, amplified, and/or expressed recombinantly. Any recombinant expression system can be used, including, in addition to mammalian cells, *e.g.*, bacterial, yeast, insect or plant systems.

Alternatively, these nucleic acids can be synthesized *in vitro* by well-known chemical synthesis techniques, as described in, *e.g.*, Carruthers, *Cold Spring Harbor Symp. Quant. Biol.* 47:411-418 (1982); Adams, *Am. Chem. Soc.* 105:661 (1983); Belousov, *Nucleic Acids Res.* 25:3440-3444 (1997); Frenkel, *Free Radic. Biol. Med.* 19:373-380 (1995); Blommers, *Biochemistry* 33:7886-7896 (1994); Narang, *Meth. Enzymol.* 68:90 (1979); Brown, *Meth. Enzymol.* 68:109 (1979); Beaucage, *Tetra. Lett.* 22:1859 (1981); U.S. Patent No. 4,458,066. Double-stranded DNA fragments may then be obtained either by synthesizing the complementary strand and annealing the strands together under appropriate conditions, or by adding the complementary strand using DNA polymerase with an appropriate primer sequence..

Techniques for the manipulation of nucleic acids, such as, for example, for generating mutations in sequences, subcloning, labeling probes, sequencing, hybridization and the like are well described in the scientific and patent literature.

See, e.g., Sambrook, ed., *Molecular Cloning: a Laboratory manual* (2nd ed.), Vols. 1-3, Cold Spring Harbor Laboratory (1989); *Current Protocols in Molecular Biology*, Ausubel, ed. John Wiley & Sons, Inc., New York (1997); *Laboratory Techniques in Biochemistry and Molecular Biology: Hybridization With Nucleic Acid Probes, Part I*,  
5 Theory and Nucleic Acid Preparation, Tijssen, ed. Elsevier, N.Y. (1993).

Nucleic acids, vectors, capsids, polypeptides, and the like can be analyzed and quantified by any of a number of general means well known to those of skill in the art. These include, e.g., analytical biochemical methods such as NMR, spectrophotometry, radiography, electrophoresis, capillary electrophoresis, high performance liquid  
10 chromatography (HPLC), thin layer chromatography (TLC), and hyperdiffusion chromatography, various immunological methods, e.g., fluid or gel precipitin reactions, immunodiffusion, immunoelectrophoresis, radioimmunoassays (RIAs), enzyme-linked immunosorbent assays (ELISAs), immuno-fluorescent assays, Southern analysis, Northern analysis, dot-blot analysis, gel electrophoresis (e.g., SDS-  
15 PAGE), RT-PCR, quantitative PCR, other nucleic acid or target or signal amplification methods, radiolabeling, scintillation counting, and affinity chromatography.

Oligonucleotide primers are used to amplify nucleic acid encoding an olfactory receptor ligand-binding region. The nucleic acids described herein can also be cloned  
20 or measured quantitatively using amplification techniques. Using exemplary degenerate primer pair sequences, (see below), the skilled artisan can select and design suitable oligonucleotide amplification primers. Amplification methods are also well known in the art, and include, e.g., polymerase chain reaction, PCR (PCR Protocols, a Guide to Methods and Applications, ed. Innis. Academic Press, N.Y.  
25 (1990) and PCR Strategies, ed. Innis, Academic Press, Inc., N.Y. (1995), ligase chain reaction (LCR) (see, e.g., Wu, *Genomics* 4:560 (1989); Landegren, *Science* 241:1077,(1988); Barringer, *Gene* 89:117 (1990)); transcription amplification (see, e.g., Kwok, *PNAS*, 86:1173 (1989)); and, self-sustained sequence replication (see, e.g., Guatelli, *PNAS*, 87:1874 (1990)); Q Beta replicase amplification (see, e.g.,  
30 Smith, *J. Clin. Microbiol.* 35:1477-1491 (1997)); automated Q-beta replicase amplification assay (see, e.g., Burg, *Mol. Cell. Probes* 10:257-271 (1996)) and other RNA polymerase mediated techniques (e.g., NASBA, Cangene, Mississauga, Ontario); see also Berger, *Methods Enzymol.* 152:307-316 (1987); Sambrook;

Ausubel; U.S. Patent Nos. 4,683,195 and 4,683,202; Sooknanan, *Biotechnology* 13:563-564 (1995).

Once amplified, the nucleic acids, either individually or as libraries, may be cloned according to methods known in the art, if desired, into any of a variety of  
5 vectors using routine molecular biological methods; methods for cloning *in vitro* amplified nucleic acids are described, *e.g.*, U.S. Pat. No. 5,426,039. To facilitate cloning of amplified sequences, restriction enzyme sites can be "built into" the PCR primer pair. For example, Pst I and Bsp E1 sites were designed into the exemplary primer pairs of the invention. These particular restriction sites have a sequence that,  
10 when ligated, are "in-frame" with respect to the 7-membrane receptor "donor" coding sequence into which they are spliced (the ligand-binding region coding sequence is internal to the 7-membrane polypeptide, thus, if it is desired that the construct be translated downstream of a restriction enzyme splice site, out of frame results should be avoided; this may not be necessary if the inserted ligand-binding domain comprises  
15 substantially most of the transmembrane VII region). The primers can be designed to retain the original sequence of the "donor" 7-membrane receptor (the Pst I and Bsp E1 sequence in the primers of the invention generate an insert that, when ligated into the Pst I/Bsp E1 cut vector, encode residues found in the "donor" mouse olfactory receptor M4 sequence). Alternatively, the primers can encode amino acid residues  
20 that are conservative substitutions (*e.g.*, hydrophobic for hydrophobic residue, see above discussion) or functionally benign substitutions (*e.g.*, do not prevent plasma membrane insertion, cause cleavage by peptidase, cause abnormal folding of receptor, and the like).

The primer pairs are designed to selectively amplify ligand-binding regions of  
25 olfactory receptor proteins. These domain regions may vary for different ligands, and more particularly odorants; thus, what may be a minimal binding region for one ligand, and more particularly odorants, may be too limiting for a second potential ligand. Thus, domain regions of different sizes comprising different domain structures may be amplified; for example, transmembrane (TM) domains II through  
30 VII, III through VII, III through VI or II through VI, or variations thereof (*e.g.*, only a subsequence of a particular domain, mixing the order of the domains, and the like), of a 7-transmembrane OR.

As domain structures and sequence of many 7-membrane proteins, particularly olfactory receptors, are known, the skilled artisan can readily select domain-flanking and internal domain sequences as model sequences to design degenerate amplification primer pairs. For example, a nucleic acid sequence encoding domain regions II through VII can be generated by PCR amplification using a primer pair. To amplify a nucleic acid comprising transmembrane domain I (TM I) sequence, a degenerate primer can be designed from a nucleic acid that encodes the amino acid sequence LFLLYL3' (SEQ ID NO: 519). Such a degenerate primer can be used to generate a binding domain incorporating TM I through TM III, TM I through TM IV, TM I through TM V, TM I through TM VI or TM I through TM VII).

To amplify a nucleic acid comprising a transmembrane domain III (TM III) sequence, a degenerate primer (of at least about 17 residues) can be designed from a nucleic acid that encodes the amino acid sequence M(A/G)(Y/F)DRYVAI 3' (SEQ ID NO: 520) (encoded by a nucleic acid sequence such as 5'-ATGG(G/C)CT(A/T)TGACCG(C/A/T)T(AT)(C/T)GT-3' (SEQ ID NO: 521)). Such a degenerate primer can be used to generate a binding domain incorporating TM III through TM IV, TM III through TM V, TM III through TM VI or TM III through TM VII.

To amplify transmembrane domain VI (TM VI) sequence, a degenerate primer (of at least about 17 residues) can be designed from nucleic acid encoding an amino acid sequence TC(G/A)SHL (SEQ ID NO: 522), encoded by a sequence such as 5'-AG(G/A)TGN(G/C)(T/A)N(G/C)C(G/A)CANGT-3' (SEQ ID NO: 522). Such a degenerate primer can be used to generate a binding domain incorporating TM I through TM VI, TM II through TM VI, TM III through TM VI or TM IV through TM VI).

Paradigms to design degenerate primer pairs are well known in the art. For example, a COnsensus-DEgenerate Hybrid Oligonucleotide Primer (CODEHOP) (SEQ ID NO: 523) strategy computer program is accessible as <http://blocks.fhcrc.org/codehop.html>, and is directly linked from the BlockMaker multiple sequence alignment site for hybrid primer prediction beginning with a set of related protein sequences, as known olfactory receptor ligand-binding regions (*see, e.g., Rose, Nucleic Acids Res.* 26:1628-1635 (1998); Singh, *Biotechniques*, 24:318-19 (1998)).

Means to synthesize oligonucleotide primer pairs are well known in the art. "Natural" base pairs or synthetic base pairs can be used. For example, use of artificial nucleobases offers a versatile approach to manipulate primer sequence and generate a more complex mixture of amplification products. Various families of artificial nucleobases are capable of assuming multiple hydrogen bonding orientations through internal bond rotations to provide a means for degenerate molecular recognition. Incorporation of these analogs into a single position of a PCR primer allows for generation of a complex library of amplification products. *See, e.g., Hoops, Nucleic Acids Res.* 25:4866-4871 (1997). Nonpolar molecules can also be used to mimic the shape of natural DNA bases. A non-hydrogen-bonding shape mimic for adenine can replicate efficiently and selectively against a nonpolar shape mimic for thymine (*see, e.g., Morales, Nat. Struct. Biol.* 5:950-954 (1998)). For example, two degenerate bases can be the pyrimidine base 6H, 8H-3,4-dihydropyrimido[4,5-c][1,2]oxazin-7-one or the purine base N6-methoxy-2,6-diaminopurine (*see, e.g., Hill, PNAS*, 95:4258-63 (1998)). Exemplary degenerate primers of the invention incorporate the nucleobase analog 5'-Dimethoxytrityl-N-benzoyl-2'-deoxy-Cytidine,3'-[(2-cyanoethyl)-(N,N-diisopropyl)]-phosphoramidite (the term "P" in the sequences, *see above*). This pyrimidine analog hydrogen bonds with purines, including A and G residues.

Exemplary primer pairs for amplification of olfactory receptor transmembrane domains II through VII include:

- (a) 5'-GGGGTCCGGAG(A/G)(C/G)(A/G)TA(A/G/T)AT(A/G/P)A(A/G/P)(A/G/P)GG-3' (SEQ ID NO: 524) and  
5'-GGGGCTGCAGACACC(A/C/G/T)ATGTA(C/T)(C/T)T(A/C/G/T)TT(C/T)(C/T)T-3' (SEQ ID NO: 525).
- (b) 5'-GGGGTCCGGAG(A/G)(C/G)T(A/G)A(A/G/T)AT(A/G/P)A(A/G/P)(A/G/P)GG-3' (SEQ ID NO: 526); and  
5'-GGGGCTGCAGACACC(AC/G/T)ATGTA(C/T)(C/T)T(A/C/G/T)TT(C/T)(C/T)T-3' (SEQ ID NO: 527)
- (c) 5'-GGGGTCCGGAG(A/G)(C/G)T(A/G)A(A/G/T)AT(A/G/C/T)A(A/G/C/T)(A/G/C/T)GG-3' (SEQ ID NO: 528) and  
5'-GGGGCTGCAGACACC(A/C/G/T)ATGTA(C/T)(C/T)T(A/C/G/T)TT(C/T)(C/T)T-3' (SEQ ID NO: 558)

Nucleic acids that encode ligand-binding regions of olfactory receptors may be generated by amplification (*e.g., PCR*) of appropriate nucleic acid sequences using



degenerate primer pairs. The amplified nucleic acid can be genomic DNA from any cell or tissue or mRNA or cDNA derived from olfactory receptor-expressing cells, e.g., olfactory neurons or olfactory epithelium.

Isolation from olfactory receptor-expressing cells is well known in the art  
5 (cells expressing naturally or inducibly expressing olfactory receptors can be used to express the hybrid olfactory receptors of the invention to screen for potential odorants and odorant effect on cell physiology, as described below). For example, cells can be identified by olfactory marker protein (OMP), an abundant cytoplasmic protein expressed almost exclusively in mature olfactory sensory neurons (see, e.g., Buiakova,  
10 *PNAS*, 93:9858-63 (1996)). Shirley, *Eur. J. Biochem.* 32:485-494 (1983), describes a rat olfactory preparation suitable for biochemical studies *in vitro* on olfactory mechanisms. Cultures of adult rat olfactory receptor neurons are described by Vargas, *Chem. Senses* 24:211-216 (1999). Because these cultured neurons exhibit typical voltage-gated currents and are responsive to application of odorants, they can also be  
15 used to express the hybrid olfactory receptors of the invention for odorant screening (endogenous olfactory receptor can be initially blocked, if desired, by, e.g., antisense, knockout, and the like). U.S. Patent No. 5,869,266 describes culturing human olfactory neurons for neurotoxicity tests and screening. Murrell, *J. Neurosci.* 19:8260-8270 (1999), describes differentiated olfactory receptor-expressing cells in  
20 culture that respond to odorants, as measured by an influx of calcium.

In one embodiment, hybrid protein-coding sequences comprising nucleic acids ORs fused to the translocation sequences described herein may be constructed. Also provided are hybrid ORs comprising the translocation motifs and ligand-binding domains of olfactory receptors. These nucleic acid sequences can be operably linked  
25 to transcriptional or translational control elements, e.g., transcription and translation initiation sequences, promoters and enhancers, transcription and translation terminators, polyadenylation sequences, and other sequences useful for transcribing DNA into RNA. In construction of recombinant expression cassettes, vectors, transgenics, and a promoter fragment can be employed to direct expression of the  
30 desired nucleic acid in all tissues. Olfactory cell-specific transcriptional elements can also be used to express the fusion polypeptide receptor, including, e.g., a 6.7 kb region upstream of the M4 olfactory receptor coding region. This region was sufficient to direct expression in olfactory epithelium with wild type zonal restriction and

distributed neuronal expression for endogenous olfactory receptors (Qasba, *J. Neurosci.* 18:227-236 (1998)). Receptor genes are normally expressed in a small subset of neurons throughout a zonally restricted region of the sensory epithelium. The transcriptional or translational control elements can be isolated from natural  
5 sources, obtained from such sources as ATCC or GenBank libraries, or prepared by synthetic or recombinant methods.

In another embodiment, fusion proteins, either having C-terminal or, more preferably, N-terminal translocation sequences, may also comprise the translocation motif described herein. However, these fusion proteins can also comprise additional  
10 elements for, *e.g.*, protein detection, purification, or other applications. Detection and purification facilitating domains include, *e.g.*, metal chelating peptides such as polyhistidine tracts or histidine-tryptophan modules or other domains that allow purification on immobilized metals; maltose binding protein; protein A domains that allow purification on immobilized immunoglobulin; or the domain utilized in the  
15 FLAGS extension/affinity purification system (Immunex Corp, Seattle WA).

The inclusion of a cleavable linker sequences such as Factor Xa (*see, e.g., Ottavi, Biochimie* 80:289-293 (1998)), subtilisin protease recognition motif (*see, e.g., Polyak, Protein Eng.* 10:615-619 (1997)); enterokinase (Invitrogen, San Diego, CA), and the like, between the translocation domain (for efficient plasma membrane  
20 expression) and the rest of the newly translated polypeptide may be useful to facilitate purification. For example, one construct can include a polypeptide-encoding nucleic acid sequence linked to six histidine residues followed by a thioredoxin, an enterokinase cleavage site (*see, e.g., Williams, Biochemistry* 34:1787-1797 (1995)), and an amino terminal translocation domain. The histidine residues facilitate  
25 detection and purification while the enterokinase cleavage site provides a means for purifying the desired protein(s) from the remainder of the fusion protein. Technology pertaining to vectors encoding fusion proteins and application of fusion proteins are well described in the scientific and patent literature (*see, e.g., Kroll, DNA Cell. Biol.* 12:441-53 (1993)).

30 Expression vectors, either as individual expression vectors or as libraries of expression vectors, comprising the olfactory binding domain-encoding sequences may be introduced into a genome or into the cytoplasm or a nucleus of a cell and expressed by a variety of conventional techniques, well described in the scientific and patent

literature (*see, e.g.*, Roberts, *Nature* 328:731 (1987); Berger *supra*; Schneider, *Protein Expr. Purif.* 6435:10 (1995); Sambrook; Tijssen; Ausubel). Product information from manufacturers of biological reagents and experimental equipment also provide information regarding known biological methods. The vectors can be isolated from  
5 natural sources, obtained from such sources as ATCC or GenBank libraries, or prepared by synthetic or recombinant methods.

The nucleic acids can be expressed in expression cassettes, vectors or viruses which are stably or transiently expressed in cells (*e.g.*, episomal expression systems). Selection markers can be incorporated into expression cassettes and vectors to confer  
10 a selectable phenotype on transformed cells and sequences. For example, selection markers can code for episomal maintenance and replication such that integration into the host genome is not required. For example, the marker may encode antibiotic resistance (*e.g.*, chloramphenicol, kanamycin, G418, bleomycin, hygromycin) or herbicide resistance (*e.g.*, chlorosulfuron or Basta) to permit selection of those cells  
15 transformed with the desired DNA sequences (*see, e.g.*, Blondelet-Rouault, *Gene* 190:315-17 (1997); Aubrecht, *J. Pharmacol. Exp. Ther.*, 281:992-97 (1997)). Because selectable marker genes conferring resistance to substrates like neomycin or hygromycin can only be utilized in tissue culture, chemoresistance genes are also used as selectable markers *in vitro* and *in vivo*.

20 A chimeric nucleic acid sequence may encode a ligand-binding domain within any 7-transmembrane polypeptide. 7-transmembrane receptors belong to a superfamily of transmembrane (TM) proteins having seven domains that traverse a plasma membrane seven times. Each of the seven domains spans the plasma membrane (TM I to TM VII). Because 7-transmembrane receptor polypeptides have  
25 similar primary sequences and secondary and tertiary structures, structural domains (*e.g.*, TM domains) can be readily identified by sequence analysis. For example, homology modeling, Fourier analysis and helical periodicity detection can identify and characterize the seven domains with a 7-transmembrane receptor sequence. Fast Fourier Transform (FFT) algorithms can be used to assess the dominant periods that  
30 characterize profiles of the hydrophobicity and variability of analyzed sequences. To predict TM domains and their boundaries and topology, a "neural network algorithm" by "PHD server" can be used, as done by Pilpel, *Protein Science* 8:969-977 (1999); Rost, *Protein Sci.* 4:521-533 (1995). Periodicity detection enhancement and alpha

helical periodicity index can be done as by, *e.g.*, Donnelly, *Protein Sci.* 2:55-70 (1993). Other alignment and modeling algorithms are well known in the art, *see, e.g.*, Peitsch, *Receptors Channels* 4:161-164 (1996); Cronet, *Protein Eng.* 6:59-64 (1993) (homology and "discover modeling"); <http://bioinfo.weizmann.ac.il/>.

5           The library sequences include receptor sequences that correspond to TM ligand-binding domains, including, *e.g.*, TM II to VII, TM II to VI, TM III to VII, and TM III to VII, that have been amplified (*e.g.*, PCR) from mRNA of or cDNA derived from, *e.g.*, olfactory receptor-expressing neurons or genomic DNA.

Libraries of olfactory receptor ligand-binding TM domain sequences can  
10 include a various TM domains or variations thereof, as described above. These sequences can be derived from any 7-transmembrane receptor. Because these polypeptides have similar primary sequences and secondary and tertiary structures, the seven domains can be identified by various analyses well known in the art, including, *e.g.*, homology modeling, Fourier analysis and helical periodicity (*see, e.g.*, Pilpel  
15 *supra*), as described above. Using this information sequences flanking the seven domains can be identified and used to design degenerate primers for amplification of various combinations of TM regions and subsequences.

The present invention also includes not only the DNA and proteins having the specified amino acid sequences, but also DNA fragments, particularly fragments of,  
20 for example, 40, 60, 80, 100, 150, 200, or 250 nucleotides, or more, as well as protein fragments of, for example, 10, 20, 30, 50, 70, 100, or 150 amino acids, or more.

Also contemplated are chimeric proteins, comprising at least 10, 20, 30, 50, 70, 100, or 150 amino acids, or more, of one of at least one of the olfactory receptors described herein, coupled to additional amino acids representing all or part of another  
25 G protein receptor, preferably a member of the 7TM superfamily. These chimeras can be made from the instant receptors and a G protein receptor described herein, or they can be made by combining two or more of the present proteins. In one preferred embodiment, one portion of the chimera corresponds to and is derived from one or more of the domains of the seven transmembrane protein described herein, and the  
30 remaining portion or portions come from another G protein-coupled receptor. Chimeric receptors are well known in the art, and the techniques for creating them and the selection and boundaries of domains or fragments of G protein-coupled receptors for incorporation therein are also well known. Thus, this knowledge of those skilled

in the art can readily be used to create such chimeric receptors. The use of such chimeric receptors can provide, for example, an olfactory selectivity characteristic of one of the receptors specifically disclosed herein, coupled with the signal transduction characteristics of another receptor, such as a well known receptor used in prior art  
5 assay systems.

For example, a domain such as a ligand-binding domain, an extracellular domain, a transmembrane domain (*e.g.*, one comprising seven transmembrane regions and corresponding extracellular and cytosolic loops), the transmembrane domain and a cytoplasmic domain, an active site, a subunit association region, etc., can be  
10 covalently linked to a heterologous protein. For instance, an extracellular domain can be linked to a heterologous GPCR transmembrane domain, or a heterologous GPCR extracellular domain can be linked to a transmembrane domain. Other heterologous proteins of choice can include, *e.g.*, green fluorescent protein,  $\beta$ -gal, glutamate receptor, and the rhodopsin presequence.

15 Polymorphic variants, alleles, and interspecies homologs that are substantially identical to an olfactory receptor disclosed herein can be isolated using the nucleic acid probes described above. It is hypothesized that allelic differences in receptors may explain why there is a difference in olfactory sensation in different human subjects. Accordingly, the identification of such alleles may be significant, especially  
20 with respect to producing receptor libraries that adequately represent the olfactory capability of the human population, *i.e.*, which take into account allelic differences in different individuals. Alternatively, expression libraries can be used to clone olfactory receptors and polymorphic variants, alleles, and interspecies homologs thereof, by detecting expressed homologs immunologically with antisera or purified antibodies  
25 made against an olfactory polypeptide, which also recognize and selectively bind to the olfactory receptor homolog.

Also within the scope of the invention are host cells for expressing the ORs, fragments, or variants of the invention. To obtain high levels of expression of a cloned gene or nucleic acid, such as cDNAs encoding the olfactory receptors,  
30 fragments, or variants of the invention, one of skill typically subclones the nucleic acid sequence of interest into an expression vector that contains a strong promoter to direct transcription, a transcription/translation terminator, and if for a nucleic acid encoding a protein, a ribosome binding site for translational initiation. Suitable

bacterial promoters are well known in the art and described, *e.g.*, in Sambrook *et al.* However, bacterial or eukaryotic expression systems can be used.

Any of the well-known procedures for introducing foreign nucleotide sequences into host cells may be used. These include the use of calcium phosphate transfection, polybrene, protoplast fusion, electroporation, liposomes, microinjection, plasma vectors, viral vectors and any of the other well known methods for introducing cloned genomic DNA, cDNA, synthetic DNA or other foreign genetic material into a host cell (*see, e.g.*, Sambrook *et al.*) It is only necessary that the particular genetic engineering procedure used be capable of successfully introducing at least one gene into the host cell capable of expressing the olfactory receptor, fragment, or variant of interest.

After the expression vector is introduced into the cells, the transfected cells are cultured under conditions favoring expression of the receptor, fragment, or variant of interest, which is then recovered from the culture using standard techniques. Examples of such techniques are well known in the art. *See, e.g.*, WO 00/06593, which is incorporated by reference in a manner consistent with this disclosure.

#### **D. Immunological Detection of OR Polypeptides**

In addition to the detection of OR genes and gene expression using nucleic acid hybridization technology, one can also use immunoassays to detect ORs, *e.g.*, to identify olfactory receptor cells, and variants of OR family members. Immunoassays can be used to qualitatively or quantitatively analyze the ORs. A general overview of the applicable technology can be found in Harlow & Lane, *Antibodies: A Laboratory Manual* (1988).

##### **1. Antibodies to OR family members**

Methods of producing polyclonal and monoclonal antibodies that react specifically with a OR family member are known to those of skill in the art (*see, e.g.*, Coligan, *Current Protocols in Immunology* (1991); Harlow & Lane, *supra*; Goding, *Monoclonal Antibodies: Principles and Practice* (2d ed. 1986); and Kohler & Milstein, *Nature*, 256:495-97 (1975)). Such techniques include antibody preparation by selection of antibodies from libraries of recombinant antibodies in phage or similar vectors, as well as preparation of polyclonal and monoclonal antibodies by

immunizing rabbits or mice (*see, e.g., Huse et al., Science, 246:1275-81 (1989); Ward et al., Nature, 341:544-46 (1989)*).

A number of OR-comprising immunogens may be used to produce antibodies specifically reactive with a OR family member. For example, a recombinant OR protein, or an antigenic fragment thereof, can be isolated as described herein. Suitable antigenic regions include, *e.g.*, the conserved motifs that are used to identify members of the OR family. Recombinant proteins can be expressed in eukaryotic or prokaryotic cells as described above, and purified as generally described above. Recombinant protein is the preferred immunogen for the production of monoclonal or polyclonal antibodies. Alternatively, a synthetic peptide derived from the sequences disclosed herein and conjugated to a carrier protein can be used as an immunogen. Naturally occurring protein may also be used either in pure or impure form. The product is then injected into an animal capable of producing antibodies. Either monoclonal or polyclonal antibodies may be generated, for subsequent use in immunoassays to measure the protein.

Methods of production of polyclonal antibodies are known to those of skill in the art. For example, an inbred strain of mice (*e.g.*, BALB/C mice) or rabbits may be immunized with the protein using a standard adjuvant, such as Freund's adjuvant, and a standard immunization protocol. The animal's immune response to the immunogen preparation is monitored by taking test bleeds and determining the titer of reactivity to the OR. When appropriately high titers of antibody to the immunogen are obtained, blood is collected from the animal and antisera are prepared. Further fractionation of the antisera to enrich for antibodies reactive to the protein can be done if desired (*see Harlow & Lane, supra*).

Monoclonal antibodies may be obtained by various techniques familiar to those skilled in the art. Briefly, spleen cells from an animal immunized with a desired antigen may be immortalized, commonly by fusion with a myeloma cell (*see Kohler & Milstein, Eur. J. Immunol., 6:511-19 (1976)*). Alternative methods of immortalization include transformation with Epstein Barr Virus, oncogenes, or retroviruses, or other methods well known in the art. Colonies arising from single immortalized cells are screened for production of antibodies of the desired specificity and affinity for the antigen, and yield of the monoclonal antibodies produced by such cells may be enhanced by various techniques, including injection into the peritoneal cavity of a

vertebrate host. Alternatively, one may isolate DNA sequences which encode a monoclonal antibody or a binding fragment thereof by screening a DNA library from human B cells according to the general protocol outlined by Huse *et al.*, *Science*, 246:1275-1281 (1989).

5           Monoclonal antibodies and polyclonal sera are collected and titrated against the immunogen protein in an immunoassay, for example, a solid phase immunoassay with the immunogen immobilized on a solid support. Typically, polyclonal antisera with a titer of 109 or greater are selected and tested for their cross reactivity against non-OR proteins, or even other OR family members or other related proteins from other  
10           organisms, using a competitive binding immunoassay. Specific polyclonal antisera and monoclonal antibodies will usually bind with a  $K_d$  of at least about 0.1 mM, more usually at least about 1 pM, optionally at least about 0.1 pM or better, and optionally 0.01 pM or better.

          Once OR family member specific antibodies are available, individual OR  
15           proteins can be detected by a variety of immunoassay methods. For a review of immunological and immunoassay procedures, see *Basic and Clinical Immunology* (Stites & Terr eds., 7th ed. 1991). Moreover, the immunoassays of the present invention can be performed in any of several configurations, which are reviewed extensively in *Enzyme Immunoassay* (Maggio, ed., 1980); and Harlow & Lane, *supra*.

## 20           2.     Immunological binding assays

          OR proteins can be detected and/or quantified using any of a number of well recognized immunological binding assays (see, e.g., U.S. Patents 4,366,241; 4,376,110; 4,517,288; and 4,837,168). For a review of the general immunoassays, see also *Methods in Cell Biology: Antibodies in Cell Biology*, volume 37 (Asai, ed. 1993);  
25           *Basic and Clinical Immunology* (Stites & Terr, eds., 7th ed. 1991). Immunological binding assays (or immunoassays) typically use an antibody that specifically binds to a protein or antigen of choice (in this case an OR family member or an antigenic subsequence thereof). The antibody (e.g., anti-OR) may be produced by any of a number of means well known to those of skill in the art and as described above.

30           Immunoassays also often use a labeling agent to specifically bind to and label the complex formed by the antibody and antigen. The labeling agent may itself be one of the moieties comprising the antibody/antigen complex. Thus, the labeling agent may be a labeled OR polypeptide or a labeled anti-OR antibody. Alternatively, the



labeling agent may be a third moiety, such a secondary antibody that specifically binds to the antibody/OR complex (a secondary antibody is typically specific to antibodies of the species from which the first antibody is derived). Other proteins capable of specifically binding immunoglobulin constant regions, such as protein A or protein G may also be used as the label agent. These proteins exhibit a strong non-immunogenic reactivity with immunoglobulin constant regions from a variety of species (*see, e.g., Kronval et al., J. Immunol., 111:1401-1406 (1973); Akerstrom et al., J. Immunol., 135:2589-2542 (1985)*). The labeling agent can be modified with a detectable moiety, such as biotin, to which another molecule can specifically bind, such as streptavidin.

10 A variety of detectable moieties are well known to those skilled in the art.

Throughout the assays, incubation and/or washing steps may be required after each combination of reagents. Incubation steps can vary from about 5 seconds to several hours, optionally from about 5 minutes to about 24 hours. However, the incubation time will depend upon the assay format, antigen, volume of solution, concentrations, and the like. Usually, the assays will be carried out at ambient temperature, although they can be conducted over a range of temperatures, such as 10°C to 40°C.

15

**a. Non-competitive assay formats**

Immunoassays for detecting an OR protein in a sample may be either competitive or noncompetitive. Noncompetitive immunoassays are assays in which the amount of antigen is directly measured. In one preferred "sandwich" assay, for example, the anti-OR antibodies can be bound directly to a solid substrate on which they are immobilized. These immobilized antibodies then capture the OR protein present in the test sample. The OR protein is thus immobilized is then bound by a labeling agent, such as a second OR antibody bearing a label. Alternatively, the second antibody may lack a label, but it may, in turn, be bound by a labeled third antibody specific to antibodies of the species from which the second antibody is derived. The second or third antibody is typically modified with a detectable moiety, such as biotin, to which another molecule specifically binds, *e.g., streptavidin*, to provide a detectable moiety.

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**b. C mpetitive assay formats**

In competitive assays, the amount of OR protein present in the sample is measured indirectly by measuring the amount of a known, added (exogenous) OR

protein displaced (competed away) from an anti-OR antibody by the unknown OR protein present in a sample. In one competitive assay, a known amount of OR protein is added to a sample and the sample is then contacted with an antibody that specifically binds to the OR. The amount of exogenous OR protein bound to the antibody is inversely proportional to the concentration of OR protein present in the sample. In a particularly preferred embodiment, the antibody is immobilized on a solid substrate. The amount of OR protein bound to the antibody may be determined either by measuring the amount of OR protein present in a OR/antibody complex, or alternatively by measuring the amount of remaining uncomplexed protein. The amount of OR protein may be detected by providing a labeled OR molecule.

A hapten inhibition assay is another preferred competitive assay. In this assay the known OR protein is immobilized on a solid substrate. A known amount of anti-OR antibody is added to the sample, and the sample is then contacted with the immobilized OR. The amount of anti-OR antibody bound to the known immobilized OR protein is inversely proportional to the amount of OR protein present in the sample. Again, the amount of immobilized antibody may be detected by detecting either the immobilized fraction of antibody or the fraction of the antibody that remains in solution. Detection may be direct where the antibody is labeled or indirect by the subsequent addition of a labeled moiety that specifically binds to the antibody as described above.

**c. Cross-reactivity determinations**

Immunoassays in the competitive binding format can also be used for cross-reactivity determinations. For example, a protein at least partially encoded by the nucleic acid sequences disclosed herein can be immobilized to a solid support. Proteins (*e.g.*, OR proteins and homologs) are added to the assay that compete for binding of the antisera to the immobilized antigen. The ability of the added proteins to compete for binding of the antisera to the immobilized protein is compared to the ability of the OR polypeptide encoded by the nucleic acid sequences disclosed herein to compete with itself. The percent cross-reactivity for the above proteins is calculated, using standard calculations. Those antisera with less than 10% cross-reactivity with each of the added proteins listed above are selected and pooled. The cross-reacting antibodies are optionally removed from the pooled antisera by immunoabsorption with the added considered proteins, *e.g.*, distantly related

homologs. In addition, peptides comprising amino acid sequences representing conserved motifs that are used to identify members of the OR family can be used in cross-reactivity determinations.

The immunoabsorbed and pooled antisera are then used in a competitive binding immunoassay as described above to compare a second protein, thought to be perhaps an allele or polymorphic variant of a OR family member, to the immunogen protein (*i.e.*, OR protein encoded by the nucleic acid sequences disclosed herein). In order to make this comparison, the two proteins are each assayed at a wide range of concentrations and the amount of each protein required to inhibit 50% of the binding of the antisera to the immobilized protein is determined. If the amount of the second protein required to inhibit 50% of binding is less than 10 times the amount of the protein encoded by nucleic acid sequences disclosed herein required to inhibit 50% of binding, then the second protein is said to specifically bind to the polyclonal antibodies generated to a OR immunogen.

Antibodies raised against OR conserved motifs can also be used to prepare antibodies that specifically bind only to GPCRs of the OR family, but not to GPCRs from other families.

Polyclonal antibodies that specifically bind to a particular member of the OR family, *e.g.*, AOLFR1, can be made by subtracting out cross-reactive antibodies using other OR family members. Species-specific polyclonal antibodies can be made in a similar way. For example, antibodies specific to human AOLFR1 can be made by, subtracting out antibodies that are cross-reactive with orthologous sequences, *e.g.*, rat OR1 or mouse OR1.

**d. Other assay formats**

Western blot (immunoblot) analysis is used to detect and quantify the presence of OR protein in the sample. The technique generally comprises separating sample proteins by gel electrophoresis on the basis of molecular weight, transferring the separated proteins to a suitable solid support, (such as a nitrocellulose filter, a nylon filter, or derivatized nylon filter), and incubating the sample with the antibodies that specifically bind the OR protein. The anti-OR polypeptide antibodies specifically bind to the OR polypeptide on the solid support. These antibodies may be directly labeled or alternatively may be subsequently detected using labeled antibodies (*e.g.*, labeled sheep anti-mouse antibodies) that specifically bind to the anti-OR antibodies.

Other, assay formats include liposome immunoassays (LIA), which use liposomes designed to bind specific molecules (*e.g.*, antibodies) and release encapsulated reagents or markers. The released chemicals are then detected according to standard techniques (*see Monroe et al., Amer. Clin. Prod. Rev.*, 5:34-41 (1986)).

5                   e.       **Reduction of non-specific binding**

One of skill in the art will appreciate that it is often desirable to minimize non-specific binding in immunoassays. Particularly, where the assay involves an antigen or antibody immobilized on a solid substrate it is desirable to minimize the amount of non-specific binding to the substrate. Means of reducing such non-specific  
10 binding are well known to those of skill in the art. Typically, this technique involves coating the substrate with a proteinaceous composition. In particular, protein compositions such as bovine serum albumin (BSA), nonfat powdered milk, and gelatin are widely used with powdered milk being most preferred.

                  f.       **Labels**

15               The particular label or detectable group used in the assay is not a critical aspect of the invention, as long as it does not significantly interfere with the specific binding of the antibody used in the assay. The detectable group can be any material having a detectable physical or chemical property. Such detectable labels have been well-developed in the field of immunoassays and, in general, most any label useful in such  
20 methods can be applied to the present invention. Thus, a label is any composition detectable by spectroscopic, photochemical, biochemical, immunochemical, electrical, optical or chemical means. Useful labels in the present invention include magnetic beads (*e.g.*, DYNABEADS<sup>TM</sup>) (SEQ ID NO: 529), fluorescent dyes (*e.g.*, fluorescein isothiocyanate, Texas red, rhodamine, and the like), radiolabels (*e.g.*, <sup>3</sup>H, <sup>125</sup>I, <sup>35</sup>S, <sup>14</sup>C,  
25 or <sup>32</sup>P), enzymes (*e.g.*, horseradish peroxidase, alkaline phosphatase and others commonly used in an ELISA), and colorimetric labels such as colloidal gold or colored glass or plastic beads (*e.g.*, polystyrene, polypropylene, latex, *etc.*).

The label may be coupled directly or indirectly to the desired component of the assay according to methods well known in the art. As indicated above, a wide variety  
30 of labels may be used, with the choice of label depending on sensitivity required, ease of conjugation with the compound, stability requirements, available instrumentation, and disposal provisions.

Non-radioactive labels are often attached by indirect means. Generally, a ligand molecule (*e.g.*, biotin) is covalently bound to the molecule. The ligand then binds to another molecule (*e.g.*, streptavidin) molecule, which is either inherently detectable or covalently bound to a signal system, such as a detectable enzyme, a fluorescent compound, or a chemiluminescent compound. The ligands and their targets can be used in any suitable combination with antibodies that recognize a OR protein, or secondary antibodies that recognize anti-OR.

The molecules can also be conjugated directly to signal generating compounds, *e.g.*, by conjugation with an enzyme or fluorophore. Enzymes of interest as labels will primarily be hydrolases, particularly phosphatases, esterases and glycosidases, or oxidotases, particularly peroxidases. Fluorescent compounds include fluorescein and its derivatives, rhodamine and its derivatives, dansyl, umbelliferone, *etc.* Chemiluminescent compounds include luciferin, and 2,3-dihydrophthalazinediones, *e.g.*, luminol. For a review of various labeling or signal producing systems that may be used, *see* U.S. Patent No. 4,391,904.

Means of detecting labels are well known to those of skill in the art. Thus, for example, where the label is a radioactive label, means for detection include a scintillation counter or photographic film as in autoradiography. Where the label is a fluorescent label, it may be detected by exciting the fluorochrome with the appropriate wavelength of light and detecting the resulting fluorescence. The fluorescence may be detected visually, by means of photographic film, by the use of electronic detectors such as charge coupled devices (CCDs) or photomultipliers and the like. Similarly, enzymatic labels may be detected by providing the appropriate substrates for the enzyme and detecting the resulting reaction product. Finally simple colorimetric labels may be detected simply by observing the color associated with the label. Thus, in various dipstick assays, conjugated gold often appears pink, while various conjugated beads appear the color of the bead.

Some assay formats do not require the use of labeled components. For instance, agglutination assays can be used to detect the presence of the target antibodies. In this case, antigen-coated particles are agglutinated by samples comprising the target antibodies. In this format, none of the components need be labeled and the presence of the target antibody is detected by simple visual inspection.

### E. Detection of Olfactory Modulators

Methods and compositions for determining whether a test compound specifically binds to a mammalian chemosensory, and more particularly, an olfactory receptor of the invention, both *in vitro* and *in vivo* are described below. Many aspects  
5 of cell physiology can be monitored to assess the effect of ligand-binding to a naturally-occurring or chimeric olfactory receptor. These assays may be performed on intact cells expressing an olfactory receptor, on permeabilized cells or on membrane fractions produced by standard methods.

Olfactory receptors are normally located on the specialized cilia of olfactory  
10 neurons. These receptors bind odorants and initiate the transduction of chemical stimuli into electrical signals. An activated or inhibited G protein will in turn alter the properties of target enzymes, channels, and other effector proteins. Some examples include the activation of cGMP phosphodiesterase by transducin in the visual system, adenylate cyclase by the stimulatory G protein, phospholipase C by Gq and other  
15 cognate G proteins, and modulation of diverse channels by Gi and other G proteins. Downstream consequences can also be examined such as generation of diacyl glycerol and IP3 by phospholipase C, and in turn, for calcium mobilization by IP3.

The OR protein of the assay will typically be selected from a polypeptide having a sequence selected from SEQ. ID. NO. 1, SEQ. ID. NO. 3, SEQ. ID. NO. 5,  
20 SEQ. ID. NO. 7, SEQ. ID. NO. 9, SEQ. ID. NO. 11, SEQ. ID. NO. 13, SEQ. ID. NO. 15, SEQ. ID. NO. 17, SEQ. ID. NO. 19, SEQ. ID. NO. 21, SEQ. ID. NO. 23, SEQ. ID. NO. 25, SEQ. ID. NO. 27, SEQ. ID. NO. 29, SEQ. ID. NO. 31, SEQ. ID. NO. 33, SEQ. ID. NO. 35, SEQ. ID. NO. 37, SEQ. ID. NO. 39, SEQ. ID. NO. 41, SEQ. ID. NO. 43, SEQ. ID. NO. 45, SEQ. ID. NO. 47, SEQ. ID. NO. 49, SEQ. ID.  
25 NO. 51, SEQ. ID. NO. 53, SEQ. ID. NO. 55, SEQ. ID. NO. 57, SEQ. ID. NO. 59, SEQ. ID. NO. 61, SEQ. ID. NO. 63, SEQ. ID. NO. 65, SEQ. ID. NO. 67, SEQ. ID. NO. 69, SEQ. ID. NO. 71, SEQ. ID. NO. 73, SEQ. ID. NO. 75, SEQ. ID. NO. 77, SEQ. ID. NO. 79, SEQ. ID. NO. 81, SEQ. ID. NO. 83, SEQ. ID. NO. 85, SEQ. ID. NO. 87, SEQ. ID. NO. 89, SEQ. ID. NO. 91, SEQ. ID. NO. 93, SEQ. ID. NO. 95,  
30 SEQ. ID. NO. 97, SEQ. ID. NO. 99, SEQ. ID. NO. 101, SEQ. ID. NO. 103, SEQ. ID. NO. 105, SEQ. ID. NO. 107, SEQ. ID. NO. 109, SEQ. ID. NO. 111, SEQ. ID. NO. 113, SEQ. ID. NO. 115, SEQ. ID. NO. 117, SEQ. ID. NO. 119, SEQ. ID. NO. 121, SEQ. ID. NO. 123, SEQ. ID. NO. 125, SEQ. ID. NO. 127, SEQ. ID.

NO. 129, SEQ. ID. NO. 131, SEQ. ID. NO. 133, SEQ. ID. NO. 135, SEQ. ID.  
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NO. 145, SEQ. ID. NO. 147, SEQ. ID. NO. 149, SEQ. ID. NO. 151, SEQ. ID.  
NO. 153, SEQ. ID. NO. 155, SEQ. ID. NO. 157, SEQ. ID. NO. 159, SEQ. ID.  
5 NO. 161, SEQ. ID. NO. 163, SEQ. ID. NO. 165, SEQ. ID. NO. 167, SEQ. ID.  
NO. 169, SEQ. ID. NO. 171, SEQ. ID. NO. 173, SEQ. ID. NO. 175, SEQ. ID.  
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NO. 193, SEQ. ID. NO. 195, SEQ. ID. NO. 197, SEQ. ID. NO. 199, SEQ. ID.  
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25 ID. NO. 327, SEQ. ID. NO. 329, SEQ. ID. NO. 331, SEQ. ID. NO. 333, SEQ. ID.  
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Alternatively, the OR protein of the assay can be derived from a eukaryote host cell and can include an amino acid subsequence having at least about 30-40% amino acid sequence identity to SEQ. ID. NO. 1, SEQ. ID. NO. 3, SEQ. ID. NO. 5, SEQ. ID. NO. 7, SEQ. ID. NO. 9, SEQ. ID. NO. 11, SEQ. ID. NO. 13, SEQ. ID. NO. 15, SEQ. ID. NO. 17, SEQ. ID. NO. 19, SEQ. ID. NO. 21, SEQ. ID. NO. 23, SEQ. ID. NO. 25, SEQ. ID. NO. 27, SEQ. ID. NO. 29, SEQ. ID. NO. 31, SEQ. ID. NO. 33, SEQ. ID. NO. 35, SEQ. ID. NO. 37, SEQ. ID. NO. 39, SEQ. ID. NO. 41, SEQ. ID. NO. 43, SEQ. ID. NO. 45, SEQ. ID. NO. 47, SEQ. ID. NO. 49, SEQ. ID. NO. 51, SEQ. ID. NO. 53, SEQ. ID. NO. 55, SEQ. ID. NO. 57, SEQ. ID. NO. 59, SEQ. ID. NO. 61, SEQ. ID. NO. 63, SEQ. ID. NO. 65, SEQ. ID. NO. 67, SEQ. ID. NO. 69, SEQ. ID. NO. 71, SEQ. ID. NO. 73, SEQ. ID. NO. 75, SEQ. ID. NO. 77, SEQ. ID. NO. 79, SEQ. ID. NO. 81, SEQ. ID. NO. 83, SEQ. ID. NO. 85, SEQ. ID. NO. 87, SEQ. ID. NO. 89, SEQ. ID. NO. 91, SEQ. ID. NO. 93, SEQ. ID. NO. 95, SEQ. ID. NO. 97, SEQ. ID. NO. 99, SEQ. ID. NO. 101, SEQ. ID. NO. 103, SEQ. ID. NO. 105, SEQ. ID. NO. 107, SEQ. ID. NO. 109, SEQ. ID. NO. 111, SEQ. ID. NO. 113, SEQ. ID. NO. 115, SEQ. ID. NO. 117, SEQ. ID. NO. 119, SEQ. ID. NO. 121, SEQ. ID. NO. 123, SEQ. ID. NO. 125, SEQ. ID. NO. 127, SEQ. ID. NO. 129, SEQ. ID. NO. 131, SEQ. ID. NO. 133, SEQ. ID. NO. 135, SEQ. ID. NO. 137, SEQ. ID. NO. 139, SEQ. ID. NO. 141, SEQ. ID. NO. 143, SEQ. ID. NO. 145, SEQ. ID.



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ID. NO. 423, SEQ. ID. NO. 425, SEQ. ID. NO. 427, SEQ. ID. NO. 429, SEQ. ID. NO. 431, SEQ. ID. NO. 433, SEQ. ID. NO. 435, SEQ. ID. NO. 437, SEQ. ID. NO. 439, SEQ. ID. NO. 441, SEQ. ID. NO. 443, SEQ. ID. NO. 445, SEQ. ID. NO. 447, SEQ. ID. NO. 449, SEQ. ID. NO. 451, SEQ. ID. NO. 453, SEQ. ID. NO. 455, SEQ. ID. NO. 457, SEQ. ID. NO. 459, SEQ. ID. NO. 461, SEQ. ID. NO. 463, SEQ. ID. NO. 465, SEQ. ID. NO. 467, SEQ. ID. NO. 469, SEQ. ID. NO. 471, SEQ. ID. NO. 473, SEQ. ID. NO. 475, SEQ. ID. NO. 477, SEQ. ID. NO. 479, SEQ. ID. NO. 481, SEQ. ID. NO. 483, SEQ. ID. NO. 485, SEQ. ID. NO. 487, SEQ. ID. NO. 489, SEQ. ID. NO. 491, SEQ. ID. NO. 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511.

Preferably, the amino acid sequence identity will be at least 50-75% preferably 85%, 90%, 95%, 96%, 97%, 98%, or 99%. Optionally, the polypeptide of the assays can comprise a domain of an OR protein, such as an extracellular domain, transmembrane region, transmembrane domain, cytoplasmic domain, ligand-binding domain, subunit association domain, active site, and the like. Either the OR protein or a domain thereof can be covalently linked to a heterologous protein to create a chimeric protein used in the assays described herein. As discussed *infra*, the family of ORs provided herein exhibits substantial sequence similarity at both the DNA and protein level, but also significant dissimilarity. In particular, the members possess an average percentage sequence identity to other members of the family when determined over the full length of the gene by about 30%. Moreover, different members of the genes at the protein level exhibit an average on the order of about 40% sequence identity to other members of the family when the full length protein sequences are compared. However, while there exist differences, there are characteristic similarities, e.g. the consensus sequence already mentioned, which further define members of this novel genus of receptors.

Modulators of OR activity can be tested using OR polypeptides as described above, either recombinant or naturally occurring. The protein can be isolated, expressed in a cell, expressed in a membrane derived from a cell, expressed in tissue or in an animal, either recombinant or naturally occurring. Modulation can be tested using one of the *in vitro* or *in vivo* assays described herein.

### 1. In vitro binding assays

Olfactory transduction can also be examined *in vitro* with soluble or solid state reactions, using a full-length OR or a chimeric molecule such as an extracellular domain or transmembrane region, or combination thereof, of a OR covalently linked  
5 to a heterologous signal transduction domain, or a heterologous extracellular domain and/or transmembrane region covalently linked to the transmembrane and/or cytoplasmic domain of an OR. Furthermore, ligand-binding domains of the protein of interest can be used *in vitro* in soluble or solid state reactions to assay for ligand binding. In numerous embodiments, a chimeric receptor will be made that comprises  
10 all or part of a OR polypeptide, as well an additional sequence that facilitates the localization of the OR to the membrane, such as a rhodopsin, *e.g.*, an N-terminal fragment of a rhodopsin protein, *e.g.* bovine or another mammalian rhodopsin.

Ligand binding to a OR protein, a domain, or chimeric protein can be tested in solution, in a bilayer membrane, attached to a solid phase, in a lipid monolayer, or in  
15 vesicles. Binding of a modulator can be tested using, *e.g.*, changes in spectroscopic characteristics (*e.g.*, fluorescence, absorbance, refractive index) hydrodynamic (*e.g.*, shape), chromatographic, or solubility properties.

Receptor-G protein interactions can also be examined. For example, binding of the G protein to the receptor or its release from the receptor can be examined. For  
20 example, in the absence of GTP, an activator will lead to the formation of a tight complex of a G protein (all three subunits) with the receptor. This complex can be detected in a variety of ways, as noted above. Such an assay can be modified to search for inhibitors, *e.g.*, by adding an activator to the receptor and G protein in the absence of GTP, which form a tight complex, and then screen for inhibitors by  
25 looking at dissociation of the receptor-G protein complex. In the presence of GTP, release of the alpha subunit of the G protein from the other two G protein subunits serves as a criterion of activation.

An activated or inhibited G protein will in turn alter the properties of target enzymes, channels, and other effector proteins. The classic examples are the  
30 activation of cGMP phosphodiesterase by transducin in the visual system, adenylate cyclase by the stimulatory G protein, phospholipase C by Gq and other cognate G proteins, and modulation of diverse channels by Gi and other G proteins.

Downstream consequences can also be examined such as generation of diacyl glycerol and IP3 by phospholipase C, and in turn, for calcium mobilization by IP3.

In another embodiment of the invention, a GTP $\gamma$ S assay may be used. As described above, upon activation of a GPCR, the G $\alpha$  subunit of the G protein complex is stimulated to exchange bound GDP for GTP. Ligand-mediated stimulation of G protein exchange activity can be measured in a biochemical assay measuring the binding of added radioactively-labeled GTP $\gamma$ <sup>35</sup>S to the G protein in the presence of a putative ligand. Typically, membranes containing the chemosensory receptor of interest are mixed with a complex of G proteins. Potential inhibitors and/or activators and GTP $\gamma$ S are added to the assay, and binding of GTP $\gamma$ S to the G protein is measured. Binding can be measured by liquid scintillation counting or by any other means known in the art, including scintillation proximity assays (SPA). In other assays formats, fluorescently-labeled GTP $\gamma$ S can be utilized.

## 2. Fluorescence Polarization Assays

In another embodiment, Fluorescence Polarization ("FP") based assays may be used to detect and monitor odorant binding. Fluorescence polarization is a versatile laboratory technique for measuring equilibrium binding, nucleic acid hybridization, and enzymatic activity. Fluorescence polarization assays are homogeneous in that they do not require a separation step such as centrifugation, filtration, chromatography, precipitation or electrophoresis. These assays are done in real time, directly in solution and do not require an immobilized phase. Polarization values can be measured repeatedly and after the addition of reagents since measuring the polarization is rapid and does not destroy the sample. Generally, this technique can be used to measure polarization values of fluorophores from low picomolar to micromolar levels. This section describes how fluorescence polarization can be used in a simple and quantitative way to measure the binding of odorants to the olfactory receptors of the invention.

When a fluorescently labeled molecule is excited with plane polarized light, it emits light that has a degree of polarization that is inversely proportional to its molecular rotation. Large fluorescently labeled molecules remain relatively stationary during the excited state (4 nanoseconds in the case of fluorescein) and the polarization of the light remains relatively constant between excitation and emission. Small fluorescently labeled molecules rotate rapidly during the excited state and the

polarization changes significantly between excitation and emission. Therefore, small molecules have low polarization values and large molecules have high polarization values. For example, a single-stranded fluorescein-labeled oligonucleotide has a relatively low polarization value but when it is hybridized to a complementary strand,  
 5 it has a higher polarization value. When using FP to detect and monitor odorant-binding which may activate or inhibit the olfactory receptors of the invention, fluorescence-labeled odorants or auto-fluorescent odorants may be used.

Fluorescence polarization (P) is defined as:

$$P = \frac{Int_{\parallel} - Int_{\perp}}{Int_{\parallel} + Int_{\perp}}$$

10 Where  $\parallel$  is the intensity of the emission light parallel to the excitation light plane and  $\perp$  is the intensity of the emission light perpendicular to the excitation light plane. P, being a ratio of light intensities, is a dimensionless number. For example, the Beacon <sup>®</sup> and Beacon 2000 <sup>™</sup> System may be used in connection with these assays. Such systems typically express polarization in millipolarization units (1  
 15 Polarization Unit = 1000 mP Units).

The relationship between molecular rotation and size is described by the Perrin equation and the reader is referred to Jolley, M. E. (1991) in Journal of Analytical Toxicology, pp. 236-240, which gives a thorough explanation of this equation. Summarily, the Perrin equation states that polarization is directly proportional to the  
 20 rotational relaxation time, the time that it takes a molecule to rotate through an angle of approximately 68.5°. Rotational relaxation time is related to viscosity ( $\eta$ ), absolute temperature (T), molecular volume (V), and the gas constant (R) by the following equation:

$$Rotational\ Relaxation\ Time = \frac{3\eta V}{RT}$$

25 The rotational relaxation time is small ( $\approx$  1 nanosecond) for small molecules (e.g. fluorescein) and large ( $\approx$  100 nanoseconds) for large molecules (e.g. immunoglobulins). If viscosity and temperature are held constant, rotational relaxation time, and therefore polarization, is directly related to the molecular volume. Changes in molecular volume may be due to interactions with other molecules,  
 30 dissociation, polymerization, degradation, hybridization, or conformational changes of the fluorescently labeled molecule. For example, fluorescence polarization has been

used to measure enzymatic cleavage of large fluorescein labeled polymers by proteases, DNases, and RNases. It also has been used to measure equilibrium binding for protein/protein interactions, antibody/antigen binding, and protein/DNA binding.

### 3. Solid state and soluble high throughput assays

5 In yet another embodiment, the invention provides soluble assays using molecules such as a domain such as ligand-binding domain, an extracellular domain, a transmembrane domain (*e.g.*, one comprising seven transmembrane regions and cytosolic loops), the transmembrane domain and a cytoplasmic domain, an active site, a subunit association region, etc.; a domain that is covalently linked to a heterologous  
10 protein to create a chimeric molecule; an OR protein; or a cell or tissue expressing an OR protein, either naturally occurring or recombinant. In another embodiment, the invention provides solid phase based in vitro assays in a high throughput format, where the domain, chimeric molecule, OR protein, or cell or tissue expressing the OR is attached to a solid phase substrate.

15 In the high throughput assays of the invention, it is possible to screen up to several thousand different modulators or ligands in a single day. In particular, each well of a microtiter plate can be used to run a separate assay against a selected potential modulator, or, if concentration or incubation time effects are to be observed, every 5-10 wells can test a single modulator. Thus, a single standard microtiter plate  
20 can assay about 100 (*e.g.*, 96) modulators. If 1536 well plates are used, then a single plate can easily assay from about 1000 to about 1500 different compounds. It is also possible to assay multiple compounds in each plate well. Further, it is possible to assay several different plates per day; assay screens for up to about 6,000-20,000 different compounds is possible using the integrated systems of the invention. More  
25 recently, microfluidic approaches to reagent manipulation have been developed.

The molecule of interest can be bound to the solid state component, directly or indirectly, via covalent or non covalent linkage, *e.g.*, via a tag. The tag can be any of a variety of components. In general, a molecule which binds the tag (a tag binder) is fixed to a solid support, and the tagged molecule of interest (*e.g.*, the olfactory  
30 transduction molecule of interest) is attached to the solid support by interaction of the tag and the tag binder.

A number of tags and tag binders can be used, based upon known molecular interactions well described in the literature. For example, where a tag has a natural

binder, for example, biotin, protein A, or protein G, it can be used in conjunction with appropriate tag binders (avidin, streptavidin, neutravidin, the Fc region of an immunoglobulin, *etc.*). Antibodies to molecules with natural binders such as biotin are also widely available and appropriate tag binders (*see*, SIGMA Immunochemicals  
5 1998 catalogue SIGMA, St. Louis MO).

Similarly, any haptenic or antigenic compound can be used in combination with an appropriate antibody to form a tag/tag binder pair. Thousands of specific antibodies are commercially available and many additional antibodies are described in the literature. For example, in one common configuration, the tag is a first antibody  
10 and the tag binder is a second antibody which recognizes the first antibody. In addition to antibody-antigen interactions, receptor-ligand interactions are also appropriate as tag and tag-binder pairs. For example, agonists and antagonists of cell membrane receptors (*e.g.*, cell receptor-ligand interactions such as transferrin, c-kit, viral receptor ligands, cytokine receptors, chemokine receptors, interleukin receptors,  
15 immunoglobulin receptors and antibodies, the cadherein family, the integrin family, the selectin family, and the like; *see, e.g.*, Pigott & Power, The Adhesion Molecule Facts Book I (1993)). Similarly, toxins and venoms, viral epitopes, hormones (*e.g.*, opiates, steroids, *etc.*), intracellular receptors (*e.g.*, which mediate the effects of various small ligands, including steroids, thyroid hormone, retinoids and vitamin D;  
20 peptides), drugs, lectins, sugars, nucleic acids (both linear and cyclic polymer configurations), oligosaccharides, proteins, phospholipids and antibodies can all interact with various cell receptors.

Synthetic polymers, such as polyurethanes, polyesters, polycarbonates, polyureas, polyamides, polyethyleneimines, polyarylene sulfides, polysiloxanes,  
25 polyimides, and polyacetates can also form an appropriate tag or tag binder. Many other tag/tag binder pairs are also useful in assay systems described herein, as would be apparent to one of skill upon review of this disclosure.

Common linkers such as peptides, polyethers, and the like can also serve as tags, and include polypeptide sequences, such as poly gly sequences of between about  
30 5 and 200 amino acids. Such flexible linkers are known to persons of skill in the art. For example, poly(ethelyne glycol) linkers are available from Shearwater Polymers, Inc. Huntsville, Alabama. These linkers optionally have amide linkages, sulfhydryl linkages, or heterofunctional linkages.

Tag binders are fixed to solid substrates using any of a variety of methods currently available. Solid substrates are commonly derivatized or functionalized by exposing all or a portion of the substrate to a chemical reagent that fixes a chemical group to the surface which is reactive with a portion of the tag binder. For example, groups that are suitable for attachment to a longer chain portion would include amines, hydroxyl, thiol, and carboxyl groups. Aminoalkylsilanes and hydroxyalkylsilanes can be used to functionalize a variety of surfaces, such as glass surfaces. The construction of such solid phase biopolymer arrays is well described in the literature. See, e.g., Merrifield, *J. Am. Chem. Soc.*, 85:2149-54 (1963) (describing solid phase synthesis of, e.g., peptides); Geysen *et al.*, *J. Immun. Meth.*, 102:259-74 (1987) (describing synthesis of solid phase components on pins); Frank & Doring, *Tetrahedron*, 44:60316040 (1988) (describing synthesis of various peptide sequences on cellulose disks); Fodor *et al.*, *Science*, 251:767-77 (1991); Sheldon *et al.*, *Clinical Chemistry*, 39(4):718-19 (1993); and Kozal *et al.*, *Nature Medicine*, 2(7):753759 (1996) (all describing arrays of biopolymers fixed to solid substrates). Non-chemical approaches for fixing tag binders to substrates include other common methods, such as heat, cross-linking by UV radiation, and the like.

#### 4. Computer-based assays

Yet another assay for compounds that modulate OR protein activity involves computer assisted compound design, in which a computer system is used to generate a three-dimensional structure of an OR protein based on the structural information encoded by its amino acid sequence. The input amino acid sequence interacts directly and actively with a preestablished algorithm in a computer program to yield secondary, tertiary, and quaternary structural models of the protein. The models of the protein structure are then examined to identify regions of the structure that have the ability to bind, e.g., ligands. These regions are then used to identify ligands that bind to the protein.

The three-dimensional structural model of the protein is generated by entering protein amino acid sequences of at least 10 amino acid residues or corresponding nucleic acid sequences encoding a OR polypeptide into the computer system. The nucleotide sequence encoding the polypeptide, or the amino acid sequence thereof, can be any of SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID



NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID  
NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID  
NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID  
NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID  
5 NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID  
NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID  
NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID  
NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID  
NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107,  
10 SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID  
NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125,  
SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID  
NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143,  
SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID  
15 NO: 153, SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID NO: 159, SEQ ID NO: 161,  
SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID  
NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID NO: 177, SEQ ID NO: 179,  
SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID  
NO: 189, SEQ ID NO: 191, SEQ ID NO: 193, SEQ ID NO: 195, SEQ ID NO: 197,  
20 SEQ ID NO: 199, SEQ ID NO: 201, SEQ ID NO: 203, SEQ ID NO: 205, SEQ ID  
NO: 207, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID NO: 213, SEQ ID NO: 215,  
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25 NO: 243, SEQ ID NO: 245, SEQ ID NO: 247, SEQ ID NO: 249, SEQ ID NO: 251,  
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NO: 261, SEQ ID NO: 263, SEQ ID NO: 265, SEQ ID NO: 267, SEQ ID NO: 269,  
SEQ ID NO: 271, SEQ ID NO: 273, SEQ ID NO: 275, SEQ ID NO: 277, SEQ ID  
NO: 279, SEQ ID NO: 281, SEQ ID NO: 283, SEQ ID NO: 285, SEQ ID NO: 287,  
30 SEQ ID NO: 289, SEQ ID NO: 291, SEQ ID NO: 293, SEQ ID NO: 295, SEQ ID  
NO: 297, SEQ ID NO: 299, SEQ ID NO: 301, SEQ ID NO: 303, SEQ ID NO: 305,  
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NO: 315, SEQ ID NO: 317, SEQ ID NO: 319, SEQ ID NO: 321, SEQ ID NO: 323,

SEQ ID NO: 325, SEQ ID NO: 327, SEQ ID NO: 329, SEQ ID NO: 331, SEQ ID NO: 333, SEQ ID NO: 335, SEQ ID NO: 337, SEQ ID NO: 339, SEQ ID NO: 341, SEQ ID NO: 343, SEQ ID NO: 345, SEQ ID NO: 347, SEQ ID NO: 349, SEQ ID NO: 351, SEQ ID NO: 353, SEQ ID NO: 355, SEQ ID NO: 357, SEQ ID NO: 359, SEQ ID NO: 361, SEQ ID NO: 363, SEQ ID NO: 365, SEQ ID NO: 367, SEQ ID NO: 369, SEQ ID NO: 371, SEQ ID NO: 373, SEQ ID NO: 375, SEQ ID NO: 377, SEQ ID NO: 379, SEQ ID NO: 381, SEQ ID NO: 383, SEQ ID NO: 385, SEQ ID NO: 387, SEQ ID NO: 389, SEQ ID NO: 391, SEQ ID NO: 393, SEQ ID NO: 395, SEQ ID NO: 397, SEQ ID NO: 399, SEQ ID NO: 401, SEQ ID NO: 403, SEQ ID NO: 405, SEQ ID NO: 407, SEQ ID NO: 409, SEQ ID NO: 411, SEQ ID NO: 413, SEQ ID NO: 415, SEQ ID NO: 417, SEQ ID NO: 419, SEQ ID NO: 421, SEQ ID NO: 423, SEQ ID NO: 425, SEQ ID NO: 427, SEQ ID NO: 429, SEQ ID NO: 431, SEQ ID NO: 433, SEQ ID NO: 435, SEQ ID NO: 437, SEQ ID NO: 439, SEQ ID NO: 441, SEQ ID NO: 443, SEQ ID NO: 445, SEQ ID NO: 447, SEQ ID NO: 449, SEQ ID NO: 451, SEQ ID NO: 453, SEQ ID NO: 455, SEQ ID NO: 457, SEQ ID NO: 459, SEQ ID NO: 461, SEQ ID NO: 463, SEQ ID NO: 465, SEQ ID NO: 467, SEQ ID NO: 469, SEQ ID NO: 471, SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID NO: 477, SEQ ID NO: 479, SEQ ID NO: 481, SEQ ID NO: 483, SEQ ID NO: 485, SEQ ID NO: 487, SEQ ID NO: 489, SEQ ID NO: 491, SEQ ID NO: 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511, and conservatively modified versions thereof.

The amino acid sequence represents the primary sequence or subsequence of the protein, which encodes the structural information of the protein. At least 10 residues of the amino acid sequence (or a nucleotide sequence encoding 10 amino acids) are entered into the computer system from computer keyboards, computer readable substrates that include, but are not limited to, electronic storage media (*e.g.*, magnetic diskettes, tapes, cartridges, and chips), optical media (*e.g.*, CD ROM), information distributed by internet sites, and by RAM. The three-dimensional structural model of the protein is then generated by the interaction of the amino acid sequence and the computer system, using software known to those of skill in the art.

The amino acid sequence represents a primary structure that encodes the information necessary to form the secondary, tertiary and quaternary structure of the

protein of interest. The software looks at certain parameters encoded by the primary sequence to generate the structural model. These parameters are referred to as "energy terms," and primarily include electrostatic potentials, hydrophobic potentials, solvent accessible surfaces, and hydrogen bonding. Secondary energy terms include van der  
5 Waals potentials. Biological molecules form the structures that minimize the energy terms in a cumulative fashion. The computer program is therefore using these terms encoded by the primary structure or amino acid sequence to create the secondary structural model.

The tertiary structure of the protein encoded by the secondary structure is then  
10 formed on the basis of the energy terms of the secondary structure. The user at this point can enter additional variables such as whether the protein is membrane bound or soluble, its location in the body, and its cellular location, *e.g.*, cytoplasmic, surface, or nuclear. These variables along with the energy terms of the secondary structure are used to form the model of the tertiary structure. In modeling the tertiary structure, the  
15 computer program matches hydrophobic faces of secondary structure with like, and hydrophilic faces of secondary structure with like.

Once the structure has been generated, potential ligand-binding regions are identified by the computer system. Three-dimensional structures for potential ligands are generated by entering amino acid or nucleotide sequences or chemical formulas of  
20 compounds, as described above. The three-dimensional structure of the potential ligand is then compared to that of the OR protein to identify ligands that bind to the protein. Binding affinity between the protein and ligands is determined using energy terms to determine which ligands have an enhanced probability of binding to the protein.

25 Computer systems are also used to screen for mutations, polymorphic variants, alleles and interspecies homologs of OR genes. Such mutations can be associated with disease states or genetic traits. As described above, GeneChip™ and related technology can also be used to screen for mutations, polymorphic variants, alleles and interspecies homologs. Once the variants are identified, diagnostic assays can be used  
30 to identify patients having such mutated genes. Identification of the mutated OR genes involves receiving input of a first nucleic acid or amino acid sequence of a OR gene, or conservatively modified versions thereof. The sequence is entered into the computer system as described above. The first nucleic acid or amino acid sequence is

then compared to a second nucleic acid or amino acid sequence that has substantial identity to the first sequence. The second sequence is entered into the computer system in the manner described above. Once the first and second sequences are compared, nucleotide or amino acid differences between the sequences are identified.

- 5 Such sequences can represent allelic differences in various OR genes, and mutations associated with disease states and genetic traits.

#### 5. Cell-based binding assays

In a preferred embodiment, an OR polypeptide is expressed in a eukaryotic cell as a chimeric receptor with a heterologous, chaperone sequence that facilitates its maturation and targeting through the secretory pathway. In a preferred embodiment, 10 the heterologous sequence is a rhodopsin sequence, such as an N-terminal fragment of a rhodopsin. Such chimeric OR receptors can be expressed in any eukaryotic cell, such as HEK-293 cells. Preferably, the cells comprise a functional G protein, *e.g.*, G $\alpha$ 15, that is capable of coupling the chimeric receptor to an intracellular signaling 15 pathway or to a signaling protein such as phospholipase C. Activation of such chimeric receptors in such cells can be detected using any standard method, such as by detecting changes in intracellular calcium by detecting FURA-2 dependent fluorescence in the cell.

Activated GPCR receptors become substrates for kinases that phosphorylate 20 the C-terminal tail of the receptor (and possibly other sites as well). Thus, activators will promote the transfer of  $^{32}\text{P}$  from gamma-labeled GTP to the receptor, which can be assayed with a scintillation counter. The phosphorylation of the C-terminal tail will promote the binding of arrestin-like proteins and will interfere with the binding of G proteins. The kinase/arrestin pathway plays a key role in the desensitization of 25 many GPCR receptors. For example, compounds that modulate the duration an olfactory receptor stays active would be useful as a means of prolonging a desired odor or cutting off an unpleasant one. For a general review of GPCR signal transduction and methods of assaying signal transduction, *see, e.g., Methods in Enzymology*, vols. 237 and 238 (1994) and volume 96 (1983); Bourne *et al.*, *Nature*, 30 10:349:117-27 (1991); Bourne *et al.*, *Nature*, 348:125-32 (1990); Pitcher *et al.*, *Annu. Rev. Biochem.*, 67:653-92 (1998).

OR modulation may be assayed by comparing the response of an OR polypeptide treated with a putative OR modulator to the response of an untreated

control sample. Such putative OR modulators can include odorants that either inhibit or activate OR polypeptide activity. In one embodiment, control samples (untreated with activators or inhibitors) are assigned a relative OR activity value of 100. Inhibition of an OR polypeptide is achieved when the OR activity value relative to the control is about 90%, optionally 50%, optionally 25-0%. Activation of an OR polypeptide is achieved when the OR activity value relative to the control is 110%, optionally 150%, 200-500%, or 1000-2000%.

Changes in ion flux may be assessed by determining changes in polarization (*i.e.*, electrical potential) of the cell or membrane expressing a OR protein. One means to determine changes in cellular polarization is by measuring changes in current (thereby measuring changes in polarization) with voltage-clamp and patch-clamp techniques, *e.g.*, the "cell-attached" mode, the "inside-out" mode, and the "whole cell" mode (*see, e.g.*, Ackerman *et al.*, *New Engl. J Med.*, 336:1575-1595 (1997)). Whole cell currents are conveniently determined using the standard. Other known assays include: radiolabeled ion flux assays and fluorescence assays using voltage-sensitive dyes (*see, e.g.*, Vestergaard-Bogind *et al.*, *J. Membrane Biol.*, 88:67-75 (1988); Gonzales & Tsien, *Chem. Biol.*, 4:269277 (1997); Daniel *et al.*, *J. Pharmacol. Meth.*, 25:185-193 (1991); Holevinsky *et al.*, *J. Membrane Biology*, 137:59-70 (1994)). Generally, the compounds to be tested are present in the range from 1 pM to 100 mM.

The effects of the test compounds upon the function of the polypeptides can be measured by examining any of the parameters described above. Any suitable physiological change that affects GPCR activity can be used to assess the influence of a test compound on the polypeptides of this invention. When the functional consequences are determined using intact cells or animals, one can also measure a variety of effects such as transmitter release, hormone release, transcriptional changes to both known and uncharacterized genetic markers (*e.g.*, northern blots), changes in cell metabolism such as cell growth or pH changes, and changes in intracellular second messengers such as  $\text{Ca}^{2+}$ , IP3, cGMP, or cAMP.

Preferred assays for GPCRs include cells that are loaded with ion or voltage sensitive dyes to report receptor activity. Assays for determining activity of such receptors can also use known agonists and antagonists for other G protein coupled receptors as negative or positive controls to assess activity of tested compounds. In

assays for identifying modulatory compounds (*e.g.*, agonists, antagonists), changes in the level of ions in the cytoplasm or membrane voltage will be monitored using an ion sensitive or membrane voltage fluorescent indicator, respectively. Among the ion-sensitive indicators and voltage probes that may be employed are those disclosed  
5 in the Molecular Probes 1997 Catalog. For G protein coupled receptors, promiscuous G proteins such as G $\alpha$ 15 and G $\alpha$ 16 can be used in the assay of choice (Wilkie *et al.*, *PNAS*, 88:10049-53 (1991)). Such promiscuous G proteins allow coupling of a wide range of receptors.

Receptor activation typically initiates subsequent intracellular events, *e.g.*,  
10 increases in second messengers such as IP3, which releases intracellular stores of calcium ions. Activation of some G protein coupled receptors stimulates the formation of inositol triphosphate (IP3) through phospholipase C-mediated hydrolysis of phosphatidylinositol (Berridge & Irvine, *Nature*, 312:315-21 (1984)). IP3 in turn stimulates the release of intracellular calcium ion stores. Thus, a change in  
15 cytoplasmic calcium ion levels, or a change in second messenger levels such as IP3 can be used to assess G protein coupled receptor function. Cells expressing such G protein coupled receptors may exhibit increased cytoplasmic calcium levels as a result of contribution from both intracellular stores and via activation of ion channels, in which case it may be desirable although not necessary to conduct such assays in  
20 calcium-free buffer, optionally supplemented with a chelating agent such as EGTA, to distinguish fluorescence response resulting from calcium release from internal stores.

Other assays can involve determining the activity of receptors which, when activated, result in a change in the level of intracellular cyclic nucleotides, *e.g.*, cAMP or cGMP, by activating or inhibiting enzymes such as adenylate cyclase. There are  
25 cyclic nucleotide-gated ion channels, *e.g.*, rod photoreceptor cell channels and olfactory neuron channels that are permeable to cations upon activation by binding of cAMP or cGMP (*see, e.g.*, Altenhofen *et al.*, *PNAS*, 88:9868-72 (1991) and Dhallan *et al.*, *Nature*, 347:184-187 (1990)). In cases where activation of the receptor results in a decrease in cyclic nucleotide levels, it may be preferable to expose the cells to agents  
30 that increase intracellular cyclic nucleotide levels, *e.g.*, forskolin, prior to adding a receptor-activating compound to the cells in the assay. Cells for this type of assay can be made by co-transfection of a host cell with DNA encoding a cyclic nucleotide-gated ion channel, GPCR phosphatase and DNA encoding a receptor (*e.g.*,

certain glutamate receptors, muscarinic acetylcholine receptors, dopamine receptors, serotonin receptors, and the like), which, when activated, causes a change in cyclic nucleotide levels in the cytoplasm.

In a preferred embodiment, OR protein activity is measured by expressing a  
5 OR gene in a heterologous cell with a promiscuous G protein that links the receptor to a phospholipase C signal transduction pathway (*see* Offermanns & Simon, *J. Biol. Chem.*, 270:15175-15180 (1995)). Optionally the cell line is HEK-293 (which does not naturally express OR genes) and the promiscuous G protein is G $\alpha$ 15/G $\alpha$ 16 (Offermanns & Simon, *supra*). Modulation of olfactory transduction is assayed by  
10 measuring changes in intracellular Ca<sup>2+</sup> levels, which change in response to modulation of the OR signal transduction pathway via administration of a molecule that associates with a OR protein. Changes in Ca<sup>2+</sup> levels are optionally measured using fluorescent Ca<sup>2+</sup> indicator dyes and fluorometric imaging.

In one embodiment, the changes in intracellular cAMP or cGMP can be  
15 measured using immunoassays. The method described in Offermanns & Simon, *J. Bio. Chem.*, 270:15175-15180 (1995), may be used to determine the level of cAMP. Also, the method described in Felley-Bosco *et al.*, *Am. J. Resp. Cell and Mol. Biol.*, 11:159-164 (1994), may be used to determine the level of cGMP. Further, an assay kit for measuring cAMP and/or cGMP is described in U.S. Patent 4,115,538, herein  
20 incorporated by reference.

In another embodiment, phosphatidyl inositol (PI) hydrolysis can be analyzed according to U.S. Patent 5,436,128, herein incorporated by reference. Briefly, the assay involves labeling of cells with 3H-myoinositol for 48 or more hrs. The labeled cells are treated with a test compound for one hour. The treated cells are lysed and  
25 extracted in chloroform-methanol-water after which the inositol phosphates were separated by ion exchange chromatography and quantified by scintillation counting. Fold stimulation is determined by calculating the ratio of cpm in the presence of agonist, to cpm in the presence of buffer control. Likewise, fold inhibition is determined by calculating the ratio of cpm in the presence of antagonist, to cpm in the  
30 presence of buffer control (which may or may not contain an agonist).

In another embodiment, transcription levels can be measured to assess the effects of a test compound on signal transduction. A host cell containing an OR protein of interest is contacted with a test compound for a sufficient time to effect any

interactions, and then the level of gene expression is measured. The amount of time to effect such interactions may be empirically determined, such as by running a time course and measuring the level of transcription as a function of time. The amount of transcription may be measured by using any method known to those of skill in the art to be suitable. For example, mRNA expression of the protein of interest may be detected using northern blots or their polypeptide products may be identified using immunoassays. Alternatively, transcription based assays using reporter gene may be used as described in U.S. Patent 5,436,128, herein incorporated by reference. The reporter genes can be, *e.g.*, chloramphenicol acetyltransferase, luciferase, '3-galactosidase and alkaline phosphatase. Furthermore, the protein of interest can be used as an indirect reporter via attachment to a second reporter such as green fluorescent protein (*see, e.g.*, Mistili & Spector, *Nature Biotechnology*, 15:961-64 (1997)).

The amount of transcription is then compared to the amount of transcription in either the same cell in the absence of the test compound, or it may be compared with the amount of transcription in a substantially identical cell that lacks the OR protein of interest. A substantially identical cell may be derived from the same cells from which the recombinant cell was prepared but which had not been modified by introduction of heterologous DNA. Any difference in the amount of transcription indicates that the test compound has in some manner altered the activity of the OR protein of interest.

#### **6. Transgenic non-human animals expressing olfactory receptors**

Non-human animals expressing one or more olfactory receptor sequences of the invention, particularly human olfactory receptor sequences, can also be used for receptor assays. Such expression can be used to determine whether a test compound specifically binds to a mammalian olfactory transmembrane receptor polypeptide *in vivo* by contacting a non-human animal stably or transiently transfected with a nucleic acid encoding an olfactory receptor or ligand-binding region thereof with a test compound and determining whether the animal reacts to the test compound by specifically binding to the receptor polypeptide.

Use of the translocation domains of the invention in the fusion polypeptides generates a cell expressing high levels of olfactory receptor. Animals transfected or infected with the vectors of the invention are particularly useful for assays to identify and characterize odorants/ligands that can bind to a specific or sets of receptors. Such



vector-infected animals expressing libraries of human olfactory sequences can be used for *in vivo* screening of odorants and their effect on, *e.g.*, cell physiology (*e.g.*, on olfactory neurons), on the CNS (*e.g.*, olfactory bulb activity), or behavior.

Means to infect/express the nucleic acids and vectors, either individually or as  
5 libraries, are well known in the art. A variety of individual cell, organ or whole animal parameters can be measured by a variety of means. For example, recording of stimulant-induced waves (bulbar responses) from the main olfactory bulb or accessory olfactory bulb is a useful tool for measuring quantitative stable olfactory responses. When electrodes are located on the olfactory bulb surface it is possible to record stable  
10 responses over a period of several days (*see, e.g.*, Kashiwayanagi, *Brain Res. Protoc.* 1:287-291 (1997)). In this study, electroolfactogram recordings were made with a four-electrode assembly from the olfactory epithelium overlying the endoturbinates bones facing the nasal septum. Four electrodes were fixed along the dorsal-to-ventral axis of one turbinate bone or were placed in corresponding positions on four turbinate  
15 bones and moved together up toward the top of the bone. *See also*, Scott, *J. Neurophysiol.* 77:1950-1962 (1997); Scott, *J. Neurophysiol.* 75:2036-2049 (1996); Ezech, *J. Neurophysiol.* 73:2207-2220 (1995). In other systems, fluorescence changes in nasal epithelium can be measured using the dye di-4-ANEPPS, which is applied on the rat's nasal septum and medial surface of the turbinates (*see, e.g.*, Youngentob, *J.*  
20 *Neurophysiol.* 73:387-398 (1995)). Extracellular potassium activity (aK) measurements can also be carried out in *in vivo*. An increase in aK can be measured in the mucus and the proximal part of the nasal epithelium (*see, e.g.*, Khayari, *Brain Res.* 539:1-5 (1991)).

The OR sequences of the invention can be for example expressed in animal  
25 nasal epithelium by delivery with an infecting agent, *e.g.*, adenovirus expression vector. Recombinant adenovirus-mediated expression of a recombinant gene in olfactory epithelium using green fluorescent protein as a marker is described by, *e.g.*, Touhara, *PNAS*, 96:4040-45 (1999).

The endogenous olfactory receptor genes can remain functional and wild-type  
30 (native) activity can still be present. In other situations, where it is desirable that all olfactory receptor activity is by the introduced exogenous hybrid receptor, use of a knockout line is preferred. Methods for the construction of non-human transgenic

animals, particularly transgenic mice, and the selection and preparation of recombinant constructs for generating transformed cells are well known in the art.

Construction of a "knockout" cell and animal is based on the premise that the level of expression of a particular gene in a mammalian cell can be decreased or completely abrogated by introducing into the genome a new DNA sequence that serves to interrupt some portion of the DNA sequence of the gene to be suppressed. Also, "gene trap insertion" can be used to disrupt a host gene, and mouse embryonic stem (ES) cells can be used to produce knockout transgenic animals (*see, e.g.,* Holzschu, *Transgenic Res* 6:97-106 (1997)). The insertion of the exogenous is typically by homologous recombination between complementary nucleic acid sequences. The exogenous sequence is some portion of the target gene to be modified, such as exonic, intronic or transcriptional regulatory sequences, or any genomic sequence which is able to affect the level of the target gene's expression; or a combination thereof. Gene targeting via homologous recombination in pluripotential embryonic stem cells allows one to modify precisely the genomic sequence of interest. Any technique can be used to create, screen for, propagate, a knockout animal, *e.g., see* Bijvoet, *Hum. Mol. Genet.* 7:53-62 (1998); Moreadith, *J. Mol. Med.* 75:208-216 (1997); Tojo, *Cytotechnology* 19:161-165 (1995); Mudgett, *Methods Mol. Biol.* 48:167-184 (1995); Longo, *Transgenic Res.* 6:321-328 (1997); U.S. Patents Nos. 5,616,491; 5,464,764; 5,631,153; 5,487,992; 5,627,059; 5,272,071; WO 91/09955; WO 93/09222; WO 96/29411; WO 95/31560; WO 91/12650.

The nucleic acid libraries of the invention can also be used as reagents to produce "knockout" human cells and their progeny. Likewise, the nucleic acids of the invention can also be used as reagents to produce "knock-ins" in mice. The human or rat OR gene sequences can replace the orthologous ORs in the mouse genome. In this way, a mouse expressing a human or rat OR can be produced. This mouse can then be used to analyze the function of human or rat ORs, and to identify ligands for such ORs.

#### F. Modulators

The compounds tested as modulators of an OR family member can be any small chemical compound, or a biological entity, such as a protein, sugar, nucleic acid or lipid. Alternatively, modulators can be genetically altered versions of an OR gene.

Typically, test compounds will be small chemical molecules and peptides. Essentially any chemical compound can be used as a potential modulator or ligand in the assays of the invention, although most often compounds can be dissolved in aqueous or organic (especially DMSO-based) solutions are used. The assays are designed to  
5 screen large chemical libraries by automating the assay steps and providing compounds from any convenient source to assays, which are typically run in parallel (e.g., in microtiter formats on microtiter plates in robotic assays). It will be appreciated that there are many suppliers of chemical compounds, including Sigma (St. Louis, MO), Aldrich (St. Louis, MO), Sigma-Aldrich (St. Louis, MO), Fluka  
10 Chemika-Biochemica Analytika (Buchs, Switzerland) and the like.

The OR modulating compounds can be used in any number of consumer products, including, but not limited to, perfumes, fragrance compositions, deodorants, air fresheners, foods, drugs, *etc.*, or ingredients thereof, to thereby modulate the odor of the product, composition, or ingredient in a desired manner. As  
15 one of skill in the art will recognize, OR modulating compounds can be used to enhance desirable odors, to block malodors, or a combination thereof.

In one preferred embodiment, high throughput screening methods involve providing a combinatorial chemical or peptide library containing a large number of potential therapeutic compounds (potential modulator or ligand compounds). Such  
20 "combinatorial chemical libraries" or "ligand libraries" are then screened in one or more assays, as described herein, to identify those library members (particular chemical species or subclasses) that display a desired characteristic activity. The compounds thus identified can serve as conventional "lead compounds" or can themselves be used as potential or actual odorant compositions.

25 A combinatorial chemical library is a collection of diverse chemical compounds generated by either chemical synthesis or biological synthesis, by combining a number of chemical "building blocks" such as reagents. For example, a linear combinatorial chemical library such as a polypeptide library is formed by combining a set of chemical building blocks (amino acids) in every possible way for a  
30 given compound length (*i.e.*, the number of amino acids in a polypeptide compound). Millions of chemical compounds can be synthesized through such combinatorial mixing of chemical building blocks.

Preparation and screening of combinatorial chemical libraries is well known to those of skill in the art. Such combinatorial chemical libraries include, but are not limited to, peptide libraries (*see, e.g.*, U.S. Patent 5,010,175, Furka, *Int. J. Pept. Prot. Res.*, 37:487-93 (1991) and Houghton *et al.*, *Nature*, 354:84-88 (1991)). Other chemistries for generating chemical diversity libraries can also be used. Such chemistries include, but are not limited to: peptoids (*e.g.*, PCT Publication No. WO 91/19735), encoded peptides (*e.g.*, PCT Publication WO 93/20242), random bio-oligomers (*e.g.*, PCT Publication No. WO 92/00091), benzodiazepines (*e.g.*, U.S. Pat. No. 5,288,514), diversomers such as hydantoins, benzodiazepines and dipeptides (Hobbs *et al.*, *PNAS*, 90:6909-13 (1993)), vinylogous polypeptides (Hagihara *et al.*, *J. Amer. Chem. Soc.*, 114:6568 (1992)), nonpeptidal peptidomimetics with glucose scaffolding (Hirschmann *et al.*, *J. Amer. Chem. Soc.*, 114:9217-18 (1992)), analogous organic syntheses of small compound libraries (Chen *et al.*, *J. Amer. Chem. Soc.*, 116:2661 (1994)), oligocarbamates (Cho *et al.*, *Science*, 261:1303 (1993)), peptidyl phosphonates (Campbell *et al.*, *J. Org. Chem.*, 59:658 (1994)), nucleic acid libraries (Ausubel, Berger and Sambrook, all *supra*), peptide nucleic acid libraries (U.S. Patent 5,539,083), antibody libraries (Vaughn *et al.*, *Nature Biotechnology*, 14(3):309-14 (1996) and PCT/US96/10287), carbohydrate libraries (Liang *et al.*, *Science*, 274:1520-22 (1996) and U.S. Patent 5,593,853), small organic molecule libraries (benzodiazepines, Baum, *C&EN*, Jan 18, page 33 (1993); thiazolidinones and metathiazanones, U.S. Patent 5,549,974; pynrolidines, U.S. Patents 5,525,735 and 5,519,134; morpholino compounds, U.S. Patent 5,506,337; benzodiazepines, 5,288,514, and the like).

Devices for the preparation of combinatorial libraries are commercially available (*see, e.g.*, 357 MPS, 390 MPS (Advanced Chem Tech, Louisville KY), Symphony (Rainin, Woburn, MA), 433A (Applied Biosystems, Foster City, CA), 9050 Plus (Millipore, Bedford, MA)). In addition, numerous combinatorial libraries are themselves commercially available (*see, e.g.*, ComGenex, Princeton, NJ; Tripos, Inc., St. Louis, MO; 3D Pharmaceuticals, Exton, PA; Martek Biosciences; Columbia, MD; *etc.*).

**G. Methods for Representing and Predicting the Perception of Odor**

The invention also preferably provides methods for representing the perception of odor (or taste) and/or for predicting the perception of odor (or taste) in a mammal, including in a human. Preferably, such methods may be performed by using the  
5 receptors and genes encoding said olfactory receptors disclosed herein.

Also contemplated as within the invention, is a method of screening one or more compounds for the presence of an odor detectable by a mammal, comprising: contacting said one or more compounds with the disclosed receptors, preferably wherein the mammal is a human. Also contemplated as within the invention is a  
10 method for representing olfactory perception of a particular smell in a mammal, comprising: providing values  $X_1$  to  $X_n$  representative of the quantitative stimulation of each of  $n$  olfactory receptors of said vertebrate, where  $n$  is greater than or equal to 4; and generating from said values a quantitative representation of olfactory perception. The olfactory receptors may be an olfactory receptor disclosed herein, the  
15 representation may constitute a point or a volume in  $n$ -dimensional space, may constitute a graph or a spectrum, and may constitute a matrix of quantitative representations. Also, the providing step may comprise contacting a plurality of recombinantly-produced olfactory receptors with a test composition and quantitatively measuring the interaction of said composition with said receptors.

Also contemplated as within the invention, is a method for predicting the olfactory perception in a mammal generated by one or more molecules or combinations of molecules yielding unknown olfactory perception in a mammal, comprising: providing values  $X_1$  to  $X_n$  representative of the quantitative stimulation of  
20 each of  $n$  olfactory receptors of said vertebrate, where  $n$  is greater than or equal to 4, for one or more molecules or combinations of molecules yielding known olfactory perception in a mammal; and generating from said values a quantitative representation of olfactory perception in a mammal for the one or more molecules or combinations  
25 of molecules yielding known olfactory perception in a mammal, providing values  $X_1$  to  $X_n$  representative of the quantitative stimulation of each of  $n$  olfactory receptors of said vertebrate, where  $n$  is greater than or equal to 4, for one or more molecules or  
30 combinations of molecules yielding unknown olfactory perception in a mammal; and generating from said values a quantitative representation of olfactory perception in a mammal for the one or more molecules or combinations of molecules yielding

unknown olfactory perception in a mammal, and predicting the olfactory perception in a mammal generated by one or more molecules or combinations of molecules yielding unknown olfactory perception in a mammal by comparing the quantitative representation of olfactory perception in a mammal for the one or more molecules or combinations of molecules yielding unknown olfactory perception in a mammal to the quantitative representation of olfactory perception in a mammal for the one or more molecules or combinations of molecules yielding known olfactory perception in a mammal. The olfactory receptors used in this method may include an olfactory receptor disclosed herein.

10 In another embodiment, novel molecules or combinations of molecules are generated which elicit a predetermined olfactory perception in a mammal by determining a value of olfactory perception in a mammal for a known molecule or combinations of molecules as described above; determining a value of olfactory perception in a mammal for one or more unknown molecules or combinations of molecules as described above; comparing the value of olfactory perception in a mammal for one or more unknown compositions to the value of olfactory perception in a mammal for one or more known compositions; selecting a molecule or combination of molecules that elicits a predetermined olfactory perception in a mammal; and combining two or more unknown molecules or combinations of molecules to form a molecule or combination of molecules that elicits a predetermined olfactory perception in a mammal. The combining step yields a single molecule or a combination of molecules that elicits a predetermined olfactory perception in a mammal.

25 In another embodiment of the invention, there is provided a method for simulating a fragrance, comprising: for each of a plurality of cloned olfactory receptors, preferably human receptors, ascertaining the extent to which the receptor interacts with the fragrance; and combining a plurality of compounds, each having a previously-ascertained interaction with one or more of the receptors, in amounts that together provide a receptor-stimulation profile that mimics the profile for the fragrance. Interaction of a fragrance with an olfactory receptor can be determined using any of the binding or reporter assays described herein. The plurality of compounds may then be combined to form a mixture. If desired, one or more of the plurality of the compounds can be combined covalently. The combined compounds

substantially stimulate at least 75%, 80% or 90% of the receptors that are substantially stimulated by the fragrance.

In another preferred embodiment of the invention, a plurality of standard compounds are tested against a plurality of olfactory receptors to ascertain the extent to which the receptors each interact with each standard compound, thereby generating a receptor stimulation profile for each standard compound. These receptor stimulation profiles may then be stored in a relational database on a data storage medium. The method may further comprise providing a desired receptor-stimulation profile for a scent; comparing the desired receptor stimulation profile to the relational database; and ascertaining one or more combinations of standard compounds that most closely match the desired receptor-stimulation profile. The method may further comprise combining standard compounds in one or more of the ascertained combinations to simulate the scent.

#### H. Kits

OR genes and their homologs are useful tools for identifying olfactory receptor cells, for forensics and paternity determinations, and for examining olfactory transduction. OR family member-specific reagents that specifically hybridize to OR nucleic acids, such as AOLFR1 probes and primers, and OR family member-specific reagents that specifically bind to an OR protein, *e.g.*, OR antibodies are used to examine olfactory cell expression and olfactory transduction regulation.

Nucleic acid assays for the presence of DNA and RNA for an OR family member in a sample include numerous techniques are known to those skilled in the art, such as southern analysis, northern analysis, dot blots, RNase protection, S1 analysis, amplification techniques such as PCR, and *in situ* hybridization. In *in situ* hybridization, for example, the target nucleic acid is liberated from its cellular surroundings in such a form so as to be available for hybridization within the cell, while preserving the cellular morphology for subsequent interpretation and analysis. The following articles provide an overview of the art of *in situ* hybridization: Singer *et al.*, *Biotechniques*, 4:230-50 (1986); Haase *et al.*, *Methods in Virology*, vol. VII, pp. 189-226 (1984); and *Nucleic Acid Hybridization: A Practical Approach* (Names *et al.*, eds. 1987). In addition, an OR protein can be detected with the various immunoassay

techniques described above. The test sample is typically compared to both a positive control (e.g., a sample expressing a recombinant OR protein) and a negative control.

The present invention also provides for kits for screening for modulators of OR family members. Such kits can be prepared from readily available materials and reagents. For example, such kits can comprise any one or more of the following materials: OR nucleic acids or proteins, reaction tubes, and instructions for testing OR activity. Optionally, the kit contains a biologically active OR receptor. A wide variety of kits and components can be prepared according to the present invention, depending upon the intended user of the kit and the particular needs of the user.

### EXAMPLES

Genomic, predicted amino acid sequence, and predicted coding sequences (cds), of novel G protein-coupled human odorant receptors, and classes of such receptors, are described. Each example describes a discrete protein and nucleic acid pair. Accordingly, Example 1 describes SEQ. ID. NOS. 1 and 2, for the human olfactory receptor protein designated AOLFR1, and the human DNA encoding AOLFR1, respectively; Example 2 describes SEQ. ID. NOS. 3 and 4, for the human olfactory receptor protein designated AOLFR2, and the human DNA encoding AOLFR2, respectively; and so on in the manner described, through the final Example sequence.

In the protein sequences presented herein, the one-letter code X or Xaa refers to any of the twenty common amino acid residues. In the DNA sequences presented herein, the one letter codes N or n refers to any of the of the four common nucleotide bases, A, T, C, or G.

### EXAMPLES

#### **AOLFR1 sequences:**

MKTFSSFLQIGRNMHQGNQTTTTEFILLGFFKQDEHQNLLFVFLGMYLVTVIGNGLIIVAISLD  
TYLHTPMYLFANLSFADISSISNSVPMKMLVNIQTKSQSISYESCITQMYFSIVFVIDNLLLGT  
AYDHFVAICHPLNYTILMRPRFGILLTVISWFLSNIALTHTLLLIQLLFCNHNTPHFFCDLAPLL  
KLSCSDTLINELVLFIVGLSVIIFPFTLSFFSYVCHRAVLRVSSTQGWKAFSTCGSHLTVVLLFY  
GTIVGVYFFPSSTHPEDTDKIGAVLFTVVTMNPFIYSLRNKDMKGALRKLINRKISSL (SEQ ID  
NO: 1)

ATGAAGACTTTTAGTTCCTTTCTTCAGATCGGCAGAAATATGCATCAAGGAAACCAAACCA  
CCATCACTGAATTCATTCTCCTGGGATTTTCAAGCAGGATGAGCATCAAAACCTCCTCTTT  
GTGCTTTTCTTGGGTATGTACCTGGTCACTGTGATTGGGAACGGGCTCATCATTGTGGCTA  
TCAGCTTGGATACGTACCTTCATACCCCCATGTATCTCTTCTTGCCAATCTATCCTTTGCT  
GATATTTCTCCATTTCCAACCTCAGTCCCCAAAATGCTGGTGAATATTCAAACCAAGAGTC



AATCCATCTCTTATGAGAGCTGCATCACACAGATGTACTTTTCTATTGTGTTTGTGCGTCATT  
 GACAAATTTGCTCTTGGGGACCATGGCCTATGACCACCTTTGTGGCGATCTGCCACCCCTCTGA  
 ATTATACAATTCTCATGCGGCCAGGTTCCGGCATTGCTCACAGTCATCTCATGGTTCCTC  
 AGTAATATTATTGCTCTGACACACACCCCTTCTGCTCATTCAATTGCTCTTCTGTAACCACAA  
 5 CACTCTCCACACTTCTTCTGTGACTTGGCCCTCTGCTCAAACCTGTCTGTTCAGATACAT  
 TGATCAATGAGCTTGTGTTGTTTATTGTGGGTTTATCAGTTATCATCTTCCCCTTTACACTC  
 AGCTTCTTTTCTATGTCTGCATCATCAGAGCTGTCCTGAGAGTATCTTCCACACAGGGAA  
 AGTGGAAGCCCTTCTCCACTTGTGGCTCTCACCTGACAGTTGTATTACTGTTCTACGGAAC  
 CATTGTAGGCGTGACTTTTTCCCCTCTCCACTCACCCCTGAGGACACTGATAAGATTGGT  
 10 GCTGTCCTATTCACTGTGGTGACACCCATGATAAACCCCTTCATCTACAGCTTGAGGAATA  
 AGGATATGAAAGGTGCCCTGAGAAAGCTCATCAATAGAAAAATTTCTTCCCCTTTGA (SEQ  
 ID NO: 2)

#### AOLFR2 sequences:

15 MMMVLRNLSMEPTFALLGFTDYPKLIQPLFLVFLLMYVITVVGNLGMIIHKINPKFHTPMYFFL  
 SHLSFVDFCYSSIVTPKLLLENLVMADKSIFYFSCMMQYFLSCTAVVTESFLLAVMAYDRFVAIC  
 NPLLYTVAMSQRLCALLVAGSYLWGMFGPLVLLCYALRLNFGSPNVNHHFFCEYTA LISVSGS  
 DILPHLLLFSFATFNEMCTLLILTSYVFVTVLKIRSVSGRHKAFSTWASHLTAITIFHGTLFL  
 YCVPNSKNSRQTVKVASVFYTVVNPMLNPPIYSLRNKDVKDAFWKLIHTQVPFH (SEQ ID NO:  
 20 3)

ATGATGATGGTTTTAAGGAATCTGAGCATGGAGCCACCTTTGCCCTTTTAGGTTTCACAG  
 ATTACCCAAAGCTTCAGATTCCTCTCTTCTTGTGTTTCTGCTCATGTATGTTATCACAGTG  
 GTAGGAAACCTTGGGATGATCATAATAATCAAGATTAAACCCCAAATTCACACTCCTATGT  
 25 ACTTTTTCTTCTAGTCACCTCTCTTTTGTGATTTTTGTACTCTTCCATTGTCACTCCCAAGC  
 TGCTTGAGAACTTGGTAATGGCAGATAAAAGCATCTTCTACTTTAGCTGCATGATGCAGTA  
 CTTCTGTCTGCACTGCTGTGGTGACAGAGTCTTTCTGCTGGCAGTGATGGCCTATGAC  
 CGCTTTGTGGCCATCTGCAATCCTCTGCTTTATACAGTGGCCATGTCACAGAGGCTCTGTG  
 CCCTGTCTGGTGGCTGGGTCATATCTCTGGGGCATGTTTGGCCCTTGGTACTCCTTTGTTAT  
 30 GCTCTCCGGTTAAACTTCTCTGGACCTAATGTAATCAACCACCTTCTTTGTGAGTATACTGC  
 TCTCATCTCTGTGTCTGGCTCTGATATACTCATCCCCACCTGCTGCTTTTCAGCTTTCGCCA  
 CCTTCAATGAGATGTGTACACTACTGATCATCTCTCACTTCTATGTTTTCATTTTGTGACT  
 GTACTAAAAATCCGTTCTGTTAGTGGGCGCCACAAAGCCTTCTCCACCTGGGCCCTCCACC  
 TGACTGCTATCACCATCTTCCATGGGACCATCCTTTTCTTTACTGTGTACCCAACTCCAAA  
 35 AACTCTCGGCAAACAGTCAAAGTGGCCTCTGTATTTTACACAGTTGTCAACCCCATGCTGA  
 ACCCTCCGATCTACAGCCTAAGGAATAAAGACGTGAAGGATGCTTCTGGAAGTTAATACA  
 TACACAAGTTCCATTTCACTGA (SEQ ID NO: 4)

#### AOLFR3 sequences:

40 MLLTDRNTSGTFTLLGFSDYPELQVPLFLVFLAIYNVTVLGNIGLIVIIKINPKLHTPMYFFLSQ  
 LSFVDFCYSSIIAPKMLVNLVVKDRITISFLGCVVQFFFCTFVVTESFLLAVMAYDRFVAICNPL  
 LYTVDMQSQKLCVLLVVGSYAWGVSCSLELTCSALKLCFHGFNTINHHFFCESSLLSLSCSDTYI  
 NQWLLFFLATFNEISTLLIVLTSYAFIVVTILKMRSVSGRRKAFSTCASHLTAITIFHGTLFLYCV  
 PNSKNSRHTVKVASVFYTVVIPMLNPLIYSLRNKDVKDTVTEILDTKVFSY (SEQ ID NO: 5)

45 ATGCTGCTGACAGATAGAAATACAAGTGGGACCACGTTACCCCTCTTGGGCTTCTCAGATT  
 ACCCAGAACTGCAAGTCCCACTCTTCTGGTTTTTCTGGCCATCTACAATGTCACTGTGCTA  
 GGAATATTGGGTTGATTGTGATCATCAAAATCAACCCCAAACCTGCATACCCCATGTACT  
 TTTTCTCAGCCAACTCTCCTTTGTGGATTTCTGCTATTCTCCATCATTGCTCCCAAGATG  
 50 TTGGTGAACCTTGTGTCAAAGACAGAACCATTTTCAATTTTAGGATGCGTAGTACAATTCT  
 TTTTCTTCTGTACCTTTGTGGTCACTGAATCCTTTTTATTAGCTGTGATGGCCTATGACCGC  
 TTCGTGGCCATTTGCAACCCCTCTGCTCTACACAGTTGACATGTCCAGAAACTCTGCGTGC  
 TGCTAGTTGTGGGATCCTATGCCTGGGGAGTCTCATGTTCTTGGAACTGACGTGCTGCTGC  
 TTTAAAGTTATGTTTTCATGGTTTCAACACAATCAATCACTTCTTCTGTGAGTTCTCCTCAC  
 55 TACTCTCCCTTTCTTGTCTGATACTTACATCAACCAGTGGCTGCTATTCTTTCTTGCCACC  
 TTTAATGAAATCAGCACACTACTCATCGTTCTCACATCTTATGCGTTCATTGTTGTAACCAT

CCTCAAGATGCGTTCAGTCAGTGGGCGCCGCAAAGCCTTCTCCACCTGTGCCTCCACCTG  
 ACTGCCATCACCATCTTCCATGGCACCATCCTTCTCCTTTACTGTGTGCCAACTCCAAAAA  
 CTCCAGGCACACAGTCAAAGTGGCCTCTGTGTTTTACACCGTGGTGATCCCATGTTGAAT  
 CCCCTGATCTACAGTCTGAGAAATAAAGATGTCAAGGATACAGTCACCGAGATACTGGAC  
 5 ACCAAAGTCTTCTCTACTGA (SEQ ID NO: 6)

**AOLFR4 sequences:**

MENQNNVTEFILLGLTENLELWKIFSAVFLVMYVATVLENLLIVVTITTSQSLRSPMYFFLTFLS  
 LLDVMFSSV VAPKIVVD TLSKSTTISLKGCLTQLFVEHFFGGVGILLTVMAYDRYVAICKPLHY  
 10 TIIMSPRVCCLMVGGAWVGGFMHAMIQLLFMYQIPFCGPNIDHFICDLFQLLTLACTDTHILGL  
 LVTLSNGMMCVAIFLILIASYTVILCSLSYSSKGRHKALSTCSSHLTVVVLFFVPCIFLYMRPV  
 VTHPIDKAMAVSDSIITPMLNPLIYTLRNAEVKSAMKKLWMKWEALAGK (SEQ ID NO: 7)

ATGGAAAAATCAAAACAATGTGACTGAATTCATTCTTCTGGGTCTCACAGAGAACCTGGAGC  
 15 TGTGGAAAAATATTTTCTGCTGTGTTTCTTGTGTCATGTATGTAGCCACAGTGTGAAAAATCT  
 ACTTATTGTGGTAACTATTATCACAAGTCAGAGTCTGAGGTCACCTATGTATTTTTTCTTA  
 CCTTCTTGTCCCTTTTGGATGTCATGTTCTCATCTGTCGTTGCCCCCAAGGTGATTGTAGAC  
 ACCCTCTCCAAGAGCACTACCATCTCTCTCAAAGGCTGCCTCACCCAGCTGTTTGTGGAGC  
 ATTTCTTTGGTGGTGTGGGGATCATCCTCCTCACTGTGATGGCCTATGACCGCTACGTGGC  
 20 CATCTGTAAGCCCTGCACTACACGATCATCATGAGTCCACGGGTGTGCTGCCTAATGGTA  
 GGAGGGGCTTGGGTGGGGGGATTATGCACGCAATGATACAACTTCTTTCATGTATCAAA  
 TACCCTTCTGTGGTCTAATATCATAGATCACTTTATATGTGATTTGTTTCAGTTGTTGACA  
 CTTGCCTGCACGGACACCCACATCCTGGGCCTCTTAGTTACCCTCAACAGTGGGATGATGT  
 GTGTGGCCATCTTTCTTATCTTAATTGCGTCTACACGGTCATCCTATGCTCCCTGAAGTCT  
 25 TACAGCTCTAAAGGGCGGCACAAAGCCCTCTCTACCTGCAGCTCCCACTCACGGTGGTTG  
 TATGTTCTTTGTCCCCTGTATTTCTTGTACATGAGGCCTGTGGTCACTACCCCATAGAC  
 AAGGCAATGGCTGTGTGCACTCAATCATCACCCCATGTTAAATCCCTTGATCTATACAC  
 TGAGGAATGCAGAGGTGAAAAGTGCCATGAAGAACTCTGGATGAAATGGGAGGCTTTGG  
 CTGGGAAATAA (SEQ ID NO: 8)

30

**AOLFR5 sequences:**

MGKENCTTVAEFILLGLSDVPELRVCLFLLFLLIYGVTLNLANLGMIALIQVSSRLHTPMYFFLSH  
 LSSVDFCYSSIIVPKMLANIFNKDKAISFLGCMVQFYLFCTCVVTEVFLLAVMAYDRFVAICNPL  
 35 LYTVTMSWKVRVELASCCYFCGTVCSLIHLCLALRIPFYRSNVINHFFCDLPPVLSLACSDITVN  
 ETLLFLVATL NESVTIMILTSYLLILTTILKMGSABGRHKAFSTCASHLTAITVFHGTVLSIYCRP  
 SSGNSGDADKVATVFYTVVIPMLNSVIYSLRNKDVKEALRKVMGSKIHS (SEQ ID NO: 9)

ATGGGCAAGGAAAACTGCACCACTGTGGCTGAGTTCATTCTCCTTGGACTATCAGATGTCC  
 40 CTGAGTTGAGAGTCTGCCTCTTCCTGCTGTTCCCTCTCATCTATGGAGTCACGTTGTTAGCC  
 AACCTGGGCATGATTGCACTGATTCAAGGTCAGCTCTCGGCTCCACACCCCATGTACTTTT  
 TCCTCAGCCACTTGTCTCTGTAGATTTCTGCTACTCCTCAATAATTGTGCCAAAAATGTTG  
 GCTAATATCTTTAACAAGGACAAAGCCATCTCCTTCTAGGGTGCATGGTGCAATTCTACT  
 TGTTTTGCACTTGTGTGGTCACTGAGGTCTTCCTGCTGGCCGTGATGGCCTATGACCGCTTT  
 GTGGCCATCTGTAACCCCTTTGCTATACACAGTCACCATGTCTTGGAAGGTGCGTGTGGAGC  
 45 TGGCTTCTGTGCTGCTACTTCTGTGGGACGGTGTGTTCTCTGATTCAATTTGTGCTTAGCTCTT  
 AGGATCCCCCTTCTATAGATCTAATGTGATTAACCACTTTTTCTGTGATCTACCTCCTGTCTT  
 AAGTCTTGCTTGTCTGATATCACTGTGAATGAGACACTGCTGTTCCCTGGTGGCCACTTTG  
 AATGAGAGTGTTACCATCATGATCATCCTCACCTCCTACCTGCTAATTCTCACCACCATCCT  
 GAAGATGGGCTCTGCAGAGGGCAGGCACAAAGCCTTCTCCACCTGTGCTTCCACCTCACA  
 50 GCTATCACTGTCTTCCATGGAACAGTCCTTTCCATTTATTGCAGGCCAGTTCAAGGCAATA  
 GTGGAGATGCTGACAAAGTGGCCACCGTGTCTACACAGTCGTGATTCTATGCTGAACTC  
 TGTGATCTACAGCCTGAGAAATAAAGATGTGAAAGAAGCTCTCAGAAAAGTGATGGGCTC  
 CAAAATTCACTCCTAG (SEQ ID NO: 10)

**AOLFR6 sequences:**

MMASERNQSSPTTFILLGFSEYPEIQVPLFLVFLFVYTVTVVGNLGMIIIIRLNSKLHTIMYFFLS  
 HLSLTDFCFSTVVPKLLNLVVEYRTISFSGCIMQFCFACIFGVTETFMFLAAMAYDRFVAVCK  
 PLLYTTIMSQKLCALLVAGSYTWGIVCSLILTYFLLDLSFCESTFINNFICDHSVIVSASYSDPYIS  
 5 QRLCFIIAIFNEVSSLIIILTSYMLIFTTIMKMRSASGRQKTFSTCASHLTAITIFHGTLFLYCVPNP  
 KTSSLIVTVASVFYTVAIPLMLNPLIYSLRNKDINNMFELVVTCLIYH (SEQ ID NO: 11)

ATGATGGCATCTGAAAGAAATCAAAGCAGCACACCCACTTTTATTCTCTTGGGTTTTTTCAG  
 AATACCCAGAAATCCAGGTTCCACTCTTTCTGGTTTTCTTGTTCGTCTACACAGTCACTGTA  
 10 GTGGGGAACCTTGGGCATGATAATAATCATCAGACTCAATTCAAACTCCATACAATCATGT  
 ACTTTTTCTTAGTCACTTGTCTTGACAGACTCTGTTTTTCCACTGTAGTTACACCTAAA  
 CTGTTGGAGAACTTGGTTGTGGAATACAGAACCATCTCTTTCTCTGGTTGCATCATGCAAT  
 TTTGTTTTGCTTGCATTTTTGGAGTGACAGAACTTTCATGTTAGCAGCGATGGCTTATGAC  
 CGTTTTGTGGCAGTTTGTAACCCCTTGCTGTATACCACTATTATGTCTCAGAAGCTCTGTGC  
 15 TCTTCTGGTGGCTGGGTCCTATACATGGGGGATAGTGTGCTCCCTGATACTCACATATTTT  
 CTTCTTGACTTATCGTTTTGTGAATCTACCTTCATAAATAATTTTATCTGTGACCACTCTGT  
 AATTGTTTTCTGCCTCCTACTCAGACCCCTATATCAGCCAGAGGCTATGCTTTATTATGCCA  
 TATTCAATGAGGTGAGCAGCCTAATTATCATTCTGACATCATATATGCTTATTTTCACTACC  
 ATTATGAAGATGCGATCTGCAAGTGGGCGCCAGAAACTTTCTCCACCTGTGCCTCCCACC  
 20 TGACAGCCATCACTATCTTCCATGGAACCTTTTCTTTACTGTGTTCCTAATCTCTAAA  
 ACTTCAGCCTCATAGTTACAGTGGCTTCTGTGTTTTACACAGTGCGCATGCTCAATGCTGA  
 ACCCATTGATCTACAGCCTTAGGAACAAAGATATCAATAACATGTTTGAAAAATTAGTTGT  
 CACCAAATTGATTTACCACTGA (SEQ ID NO: 12)

**AOLFR7 sequences:**

MSYFYRLKLMKEAVLVKLPFTSLPLLQTLRKSRLDMEIKNYSSSTSGFILLGLSSNPQLQKPLF  
 AIFLIMYLLAAVGNVLIPAIYSDPRLHTPMYFFLSNLSFMDICFTTVIVPKMLVNFLSETKVISY  
 VGCLAQMYFFMAFGNTDSYLLASMAIDRLVAICNPLHYDVVMKPRHCLLMLLGSCSISHLHSL  
 FRVLLMSRLSFCASHIHKHFFCDTQPVLKLSGSDTSSSQMVVMTETLAVIVTPFLCIIFSYLIMV  
 30 TVLRIPSAAGWKAFSTCGSHLTAVALFYGSIIYVYFRPLSMYSVVRDRVATVMYTVVTPMLN  
 PFYISLRNKDMKRGKLLQDRIYR (SEQ ID NO: 13)

ATGAGCTATTTTTACAGGCTTAAGCTTATGAAAGAAGCTGTCTTGGTCAAACCTGCCCTTTA  
 CATCTCTCCCACTGCTTCTCCAAACCCTATCCAGGAAGTCCAGAGACATGGAGATAAAGAA  
 35 CTACAGCAGCAGCACCTCAGGCTTCATCCTCCTGGGCCTCTCTTCCAACCCTCAGCTGCAG  
 AAACCTCTCTTTGCCATCTTCCTCATCATGTACCTGCTCGCTGCGGTGGGGAATGTGCTCAT  
 CATCCCGGCCATCTACTCTGACCCCAAGGCTCCACACCCCTATGTACTTTTTTCTCAGCAACT  
 TGTCTTTTCATGGATATCTGCTTCAACAGTCATAGTGCCTAAGATGCTGGTGAATTTTCTA  
 TCAGAGACAAAGGTTATCTCCTATGTGGGCTGCCTGGCCAGATGTACTTCTTTATGGCAT  
 40 TTGGGAACACTGACAGCTACCTGCTGGCCTCTATGGCCATCGACCGGCTGGTGGCCATCTG  
 CAACCCCTTACACTATGATGTGGTTATGAAACCACGGCATTGCCTGCTCATGCTATTGGGT  
 TCTTGCAGCATCTCCACCTACATTCCCTGTTCCGCGTGCTACTTATGTCTCGCTTGTCTTT  
 CTGTGCCTCTCACATCATTAAAGCACTTTTTCTGTGACACCCAGCCTGTGCTAAAGCTCTCCT  
 GCTCTGACACATCCTCCAGCCAGATGGTGGTGATGACTGAGACCTTAGCTGTCATTGTGAC  
 45 CCCCTTCTGTGTATCATCTTCTCCTACCTGCGAATCATGGTCACTGTGCTCAGAATCCCCT  
 CTGCAGCCGGGAAGTGGAAGGCCTTCTACCTGTGGCTCCCACCTCACTGCAGTAGCCCT  
 TTTCTATGGGAGTATTATTTATGTCTATTTTAGGCCCTGTCCATGTACTCAGTGGTTAGGG  
 ACCGGGTAGCCACAGTTATGTACACAGTAGTGACACCCATGCTGAACCCCTTTCATCTACAG  
 CCTGAGGAACAAAGATATGAAGAGGGGTTTGAAGAAATTACAGGACAGAAATTTACCGGTA  
 50 A (SEQ ID NO: 14)

**AOLFR8 sequences:**

MATSNHSSGAEFILAGLTQRPELQLPLFLLFLGIYVTVTVVGNLGMIFLIALSSQLYPPVYYFLSH  
 LSFIDLCYSSVITPKMLVNFPVENIISFLECITQLYFFLIFVIAEGYLLTAMEYDRYVAICRPLLY  
 55 NIVMSHRVCSIMMAVVYSLGFLWATVHTTRMSVLSFCRSHTVSHYFCDILPLLTLSCSSTHINEI

LLFIIGGVNTLATTILAVLISYAFIFSSILGIHSTEGQSKAFGTCSSHLLAVGIFFGSITFMFKPPSS  
TTMEKEKVSSVFYTTIPMLNPLIYSLRNKDVKNALKKMTRGRQSS (SEQ ID NO: 15)

5 ATGGCTACTTCAAACCATTCCTTCAGGGGCTGAGTTTATCCTGGCAGGCTTGACACAACGCC  
CAGAACTTCAACTGCCACTCTTCCTCTGTTCTTGAATATATGTGGTCACAGTGGTGGG  
GAACCTGGGCATGATCTTCTTAATTGCTCTCAGTTCTCAACTTTACCCTCCAGTGATTATT  
TTCTCAGTCATTTGTCTTTCATTGATCTCTGCTACTCCTCTGTCATTACCCCTAAGATGCTG  
GTGAACTTTGTTCCAGAGGAGAACATTATCTCCTTTCTGGAATGCATTACTCAACTTTATTT  
10 CTTCTTATTTTGTAAATTGCAGAAGGCTACCTTCTGACAGCCATGGAATATGACCGTTAT  
GTTGCTATCTGTGCGCCACTGCTTTACAATATTGTCATGTCCACAGGGTCTGTTCCATAAT  
GATGGCTGTGGTATACTCACTGGGTTTTCTGTGGGCCACAGTCCATACTACCCGCATGTCA  
GTGTTGTCATTCTGTAGGTCTCATACGGTCAGTCATTATTTTGTGATATTCTCCCTTATT  
GACTCTGTCTTGCTCCAGCACCCACATCAATGAGATTCTGCTGTTCAATTATTGGAGGAGTT  
AATACCTTAGCAACTACACTGGCGGTCCTTATCTCTTATGCTTTCATTTTCTCTAGTATCCT  
15 TGGTATTCAATCCACTGAGGGGCAATCCAAAGCCTTTGGCACTTGTAGCTCCCATCTCTTG  
GCTGTGGGCATCTTTTTTGGGTCTATAACATTCATGTATTTCAAGCCCCCTTCCAGCACTAC  
TATGGAAAAAGAGAAGGTGTCTTCTGTGTTCTACATCACAATAATCCCCATGCTGAATCCT  
CTAATCTATAGCCTGAGGAACAAGGATGTGAAAAATGCACTGAAGAAGATGACTAGGGGA  
AGGCAGTCATCCTGA (SEQ ID NO: 16)

20

**AOLFR9 sequences:**

MLARNNSLVTEFILAGLTDRPEFWQPFFFLFLVIYIVTMVGNLGLITLFLNSHLHTPMYYFLFN  
LSFIDL CYSSVFTPKMLMNFVSKKNISNVGCMTRLFFFLFFVISECYMLTSMAYDRYVAICNPL  
LYKVTMSHQVCSMLTFAAYIMGLAGATAHTGCMFRLTFCSANINHYLCDILPLLQLSCTSTYV  
25 NEVVVLIVVGNTNITVPSCITLISYVFIVTSILHIKSTQGRSKAFSTCSSHVIALSLFFGSAAFMYIKY  
SSGSMEBQKGVFSVFYTNVVPMLNPLIYSLRNKDVKVALRKALIKIQRRNIF (SEQ ID NO: 17)

30 ATGCTGGCTAGAAACAACCTCCTTAGTGACTGAATTTATTCTTGCTGGATTAACAGATCGTC  
CAGAGTTCTGGCAACCCTTCTTTTTCTGTTCTTAGTGATCTACATTGTCAACCATGGTAGGC  
AACCTTGGCTTGATCACTCTTTTCGGTCTAAATTCTCACCTCCACACACCAATGTACTATTT  
CCTCTTCAATCTCTCCTTCATTGATCTCTGTTACTCCTCTGTTTTCACTCCCAAAATGCTAAT  
GAACTTTGTGTCAAAAAAGAATATTATCTCCAATGTTGGGTGCATGACTCGGCTGTTTTTC  
TTTCTCTTTTTCGTCATCTCTGAATGTTACATGTTGACCTCAATGGCATATGATCGCTATGT  
GGCCATCTGTAATCCATTGCTGTATAAGGTCACCATGTCCCATCAGGTCTGTTCTATGCTCA  
35 CTTTTGCTGCTTACATAATGGGATTGGCTGGAGCCACGGCCACACCGGGTGCATGTTTAG  
ACTCACCTTCTGCAGTGCTAATATCATTAAACCATTACTTGTGTGACATACTCCCCCTCCTCC  
AGCTTTCCTGCACCAGCACCTATGTCAACGAGGTGGTTGTTCTCATTGTTGTGGGTACTAA  
TATCACGGTACCAGTTGTACCATCTCATTCTTATGTTTTCATTGTCACTAGCATTCTTC  
ATATCAAATCCACTCAAGGAAGATCAAAAGCCTTCAGTACTTGTAGCTCTCATGTCAATTGC  
40 TCTGTCTCTGTTTTTGGGTGAGCGGCATTATGTATATTAAATATTCTTCTGGATCTATGG  
AGCAGGGAAAAGTTTTTCTGTTTTCTACACTAATGTGGTGCCCATGCTCAATCCCCCTCATC  
TACAGTTTGAGGAACAAGGATGTCAAAGTTGCACTGAGGAAAGCTCTGATTAAAATTCAG  
AGGAGAAATATATTCTAA (SEQ ID NO: 18)

45 **AOLFR10 sequences:**

MLARNNSLVTEFILAGLTDRPEFRQPLFFLFLVIYIVTMVGNLGLIILFGLNSHLHTPMYYFLFN  
SFIDL CYSSVFTPKMLMNFVSKKNISYVGCMTQLFFFLFFVISECYILTSMAYDRYVAICNPLLY  
KVTMSHQVCSMLTFAAYIMGLAGATAHTGCMRLTLFCSANINHYLCDILPLLQLSCTSTYVN  
EVVVLIVVGINIMVPSCITLISYVFIVTSILHIKSTQGRSKAFSTCSSHVIALSLFFGSAAFMYIKYS  
50 SGSMEBQKGVSSVFYTNVVPMLNPLIYSLRNKDVKVALRKALIKIQRRNIF (SEQ ID NO: 19)

55 ATGCTGGCTAGAAACAACCTCCTTAGTGACTGAATTTATTCTTGCTGGATTAACAGATCGTC  
CAGAGTTCCGGCAACCCTCTTTTTCTGTTTCTAGTGATCTACATTGTCAACCATGGTAGGC  
AACCTTGGCTTGATCACTCTTTTCGGTCTAAATTCTCACCTCCACACACCAATGTACTATTT  
CCTCTTCAATCTCTCCTTCATTGATCTCTGTTACTCCTCTGTTTTCACTCCCAAAATGCTAAT  
GAACTTTGTATCAAAAAAGAATATTATCTCTATGTTGGGTGCATGACTCAGCTGTTTTTCT



AAATCACAGTAATGACAGAAGGCTTGGCTGTCATAATGACCCCGTTTTTCATGCATCATCAT  
CTCTTATTTAAGAATCCTCATCACTGTTCTGAAGATTCCCTTCAGCTGCTGGAAAGCGTAAA  
GCATTTTCTACCTGTGGCTCTCATCTCACAGTGGTGACCCTGTTTTATGGAAGCATTAGCTA  
TGTCTATTTTCAGCCCCCTGTCCAATACTGTCAAGGATCAAAATAGCAACAATTATCTAC  
5 ACCGTA CTGACTCCTATGCTAAATCCATTTATCTATAGTCTGAGGAACAAAGACATGAAGC  
AGGGTTTGGCAAAGTTGATGCACAGGATGAAATGTCAGTAA (SEQ ID NO: 24)

**AOLFR13 sequences:**

MDQKNGSSFTGFILLGFSDRPQLELVLFVLLIFYIFTLLGNKTIIVLSHLDPHLHNP MYFFFSNL  
10 SFLDLCYTTGIVPQLLVNLRGADKSISYGGCVVQLYISLGLGSTECVLLGVMAFDRYAAVCRPL  
HYTVVMHPCLYVLMASSTWVIGFANSLLQTVLILLTLGRNKL EHFLEVPPLKLACVDTT  
MNESELFFVSVIII LPVALIIFSYSQIVRAVVRK SATGQRKVFGTCGSHLTVVSLFYGTAIYAY  
LQPGNNYSQDQGXISLFYTIITP MINPLIYTLRNKDVKGALKKVLWKNYDSR (SEQ ID NO:  
25)

15 ATGGATCAGAAAAATGGAAGTTCTTTCACTGGATTTATCCTACTGGGTTTCTCTGACAGGC  
CTCAGCTGGAGCTAGTCCTCTTTGTGGTTCTTTTGATCTTCTATATCTTCACTTTGCTGGGG  
AACAAAACCATCATTTGTATTATCTCACTTGGACCCACATCTTCACAATCCTATGTATTTTT  
CTTCTCCAACCTAAGCTTTTTGGATCTGTGTTACACAACCGGCATTGTTCCACAGCTCCTGG  
20 TTAATCTCAGGGGAGCAGACAAATCAATCTCCTATGGTGGTTGTGTAGTTCACTGTACAT  
CTCTCTAGGCTTGGGATCTACAGAATGCGTTCTCTTAGGAGTGATGGCATTGACCGCTAT  
GCAGCTGTTTGCAGGCCCTCCACTACACAGTAGTCATGCACCCTTGTCTGTATGTGCTGA  
TGGCTTCTACTTCATGGGTCATTGGTTTTGCCAACTCCCTATTGCAGACGGTGCTCATCTTG  
CTTTTAACACTTTGTGGAAGAAATAAATTAGAACACTTTCTTTGTGAGGTTCTCCATTGCT  
25 CAAGCTTGCTGTGTTGACACTACTATGAATGAATCTGAACTCTTCTTTGTGAGTGTCATTA  
TTCTTCTTGTACCTGTTGCATTAATCATATTCTCCTATAGTCAGATTGTGAGGCAGTCGTG  
AGGATAAAGTCAGCAACAGGGCAGAGAAAAGTGTGTTGGGACATGTGGCTCCACCTCACA  
GTGGTTTCCCTGTTCTACGGCACAGCTATCTATGCTACCTCCAGCCCGGCAACAATACTC  
TCAGGATCAGGGCAAGKTCATCTCTCTCTCTACACCATCATTACACCCATGATCAACCCC  
30 CTCATATATACACTGAGGAACAAGGATGTGAAAGGAGCACTTAAGAAGGTGCTCTGGAAG  
AACTACGACTCCAGATGA (SEQ ID NO: 26)

**AOLFR14 sequences:**

MALPLLLSPSCFASSQSLSSRMNSENLTAAVAPAEFVLLGITNRWDLRVALFLTCLPVYLVSL  
35 LGNMGMALLIRMDARLHTPMYFFLANLSLLDACYS SAIGPKMLVDLLLPRATIPYTACALQMF  
VFAGLADTECCLLAAMAYDRYVAIRNPLLYTTAMSQRLCLALLGASGLGGA VSAFVHTTLTF  
RLSFCRSRKINSFFCDIPLLAISCSDTSLNELL LFAICGFIQTATVLAITVSYGFIAGAVIHMRSVE  
GSRRAASTGGSHLTAVAMMYGTLIFMYLRPSSSYALDTDKMASVFYTLVIPSLNPLIYSLRNKE  
VKEALRQTWSRFHCPGQGSQ (SEQ ID NO: 27)

40 ATGGCCTTGCCATTGCTCTTATCTCCCTCCTGCTTTGCCTCTTCTCAGTCTCTGTCCAGTAG  
GATGAACTCAGAGAACCTCACCCGGGCCGCGGTTGCCCTGCTGAATTCGTCCTCCTGGGC  
ATCACAAATCGCTGGGACCTGCGTGTGGCCCTCTTCTGACCTGCCTGCCTGTCTACCTGG.  
TGAGCCTGCTGGGAAACATGGGCATGGCGTGTGATCCGCATGGATGCCCGGCTCCACA  
45 CACCTATGTACTTCTTCTGGCCAACCTCTCCCTGCTGGATGCCTGCTATTCTCCGCCATC  
GGCCCCAAGATGCTAGTGGACCTGCTGCTGCCCCGAGCCACCATCCCTTACACAGCCTGTG  
CCCTCCAGATGTTTGTCTTTGCAGGTCTGGCTGATACTGAGTGTTGCTTGTGTCAGCCAT  
GGCCTATGACCGCTACGTGGCCATCAGAAACCCACTTCTCTATACAACAGCTATGTGCGAG  
CGTCTATGCCTGGCCTTGCTGGGAGCATCAGGCCTGGGTGGGGCAGTGAGTGCCCTTTGTTC  
50 ACACAACCCCTCACCTTCCGCCTGAGCTTCTGCCGCTCCCGGAAGATCAATAGCTTCTTCTG  
CGATATCCCTCCACTGCTGGCCATCTCGTGACGTGACACCACTCTCAATGAACTCCTTCTCT  
TCGCCATCTGTGGCTTCATCCAGACAGCCACGGTGTAGCTATCACGGTGTCTTATGGCTT  
CATCGCTGGGCTGTGATCCACATGCGCTCGGTCGAGGGCAGTCGGCGAGCAGCCTCCAC  
CGGTGGTTCCACCTCACAGCCGTGGCCATGATGTACGGGACACTCATTTTTCATGTACCTG  
55 CGCCCCAGCTCCAGCTATGCCCTGGACACTGACAAGATGGCCTCTGTGTTCTATACCCTGG

TCATCCCGTCTCTCAACCCACTCATCTACAGCCTCCGCAATAAGGAGGTCAAGGAGGCCCT  
CAGGCAGACCTGGAGCCGATTCCACTGTCCAGGGCAGGGGTCCCAGTGA (SEQ ID NO: 28)

**AOLFR15 sequences:**

5 MRENNQSSTLEFILLGVTGQEQEDFFYLFLFYPTITLIGNLLIVLAICSDVRLHNPMPYFLLANLS  
LVDIFFSSVTIPKMLANHLLGSKSISFGGCLTQMYFMIALGNTDSYLAAMAYDRAVAISHPLH  
YTTIMSPRSCTWLIAGSWVIGNANALPHTLLTASLSFCGNQEVANFYCDITPLKLSCSDIHFHV  
KMMYLGVGIFSVPLLCIIVSYIRVFSTVFPSTKGVLKAFSTCGSHLTVVSLYYGTVMGTYFR  
PLTNYSLKDAVITVMTAVTPMLNPFYSLRNRDMKAALRKLFNKRIS (SEQ ID NO: 29)

10 ATGAGGGAAAAATAACCAGTCCTCTACACTGGAATTCATCCTCCTGGGAGTTACTGGTCAGC  
AGGAACAGGAAGATTTCTTCTACATCCTCTTCCTGTTCAATTTACCCCATCACATTGATTGGA  
AACCTGCTCATTGTCTAGCCATTTGCTCTGATGTTGCGCTTCACAACCCCATGTATTTTCT  
CCTTGCCAACCTCTCCTTGGTTGACATCTTCTTCTCATCGGTAACCATCCCTAAGATGCTGG  
15 CCAACCATCTCTTGGGCAGCAAATCCATCTCTTTTGGGGGATGCCTAACGCAGATGTATTT  
CATGATAGCCTTGGGTAACACAGACAGCTATATTTTGGCTGCAATGGCATATGATCGAGCT  
GTGGCCATCAGCCACCCACTTCACTACACAACAATTATGAGTCCACGGTCTTGTATCTGGC  
TTATTGCTGGGTCTTGGGTGATTGGAAATGCCAATGCCCTCCCCACACTCTGCTCACAGC  
TAGTCTGTCCTTCTGTGGCAACCAGGAAGTGGCCAACCTTCTACTGTGACATTACCCCTTG  
20 CTGAAGTTATCCTGTTCTGACATCCACTTTTATGTGAAGATGATGTACCTAGGGGTGGCA  
TTTTCTCTGTGCCATTACTATGCATCATTGTCTCCTATATTCGAGTCTTCTCCACAGTCTTCC  
AGGTTCCCTCCACCAAGGGCGTGCTCAAGGCCTTCTCCACCTGTGGTTCACCTCACGGT  
TGTCTCTTTGTATTATGGTACAGTCATGGGCACGTATTTCCGCCCTTGACCAATTATAGCC  
TAAAAGACGCAGTGATCACTGTAATGTACACGGCAGTGACCCCAATGTTAAATCCTTTTAT  
25 CTACAGCTGAGAAATCGGGACATGAAGGCTGCCCTGCGGAAACTCTTCAACAAGAGAAT  
CTCCTCGTAA (SEQ ID NO: 30)

**AOLFR16 sequences:**

30 MRRNCTLVTEFILLGLTSRRELQILLFTLFLAIYMTVAGNLGMIVLIQANAWLHMPMPYFFLSH  
LSFVDLCFSSNVTPKMLEIFLSEKKSISYPACLVCYLFIALVHVEIYLAVMAFDHYMAICNPLL  
YGSRMKSVCFLITVPYVYGALTGLMETMWTYNLAFCGPNEINHFCADPPLIKLACSDTYN  
KELSMFIVAGWNLSFSLFIICISYLYIFPAILKIRSTEGRQKAFSTCGSHLTAVTIFYATLFFMYLR  
PPSKESVEQGKMAVVFYTTVIPMLNLIYSLRNKNVKEALIKELSMKIYFS (SEQ ID NO: 31)

35 ATGAGAAGAACTGCACGTTGGTGACTGAGTTCATTCTCCTGGGACTGACCAGTCGCCGG  
GAATTACAAATTCTCCTCTTCACGCTGTTTCTGGCCATTTACATGGTCACGGTGGCAGGGA  
ACCTTGGCATGATTGTCTCATCCAGGCCAACGCCTGGCTCCACATGCCCATGTACTTTTTC  
CTGAGCCACTTATCCTTCGTGGATCTGTGCTTCTCTTCCAATGTGACTCCAAAGATGCTGG  
40 AGATTTTCTTTCAGAGAAGAAAAGCATTTCCTATCCTGCCTGTCTTGTGCAGTGTTACCTT  
TTTATCGCCTTGGTCCATGTTGAGATCTACATCCTGGCTGTGATGGCCTTTGACCGGTACAT  
GGCCATCTGCAACCCTCTGCTTTATGGCAGCAGAATGTCCAAGAGTGTGTGCTCCTTCCTC  
ATCACGGTGCCTTATGTGTATGGAGCGCTCACTGGCCTGATGGAGACCATGTGGACCTACA  
ACCTAGCCTTCTGTGGCCCAATGAAATTAATCACTTCTACTGTGCGGACCCACCACTGAT  
TAAGCTGGCTTGTCTGACACCTACAACAAGGAGTTGTCAATGTTTATTGTGGCTGGCTGG  
45 AACCTTTCTTTTTCTCTCTTCATCATATGATTTTCTACCTTTACATTTTCCCTGCTATTTTA  
AAGATTCGCTCTACAGAGGGCAGGCAAAAAGCTTTTCTACCTGTGGCTCCCATCTGACAG  
CTGTCACTATATTCTATGCAACCCTTTTCTTCATGTATCTCAGACCCCCCTCAAAGGAATCT  
GTTGAACAGGGTAAAATGGTAGCTGTATTTTATACCACAGTAATCCCTATGCTGAACCTTA  
TAATTTATAGCCTTAGAAATAAAAATGTAAAAGAAGCATTAATCAAAGAGCTGTCAATGA  
50 AGATATACTTTTCTTAA (SEQ ID NO: 32)

**AOLFR17 sequences:**

55 MLNFTDVTTEFILLGLTSRREWQVLFFIIFLVVYIITMVGNIGMMVLKIVSPQLNNPMPYFFLSHLS  
FVDVWFSSNVTPKMLENLFSDKKTITYAGCLVQCFFIALVHVEIFILAAMAFDRYMAIGNPLL  
YGSKMSRVVCIRLITFPYTYGFLTSLAATLWTYGLYFCGKIEINHFCADPPLIKMACAGTFVKE

YTMILAGINFTYSLTVIIISYLFILIAILRMRSAEGRQKAFSTCGSHLTAVIIFYGTLIFMYLRRPTE  
ESVEQGMVAVFYTTVIPMLNPMIYSLRNKDVKKAMMKVISRSC (SEQ ID NO: 33)

5 ATGCTCAATTTACCGATGTGACAGAGTTCATTCTTTTGGGGCTAACGAGCCGTCGAGAAT  
GGCAAGTTCTCTTCTTCATCATCTTTCTTGTGGTCTACATCATCACCATGGTGGGCAATATC  
GGCATGATGGTGTAAATCAAGGTCAGTCCTCAGCTTAACAACCCCATGTACTTTTCTCTCA  
GTCACITGTCAATTTGTTGATGTGTGGTTTTCTTCCAATGTCACCCCTAAAATGTTGGAAAAC  
CTGTTTTAGATAAAAAAACAATTACTTATGCTGGTTGTTAGTACAGTGTCTTCTTCTCAT  
10 TGCTCTTGTCCATGTGGAAATTTTATTCTTGTGCGATGGCCTTTGATAGATACATGGCAA  
TTGGGAATCCTCTGCTTTATGGCAGTAAAAATGTCAAGGGTTGTCTGTATTGACTGATTAC  
TTTCCCTTACATTTATGGTTTTCTGACGAGTCTGGCAGCAACATTATGGACTTACGGCTTGT  
ACTTCTGTGGAAAAATTGAGATCAACCATTTCTACTGTGCAGATCCACCTCTCATCAAAAT  
GGCCTGTGCCGGGACCTTTGTAAGAATATACAATGATCATACTTGCCGGCATTAACCTC  
ACATATTCCTGACTGTAATTATCATCTTACTTATTCATCCTCATTGCCATTCTGCGAAT  
15 GCGCTCAGCAGAAGGAAGGCAGAAGGCCCTTTCCACATGTGGGTCCCATCTGACAGCTGT  
CATATATTCTATGGTACTCTGATCTTCATGTATCTCAGACGTCCACAGAGGAGTCTGTG  
GAGCAGGGGAAGATGGTGGCTGTGTTCTATACACAGTGATCCCCATGTTGAATCCCATGA  
TCTACAGTCTGAGGAACAAGGATGTGAAAAAGGCCATGATGAAAGTGATCAGCAGATCAT  
GTAA (SEQ ID NO: 34)

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**AOLFR18 sequences:**

MSNTNGSAITEFILLGLTDCPELQSLFLVFLVYYLVTLGNLGMIMLMRLDSRLHTPMYFFLT  
NLAFLVLCYTSNATPQMSTNIVSEKTISFAGCFTQCYIFIALLLTEFYMLAAMAYDRYVAIYDP  
LRYSVKTSRRVCICLATFPYVYGFSDGLFQAILTFRLTFCRSNVINHFCADPPLIKLSCSDTYVK  
25 EHAMFISAGFNLSSSLTIVLSYAFILAILRIKSAEGRHKAFSTCGSHMMAVTLFYGTLCFMYI  
RPPTDKTVEESKIIAVFYTFVSPVLNPLIYSLRNKDVKKALKNVLR (SEQ ID NO: 35)

30 ATGTCCAACACAAATGGCAGTGCAATCACAGAATTCATTTTACTTGGGCTCACAGATTGCC  
CGGAAGTCCAGTCTCTGCTTTTGTGCTGTTTCTGGTTGTTTACCTEGTCACCTGCTAGGC  
AACCTGGGCATGATAATGTTAATGAGACTGGACTCTCGCCTTACACGCCCCATGTACTTCT  
TCCTCACTAAGCTTAGCCTTTGTGGATTTGTGCTATACATCAAATGCAACCCCGCAGATGTC  
GACTAATATCGTATCTGAGAAGACCATTTCTTTGCTGGTTGCTTTACACAGTGCTACATTT  
TCATTGCCCTTCTACTCACTGAGTTTTACATGCTGGCAGCAATGGCCTATGACCGCTATGT  
GGCCATATATGACCTCTGCGCTACAGTGTGAAAACGTCCAGGAGAGTTTGCATCTGCTTG  
35 GCCACATTTCCCTATGTCTATGGCTTCTCAGATGGACTCTTCCAGGCCATCCTGACCTTCCG  
CCTGACCTTCTGTAGATCCAATGTCATCAACCACTTCTACTGTGCTGACCCGCCGCTCATT  
AGCTTCTTGTCTGATACTTATGTCAAAGAGCATGCCATGTTTATATCTGCTGGCTTCAAC  
CTCTCCAGCTCCCTCACCATCGTCTTGGTGTCTATGCCCTCATTCTTGCTGCCATCCTCCG  
GATCAAATCAGCAGAGGGAAGGCACAAGGCATTCTCCACCTGTGGTTCCCATATGATGGC  
40 TGTCACCCTGTTTTATGGGACTCTCTTTGTCATGTATATAAGACCACCAACAGATAAGACT  
GTTGAGGAATCTAAAATAATAGCTGTCTTTTACACCTTTGTGAGTCCGGTACTTAATCCAT  
TGATCTACAGTCTGAGGAATAAAGATGTGAAGCAGGCCTGAAGAATGTCTGAGATGA  
(SEQ ID NO: 36)

45

**AOLFR19 sequences:**

METKNYSSSTSGFILLGLSSNPQLQKPLFAIFLIMYLLTAVGNVLILAIYSDPRLHTPMYFFLSNL  
SFMDICFTTVIVPKMLVNFLSETKIISYVGCLIQMYFFMAFGNTDSYLLASMAJDLVAICNPLH  
YDVVMKPWHCLLMILGSCSISHLHSLFVLLMSRLSFCASHIHKHFFCDTQPVLLKSCSDTSSSQ  
MVVMTETLAVIVTPFLCTIFSYLQIVTVLRIPSAAGKWKAFSTCGSHLTVVVLFGSVIYVYFR  
50 PLSMYSVMKGRVATVMYTVVTPMLNPFIIYSLRNKDMKRGKLRHRIYS (SEQ ID NO: 37)

ATGGAGACAAAGAATTATAGCAGCAGCACCTCAGGCTTCATCCTCCTGGGCCTCTCTTCCA  
ACCCTAAGCTGCAGAAACCTCTCTTTGCCATCTTCTCATCATGTACCTACTCACTGCGGTG  
GGGAATGTGCTCATCATCCTGGCCATCTACTCTGACCCAGGCTCCACACCCCTATGTACT  
55 TTTTCTCAGCAACTTGTCTTTTATGGATATCTGCTTCAACAGTCATAGTGCCTAAGATG  
CTGGTGAATTTTCTATCAGAGACAAAGATTATCTCTTATGTGGGCTGCCTGATCCAGATGT



ACTTCTTCATGGCATTGTTGGGAACACTGACAGCTACCTGCTGGCCTCTATGGCCATCGACCG  
 GCTGGTGGCCATCTGCAACCCCTTACACTATGATGTGGTTATGAAACCATGGCATTGCCTA  
 CTCATGCTATTGGGTTCTTGCAGCATCTCCACCTACATTCCCTGTTCCGCGTGTCTACTTAT  
 GTCTCGCTTGTCTTTCTGTGCCTCTCACATCATTAAGCACTTTTTCTGTGACACCCAGCCTG  
 5 TGCTAAAGCTCTCCTGCTCTGACACATCCTCCAGCCAGATGGTGGTGATGACTGAGACCTT  
 AGCTGTCAATTGTGACCCCTTCCCTGTGTACCATCTTCTCCTACCTGCAAAATCATCGTCACTG  
 TGCTCAGAATCCCCTCTGCAGCCGGGAAGTGGAAAGGCCTTCTCTACCTGTGGCTCCACCT  
 CACTGTAGTGGTCTGTCTATGGGAGTGTCTATGTCTATTTAGGCCTCTGTCCATGT  
 ACTCAGTGATGAAGGGCCGGGTAGCCACAGTTATGTACACAGTAGTGACACCCATGCTGA  
 10 ACCCTTTCATCTACAGCCTGAGGAACAAAGATATGAAAAGGGGTTTGAAGAAATTAAGAC  
 ACAGAAATTTACTCATAG (SEQ ID NO: 38)

**AOLFR20 sequences:**

MVEENHTMKNEFILTGFTHPELKTLLFVFFFAIYLITVVGNISLVALIFTHCRLHTPMYIFLGN  
 15 LALVDSCCACATPKMLENFFSEGKRISLYECAVQFYFLCTVETADCFLLAAVAYDRYVAICNP  
 LQYHIMMSKKLCIQMTTGAFIAGNLHSMIHVGLVFRLVFCGLNHINHFYCDTLPYRLSCVDPF  
 INELVLFIFSGSVQVFTIGSVLISYLYILLTIFRMKSKEGRAKAFSTCASHFSSVSLFYGSIFFLYIRP  
 NLLEEGNDIPAAILFTTVPLLNPFYISLRNKEVISVLRKILLIKSQSGSVNK (SEQ ID NO: 39)

20 ATGGTTGAAGAAAATCATACCATGAAAAATGAGTTTATCCTCACAGGATTACAGATCACC  
 CTGAGCTGAAGACTCTGCTGTTTGTGGTGTCTTTGCCATCTATCTGATCACCGTGGTGGG  
 GAATATTAGTTTGGTGGCACTGATATTTACACACTGTCGGCTTCACACACCAATGTACATC  
 TTTCTGGGAAATCTGGCTCTTGTGGATTCTTGTCTGTGCCTGTGCTATTACCCCCAAAATGTT  
 AGAGAATCTCTTTCTGAGGGCAAAAGGATTTCCTCTATGAATGTGCAGTACAGTTTTAT  
 25 TTTCTTTGCACTGTGGAAACTGCAGACTGCTTTCTTCTGCGCAGCAGTGGCCTATGACCGCT  
 ATGTGGCCATCTGCAACCCACTGCAGTACCACATCATGATGTCCAAGAAACTCTGCATTCA  
 GATGACCACAGGCGCCTTCATAGCTGGAAATCTGCATTCCATGATTCATGTAGGGCTTGTA  
 TTTAGGTTAGTTTTCTGTGGATTGAATCACATCAACCACTTTTACTGTGATACTCTTCCCTT  
 GTATAGACTCTCCTGTGTTGACCTTTTCATCAATGAACTGGTTCTATTTCATCTTCTCAGGTT  
 30 CAGTTCAAGTCTTTACCATAGGTAGTGTCTTAATATCTTATCTCTATATTCTTCTTACTATT  
 TTCAGAATGAAATCCAAGGAGGGAAGGGCCAAAGCCTTTCTACTTGTGCATCCCACCTTTT  
 CATCAGTTTCATTATTCTATGGATCTATTTTTTCTTATACATTAGACCAAATTTGCTTGAA  
 GAAGGAGGTAATGATATACCACTGCTATTTTATTTACAATAGTAGTTCCTTACTAAATC  
 CTTTCAATTTAGTCTGAGAAACAAGGAAGTAAGTGTCTTAAGAAAAATTCGTCTGAA  
 35 AATAAAATCTCAAGGAAGTGTGAACAAATGA (SEQ ID NO: 40)

**AOLFR21 sequences:**

MEPRKNVTDVLLGFTQNPKEQKVLVFMFLFYILTMVGNLLIVTVTVSETLGSPMSFFLAGL  
 TFDIIYSSSISPRLLISDLFFGNNSISFQSFMAQLFIEHLFGGSEVFLLLVMAVDRYVAICKPLHYLV  
 40 IMRQWVCVLLLVSWSVGGFLQSVFQLSIIYGLPFCGPNVIDHFFCDMYPLKLACTDTHVIGLL  
 VVANGGLSCTIAFLLLISYGVLHSLKKLSQKGRQKAHSTCSSHITVVVFFVPCIFMCARPAR  
 TFSIDKSVSVFYTVITPMLNPLIYTLRNSEMTSAMKKL (SEQ ID NO: 41)

45 ATGGAGCCAAGGAAAAATGTGACTGACTTTGTCTCTTGGGCTTCACACAGAATCCAAAG  
 GAGCAGAAAGTACTTTTTGTTATGTTCTTGTCTTCTACATTTTGACCATGGTGGGCAACCT  
 GCTCATTGTAGTGACCGTAAGTGTGAGTGTGAGACCTGGGCTCACCAATGTCCTTCTTTCTT  
 GCTGGCTTAACATTTATAGATATCATTTATTCTTCATCCATTTCCCCCAGATTGATTTTCA  
 CTGTTCTTTGGGAATAATTCCATATCCTTCCAATCTTTCATGGCCCAGCTCTTTATCGAGC  
 50 ACCTTTTGGTGGGTCAGAGGTCTTCTCCTGTTGGTGATGGCCTATGACCGCTATGTGGC  
 CATCTGTAAGCCCTTGCATTATTTGGTTATCATGAGACAATGGGTGTGTGTTTGTGCTGTG  
 GTAGTGTCTGGGTTGGAGGATTTCTGCAATCAGTATTTCAACTTAGCATTATTTATGGGC  
 TCCCATTTCTGTGGCCCCAATGTCATTGATCATTTTTTCTGTGACATGTATCCCTTATTGAAA  
 CTGGCCTGCAGTACACCCATGTTATGGCCTCTTAGTGGTGGCCAATGGAGGACTGTCTT  
 GCACTATTGCGTTTCTGCTCTTACTCATCTCTTATGGTGTGTCATCTGCACTCTCTAAAGAAA  
 55 CTTAGTCAGAAAGGGAGGCAAAAAGCCCACTCAACCTGCAGTTCCACATCACTGTGGTTG  
 TCTTCTTCTTTGTTCTTGTATTTTTATGTGTGCTAGACCTGCTAGGACCTTCTCCATTGAC

AAATCAGTGAGTGTGTTTTATACAGTCATAACCCCAATGCTGAACCCCTTAATCTACACTC  
TGAGAAATTCTGAGATGACAAGTGCTATGAAGAAGCTTTAG (SEQ ID NO: 42)

**AOLFR22 sequences:**

5 MRXXNXXTEFVLLGFSQDPGVXKALFVMFLLTYXXTVVGNLLIVVDIIASPLXGSPMYFFLAC  
LSFIDAAYSTTISPKLIVGLFCDKKTISFQCGMGQLFIDHFFGGAEVFLLVVMACDRYVAICKPL  
HYLTIMNRQVCFLLLVXXMIGGFVHSAFQIVVYSLPFCGPXVIVHFSCDMHPLLELACTDTYFI  
GLTVVVNSGAICMVIFNLLISYGVILSSLKYSQEKRGKALSTCSSGSTVVVLFVPCIFIYVRP  
10 VSNFPTDKFMTVFYTIITHMLSPLIYTLRNSEMRNAIEKLLGKKLTIFIHGGVSVLM (SEQ ID NO:  
43)

ATGAGACANNNNNAACAATATNACAGAATTTGTCCTCCTGGGCTTTTCTCAGGATCCTGGTG  
TGNNNAAAGCATTATTTGTCATGTTTTACTCACATAACNNNNNACAGTGGTGGGGAACT  
15 GCTCATTGTNGTGGATATTATTGCCAGCCCTINNTTGGGTTCCTCCAATGTATTTCTTCCTTG  
CCTGCCTGTCAATTTATAGATGCTGCATATCCACTACCATTTCTCCCAAGTTAATTGTAGGC  
TTATTCTGTGATAAAAAGACTATTTCTTCCAAGGTTGCATGGGCCAGCTATTTATAGACC  
ATTTCTTTGGTGGGGCTGAGGCTCTTCTTCTGGTGGTGATGGCCTGTGATCGCTATGTGGC  
CATCTGTAAGCCACTGCACTATTTGACCATCATGAATCGACAGGTTTGCTTCTCTGTGG  
20 TNNTNNCCATGATTGGAGGTTTTGTACATTCTGCGTTTCAAATTGTTGTGTACAGTCTCCCT  
TTCTGTGGTCCCNATGTCATTGTTTCATTTCAAGTTGTGACATGCACCCATTACTGGAAGTGGC  
ATGCACTGACACCTACTTTATAGGCCTCACTGTTGTTGTCAATAGTGGAGCAATCTGTATG  
GTCATTTTCAACCTTCTGTAAATCTCCTATGGAGTCATCCTAAGCTCCCTTAAACTTACAG  
TCAGGAAAAGAGGGGTAAAGCCTTGTCTACCTGCAGCTCCGGCAGTACCGTTGTTGTCTC  
25 TTTTTGTACCCTGTATTTTCATATATGTTAGACCTGTTTCAAACCTTCTACTGATAAGTT  
CATGACTGTGTTTTATACCATTATCACACACATGCTGAGTCCTTTAATATATACGTTGAGA  
AATTCAGAGATGAGAAATGCTATAGAAAACTCTTGGGTAAAAAGTTAACTATATTTATTA  
TAGGAGGAGTGTCCGTCCTCATGTAG (SEQ ID NO: 44)

**AOLFR23 sequences:**

30 MAKNNLTRVTEFILMGFMDHPKLEIPLFLVFLSFYLVTLGNVGMIMLIQVDVKLYTPMYFFLS  
HLSLLDACYTSVITPQILATLATGKTVISYGHCAAQFFLFTICAGTECFLLAVMAYDRYAAIRNP  
LLYTVAMNPRLCWSLVVGAYVCGVSGAILRTTCTFTLSFCKDNQINFFCDLPPLKLACSDTA  
NIEIVIFFGNFVILANASVILISYLLIKTILKVKSSGGRAKTFSTCASHITAVAFFGALIFMYLQS  
35 GSGKSLEEDKVVSVFYTVVIPMLNPLIYSLRNKDVKDAFRKVARRLQVSLSM (SEQ ID NO: 45)

ATGGCCAAGAATAATCTCACCAGAGTAACCGAATTCATTCTCATGGGCTTTATGGACCACC  
CCAAATTGGAGATTCCCCTCTTTCTGGTGTCTTCTGAGTTTCTACCTAGTCACCCTTCTTGGG  
AATGTGGGGATGATTATGTTAATCCAAGTAGATGTCAAACCTCTACACCCCAATGTACTTCT  
40 TCTGAGCCACCTCTCCCTGCTGGATGCTGTACACCTCAGTCATCACCCCTCAGATCCTA  
GCCACATTGGCCACAGGCAAAACGGTCATCTCCTACGGCCACTGTGCTGCCAGTTCTTTT  
TATTCACCATCTGTGCAGGCACAGAGTGCTTTCTGCTGGCAGTGATGGCCTATGATCGCTA  
TGCTGCCATTGCAACCCACTGCTCTATACCGTGGCCATGAATCCCAGGCTCTGCTGGAGC  
CTGGTGGTAGGAGCCTATGTCTGTGGGGTGTGAGGAGCCATCCTGCGTACCCTTGCACCT  
TCACCCCTCTCCTTCTGTAAGGACAATCAAATAAACTTCTTCTTCTGTGACCTCCCACCCCTG  
45 CTGAAGCTTGCTGCAGTGACACAGCAAACATCGAGATTGTCATCATCTTCTTTGGCAATT  
TTGTGATTTTGGCCAATGCCTCCGTATCCTGATTTCCTATCTGCTCATCATCAAGACCATT  
TTGAAAGTGAAGTCTTCAGGTGGCAGGGCCAAGACTTTCTCCACATGTGCCTCTCACATCA  
CTGCTGTGGCCCTTTTCTTTGGAGCCCTTATCTTCATGTATCTGCAAAGTGGCTCAGGCAAA  
TCTCTGGAGGAAGACAAAGTCGTGTCTGTCTTCTATACAGTGGTCATCCCCATGCTGAACC  
50 CTCTGATCTACAGCTTAAGAAACAAAGATGTAAAAGACGCCTTCAGAAAGGTCGCTAGGA  
GACTCCAGGTGTCCCTGAGCATGTAG (SEQ ID NO: 46)

**AOLFR25 sequences:**

55 METGNLTWVSDFVFLGLSQTRELQRFLFLMFLFVYITTVMGNILIITVTSDSQLHTPMYFLLRN  
LAVLDLCFSSVTPKMLVDLLSEKKTISYQCGMGQIFFHFLGGAMVFFLSVMAFDRLIAISRPL  
RYVTVMNTQLWVGLVVATWVGGFVHSIVQLALMLPLPFCGPNILDNFYCDVPQVRLACTDT

SLLEFLKISNSGLLDVVWFLLMSYLFILVMLRSHPGEARRKAASTCTTHIIVVSMIFVPSIYLY  
ARPFPTFPMDKLVSIGHTVMTPMLNPMIYTLRNQDMQAAVRRLGRHRLV (SEQ ID NO: 47)

5 ATGGAAACAGGGAACCTCACGTGGGTATCAGACTTTGTCTTCCTGGGGCTCTCGCAGACTC  
GGGAGCTCCAGCGTTTCCTGTTTCTAATGTTCCCTGTTTGTCTACATCACCAGTGTATGGGA  
AACATCCTTATCATCATCACAGTGACCTCTGATTCCTCAGCTCCACACACCCATGTACTTTCT  
GCTCCGAAAACCTGGCTGTCTAGACCTCTGTTTCTCTTCAGTCACTGCTCCCAAAATGCTAG  
TGGACCTCCTCTCTGAGAAGAAAACCATCTCTTACCAGGGCTGCATGGGTGAGATCTTCTT  
10 CTTCCACTTTTTGGGAGGTGCCATGGTCTTCTTCCTCTCAGTGATGGCCTTTGACCGCCTCA  
TTGCCATCTCCCGGCCCTCCGCTATGTCAACGTCATGAACACTCAGCTCTGGGTGGGGCT  
GGTGGTAGCCACCTGGGTGGGAGGCTTTGTCCACTCTATTGTCCAGCTGGCTCTGATGCTC  
CCACTGCCCTTCTGTGGCCCAACATTTTGATAAATTCTACTGTGATGTTCCCAAGTACT  
GAGACTTGCTGCACTGACACCTCACTGCTGGAGTTCCTCAAGATCTCCAACAGTGGGCTG  
15 CTGGATGTGCTCTGGTCTTCTCCTCCTCTGATGTCCTACTTATTCATCCTGGTGATGCTGAG  
GTCACATCCAGGGGAGGCAAGAAGGAAGGCAGCTTCCACCTGCACCAACCACATCATCGT  
GGTTTCCATGATCTTCGTTCCAAGCATTTACCTCTATGCCCGGCCCTTCACTCCATTCCCTA  
TGGACAAGCTTGTGTCCATCGGCCACACAGTCATGACCCCATGCTCAACCCCATGATCTA  
TACCTGAGGAACAGGACATGCAGGCAGCAGTGAGAAGATTAGGGAGACACCGGCTGGT  
20 TTGA (SEQ ID NO: 48)

**AOLFR26 sequences:**

MAAKNSSVTEFILEGLTHQPGLRIPFLFLGFYTVTVVGNLGLITLIGLNSHLHTPMYFFLFNLS  
LIDFCSTTTTPKMLMSFVSRKNISFTGCMTQLFFCFVVSSEFILLSAMAYDRYVAICNPLLYT  
VTMSCQVCLLLLGA YGMGFAGAMAHTGSIMNLTFCADNLVNHFMCDILPLELSCNSSYMN  
25 ELVVFTVAVDVGMPIVTVFISYALILSSILHNSSTEGRSKAFSTCSSHIIVVSLFFGSGAFMYLKP  
LSILPLEQKGVSSLFYTHVPVLNPLIYSLRNKDVKVALRRTLGRKIFS (SEQ ID NO: 49)

30 ATGGCAGCCAAAACTCTTCTGTGACAGAGTTTATCCTCGAAGGCTTAACCCACCAGCCGG  
GACTGCGGATCCCCCTCTTCTTCCTGTTTCTGGGTTCCTACACGGTCACCGTGGTGGGGAA  
CCTGGGCTTGATAACCCCTGATTGGGCTGAACCTCTCACCTGCACACTCCCATGTACTTCTTCC  
TTTTTAACCTCTCTTTAATAGATTTCTGTTTCTCCACTACCATCACTCCCAAAATGCTGATG  
AGTTTTGTCTCAAGGAAGAACATCATTTCTTTCACAGGGTGTATGACTCAGCTCTTCTTCTT  
CTGCTTCTTTGTGCTCTCTGAGTCCTTCATCCTGTCAGCGATGGCGTATGACCGCTACGTGG  
35 CCATCTGTAACCCACTGTTGTACACAGTCACCATGTCTTGCCAGGTGTGTTTGCTCCTTTTG  
TTGGGTGCCTATGGGATGGGGTTTGTCTGGGGCCATGGCCACACAGGAAGCATAATGAAC  
CTGACCTTCTGTGCTGACAACCTTGTCATATGAGCTGGTGGTCTTTATTGTTGGTGGCTGTTGAC  
GCTCTCCTGCAACAGCTCTTACATGAATGAGCTGGTGGTCTTTATTGTTGGTGGCTGTTGAC  
GTTGGAATGCCATTGTCACTGTCTTTATTTCTTATGCCCTCATCCTCTCCAGCATTCTACA  
CAACAGTTCTACAGAAGGCAGGTCCAAAGCCTTTAGTACTTGCAATTCCACATAATTGTA  
40 GTTTCTCTTTTCTTTGGTCTGGTGTCTTCATGTATCTCAAACCCCTTTCCATCCTGCCCTC  
GAGCAAGGGAAGTGTCTCCTGTTCTATACCATAATAGTCCCGTGTAAACCCATTAA  
TCTATAGCTTGAGGAACAAGGATGTCAAAGTTGCCCTGAGGAGAACTTTGGGCAGAAAAA  
TCTTTTCTTAA (SEQ ID NO: 50)

**AOLFR27 sequences:**

45 MPSQNYSISEFNLFGFSAFPQHLLPILFLLYLLMFLFTLLGNLLIMATTWIEHRLHTPMYFLCTL  
SVSEILFTVAITPRMLADLLSTHHSITFVACANQMFFSFMFGFTHSFLLLVMGYDRYVAICHPLR  
YNVLMSPRDCAHLVACTWAGGSVMGMMVTTTFVHLTFCGSNVIHHFFCHVLSLLKLACENKT  
SSVIMGVMVLCVTALIGCLFLILSYVFIVAAILRIPSABGRHKTFSTCVSHLTVVVTHYSFASFIY  
50 LKPKGLHSMYS DALMATTYTVTFPLSPIIFSLRNKBLKNAINKNFYRKFCPPSS (SEQ ID NO:  
51)

55 ATGCCTAGTCAGAACTATAGCATCATATCTGAATTTAACCTCTTTGGCTTCTCAGCCTTCCC  
CCAGCACCTCCTGCCATCTTGTTCCTGCTGTACCTCCTGATGTTCTGTTACATTGCTGG  
GCAACCTTCTCATCATGGCCACAATCTGGATTGAACACAGACTCCACACACCCATGTACCT  
CTTCTTGTGCACCTCTCCGTCTCTGAGATTCTGTTCACTGTTGCCATCACCCCTCGCATGC

TGGCTGATCTGCTTTCCACCCATCATTCCATCACCTTTGTGGCTTGTGCCAACCAGATGTTT  
TTCTCCTTCATGTTTGGCTTCACTCACTCCTTCCTTCTCCTGGTCATGGGCTATGATCGCTA  
TGTGGCCATCTGCCACCCACTGCGTTACAATGTGCTCATGAGCCCCCGTGA CTGTGCCCAT  
CTTGTGGCCTGTACCTGGGCTGGTGGCTCAGTCATGGGGATGATGGTGACAACGATAGTTT  
5 TCCACCTCACTTTCTGTGGGTCTAATGTGATCCACCATT TTTTCTGTGTCATGTGCTTTCCCTCT  
TGAAGTTGGCCTGTGAAAACAAGACATCATCTGTATCATGCGGTGTGATGCTGGTGTGTGT  
CACAGCCCTGATAGGCTGTTTATTCCTCATCATCCTCTCCTATGTCTTCATTGTGGCTGCCA  
TCTTGAGGATTCCCTCTGCCGAAGGCCGACACAAGACATTTTCTACGTGTGTATCCACCT  
CACTGTGGTGGTCACGCACTATAGTTTTCCTCCTTTATCTACCTCAAGCCCAAGGGCCTCC  
10 ATTCTATGTACAGTGACGCCTTGATGGCCACCACCTATACTGTCTTCACCCCTTCTTAGC  
CCAATCATTTTCAGCCTAAGGAACAAGGAGCTGAAGAATGCCATAAATAAAAACTTTTACA  
GAAAATTCTGTCTCCAAGTTCCTGA (SEQ ID NO: 52)

**AOLFR28 sequences:**

15 MPNFTDVTEFTLLGLTCRQELQVLFVFLAVYMITLLGNIGMILISISPQLQSPMYFFLSHLSF  
ADVCFSNNVTPKMLENLLSETKTISYVGCLVQCYFFIAVVHVEVYLAVMAFDHYMAGCXPLL  
YGSKMSRTVCVRLISVXYXYGFSVSLICTLWYGLYFCGNFEINH FYCADPPLIQIACGRVHIKE  
ITMVIAGINFTYSLSVLISYTLIVAVLRMRSADGRRKAFSTCGSHLTA VSMFYGTPIFMYLR  
RPTEESVEQGMVA VFYTTVIPMLNPMIYSLRNKDVKEAVNKAITKTYVRQ (SEQ ID NO: 53)

20 ATGCCTAATTTACGGATGTGACAGAATTTACTCTCCTGGGGCTGACCTGTCTCGTCAGGAGC  
TACAGGTTCTCTTTTTTGTGGTGTTCCTAGCGGTTACATGATCACTCTGTTGGGAAATATT  
GGTATGATCATTTTGATTAGCATCAGTCCTCAGCTTCAGAGTCCCATGTACTTTTTCTGAG  
TCATCTGTCTTTTGGCGACGTGTGCTTCTCCTCCAACGTTACCCCAAAATGCTGGA AAAACT  
25 TATTATCAGAGACAAAAACCATTTCCTATGTGGGATGCTTGGTGCAGTGCTACTTTTTTCAT  
TGCCGTTGTCCACGTGGAGGTCTATATCCTGGCTGTGATGGCCTTTGACAGGTACATGGCC  
GGCTGCAANCCTCTGCTTTATGGCAGTAAAATGTCTAGGACTGTGTGTGTTCCGGCTCATCT  
CTGTGNNNTATGNNNTATGGATTCTCTGTCAGCCTAATATGCACACTATGGACTTATGGCTT  
ATACTTCTGTGGA AACTTTGAAATCAATCACTTCTATTGTGCAGATCCCCCTCTCATCCAGA  
30 TTGCCTGTGGGAGAGTGACATCAAAGAAATCACAATGATTGTTATTGCTGGAATTAACCTT  
CACATATTCCTCTCGGTGGTCCTCATCTCCTACACTCTCATTGTAGTAGCTGTGCTACGCA  
TGCGCTCTGCCGATGGCAGGAGGAAGCGGTTCTCCACCTGTGGGTCCCACTGACGGCTGT  
TTCTATGTTTTATGGGACCCCATCTTCATGTATCTCAGGAGACCCACTGAGGAATCCGTA  
GAGCAGGGCAAAATGGTGGCTGTGTTTTACACCACAGTAATTCCTATGTTGAATCCCATGA  
35 TCTACAGTCTGAGAAATAAGGATGTAAAAGAAGCAGTCAACAAAGCAATCACCAAGACAT  
ATGTGAGGCAGTAA (SEQ ID NO: 54)

**AOLFR29 sequences:**

40 MMSFAPNASHSPVFLLLGFSTRANISYTLFFLEFLA IYLTTLGNVTLVLLISWDSRLHSPMYYLLR  
GLSVIDMGLSTVTL PQLLAHLVSHYPTIPAARCLAQFFFFYA FGVTDTLVIAVMALDRYVAICD  
PLHYALVMNHQRCACLLALSWVVSILHTMLRVGLVPLCWTGDAGGNVNLPHFFCDHRPLL R  
ASCSDIHSNELAIFFE GGFMLGPCALIVLSYVRIGAAILRLPSAAGRRAVSTCGSHLTMVGFL  
YGTIICVYFQPPFQNSQYQDMVASVMYTAITPLANPFVYSLHNKDVKGALCRLLEWVKVDP  
(SEQ ID NO: 55)

45 ATGATGAGCTTTGCCCTAATGCTTCACACTCTCCGGTTTTTTTGCTCCTTGGGTTCTCGAG  
AGCTAACATCTCCTACACTCTCCTCTTCTTCTCCTGTTCTCTGGCTATTTACCTGACCACCATA C  
TGGGGAATGTGACACTGGTGTCTGCTCATCTCCTGGGACTCCAGACTGCACTCACC CATGTA  
TTATCTGCTTCGTGGCCTCTCTGTGATAGACATGGGGCTATCCACAGTTACACTGCCCCAG  
50 TTGCTGGCCCATTTGGTCTCTCATTACCCAACCATTCCTGCTGCCCGCTGCTTGGCTCAGTT  
CTTTTTCTTCTATGCATTTGGGGTTACAGATACTTGTCTATTGCTGTCTGCTGCTGATC  
GCTATGTGGCCATCTGTGACCCCTGCACTATGCTTGGTAATGAATCAACCAACGGTGTGC  
CTGCTTACTAGCCTTGAGCTGGGTGGTGTCCATACTGCACACCATGTTGCGTGTGGGACTC  
GTCCTGCCTCTTTGCTGGACTGGGGATGCTGGGGGCAACGTTAACCTTCTCACTTCTTTTG  
55 TGACCACCGGCCACTTCTGCGAGCCTCTTGTCTGACATACATTCTAATGAGCTGGCCATA  
TTCTTTGAGGGTGGCTTCCTTATGCTGGGCCCCCTGTGCCCTCATTGTACTCTCTTATGTCCG

AATTGGGGCCGCTATTCTACGTTTGCCTTCAGCTGCTGGTCGCCGCCGAGCAGTCTCCACC  
TGTGGATCCCACCTCACCATGGTTGGTTTCTCTACGGCACCATCATTGTGTCTACTTCCA  
GCCTCCCTTCCAGAACTCTCAGTATCAGGACATGGTGGCTTCAGTAATGTATACTGCCATT  
ACACCTTTGGCCAACCCATTTGTGTATAGCCTCCACAATAAGGATGTCAAGGGTGCACCTCT  
5 GCAGGCTGCTTGAATGGGTGAAGGTAGACCCTGA (SEQ ID NO: 56)

**AOLFR30 sequences:**

MGFLSPMHPCRPPTQRRMAAGNHSTVTEFILKGLTKRADLQLPLFLLFLGIYLVTVGNLGMT  
LICLNSQLHTPMYYFLSNLSLMDLCYSSVITPKMLVNFVSEKNISYAGCMSQLYFFLVFVIAEC  
10 YMLTVMAYDRYVXXCHPLLYNIIMSHHTCLLLVAVVYAIGLIGSTIETGLMLKLPYCEHLISHY  
FCDILPLMKLSCSSYTDVEMTVFFSAGFNIVTSLTVLVSYTFILSSILGISTTEGRSKAFSTCSSHL  
AAVGMFYGSTAFMYLKPSTISSLTQENVASVFYTTVIPMLNPLIYSLRNKEVKAAVQKTLRGK  
LF (SEQ ID NO: 57)

15 ATGGGGTTCTTGTCTCCCATGCATCCCTGCAGGCCTCCCACCCAGAGGAGAATGGCTGCAG  
GAAATCACTCTACAGTGACAGAGTTTCTTCAAGGGTTTAAACGAAGAGAGCAGACCTCC  
AGCTCCCCCTCTTTCTCCTCTTCTCGGGATCTACTTGGTCACCATCGTGGGGAACCTGGGC  
ATGATCACTCTAATTTGTCTGAACTCTCAGCTGCACACCCCATGTACTACTTTCTCAGCAA  
TCTGTCACTCATGGATCTCTGCTACTCCTCCGTCAATTACCCCTAAGATGCTGGTGAACTTTG  
20 TGTCAGAGAAAAACATCATCTCCTACGCAGGGTGCATGTCACAGCTCTACTTCTTCTTGT  
TTTTGTCAATTGCTGAGTGTTACATGCTGACAGTGATGGCCTACGACCGCTATGTTGNCNTC  
TGCCACCCCTTGTCTTACAACATCATTATGTCTCATCACCTGCCTGCTGCTGGTGGCTGT  
GGTCTACGCCATCGGACTCATTGGCTCCACAATAGAACTGGCCTCATGTTAAAACTGCC  
TATTGTGAGCACCTCATCAGTCACTACTTCTGTGACATCCTCCCTCTCATGAAGCTGTCCTG  
25 CTCTAGCACCTATGATGTTGAGATGACAGTCTTCTTTTCGGCTGGATTCAACATCATAGTC  
ACGAGCTTAACAGTCTTGTGTTTCTTACACCTTCATTCTCTCCAGCATCCTCGGCATCAGCAC  
CACAGAGGGGAGATCCAAAGCCTTCAGCACCTGCAGCTCCACCTTGCAGCCGTGGGAAT  
GTTCTATGGATCAACTGCATTCATGTACTTAAACCCTCCACAATCAGTTCCTTGACCCAG  
GAGAATGTGGCCTCTGTGTTCTACACCACGGTAATCCCCATGTTGAATCCCTAATCTACA  
30 GCCTGAGGAACAAGGAAGTAAAGGCTGCCGTGCAGAAAACGCTGAGGGGTAAACTGTTTT  
GA (SEQ ID NO: 58)

**AOLFR31 sequences:**

MGTGNDTTVVEFTLLGLSEDTTVCAILFLVFLGIYVVTLMGNISIVLIRRSHTLHTPMYIFLCHL  
35 AFVDIGYSSSVTPVMLMSFLRKETSLPVAGCVAQLCSVVTFGTAEFCFLAAMAYDRYVAICSP  
LLYSTCMSPGVCILVGMSSYLGGCVNAWTFIGCLLRSLFCGPNKVNHFCDYSPLLKLACSHDF  
TFEIPAISSGSIVATVCVIAISYIYLITILKMHSTKGRHKAFTCTSHLTAVTLFYGTITFIYVMP  
KSSYSTDQNKVVSVFYTVVIPMLNPLIYSLRNKEIKGALKRELRIKIFS (SEQ ID NO: 59)

40 ATGGGGACTGGAAATGACACCACTGTGGTAGAGTTTACTCTTTTGGGGTTATCTGAGGATA  
CTACAGTTTGTGCTATTTTATTTCTTGTGTTTCTAGGAATTTATGTTGTACCTTAATGGGT  
AATATCAGCATAATTGTATTGATCAGAAGAAGTCAATCATCTTCATACACCCATGTACATTT  
TCCTCTGCCATTTGGCCTTTGTAGACATGGGTACTCCTCATCAGTCACACCTGTATGCTC  
45 ATGAGCTTCTAAGGAAAGAAACCTCTCTCCCTGTTGCTGGTTGTGTGGCCAGCTCTGTT  
CTGTAGTGACGTTTGGTACGGCCGAGTGCTTCTGCTGGCTGCCATGGCCTATGATCGCTA  
TGTGGCCATCTGCTCACCCCTGCTCTACTCTACCTGCATGTCCCCTGGAGTCTGCATCATCT  
TAGTGGGCATGTCCTACCTGGGTGGATGTGTGAATGCTTGGACATTCAATTGGCTGCTTATT  
AAGACTGTCTTCTGTGGGCCAAATAAAGTCAATCACTTTTTCTGTGACTATTACCACTTT  
TGAAGCTTGCTTGTTCCTCATGATTTTACTTTTGAATAATTCAGCTATCTCTTCTGGATCT  
50 ATCATTGTGGCCACTGTGTGTGTCATAGCCATATCTACATCTATATCTCATCACCATCCT  
GAAGATGCACTCCACCAAGGGCCGCCACAAGGCCTTCTCCACCTGCACCTCCACCTCACT  
GCAGTCACTCTGTTCTATGGGACCATTACCTTCATTTATGTGATGCCAAAGTCCAGCTACTC  
AACTGACCAGAACAAGGTGGTGTCTGTGTTCTACACCGTGGTGATTCCCATGTTGAACCCC  
CTGATCTACAGCCTCAGGAACAAGGAGATTAAGGGGGCTCTGAAGAGAGAGCTTAGAATA  
55 AAAATATTTTCTTGA (SEQ ID NO: 60)

**AOLFR32 sequences:**

MNSLKDGNHTALTGFILLGLTDDPILRVILFMILSGNLSIHLIRISSQLHHPMYFFLSHLAFADM  
 AYSSSVTPNMLVNFLVERNTVSYLGCAIQLGSAAFFATVECVLLAAMAYDRFVAICSPLLYSTK  
 MSTQVSVQLLLVVYIAGFLIAVSYTTSFYLLFCGPNQVNHFFCDFAPLLELSCSDISVSTVVLSF  
 5 SSGSIIVVTVCVIAVCYIYILITILKMRSTEGHHKAFSTCTSHLTVVTLFYGTITFIYVMPNFSYST  
 DQNKVVSVLYTVVIPMLNPLIYSLRNKEIKGALKRELVRKILSHDACYFSRTSNNIT (SEQ ID  
 NO: 61)

ATGAATTCCCTGAAGGACGGGAATCACACCGCTCTGACGGGGTTCATCCTATTGGGCTTAA  
 10 CAGATGATCCAATCCTTCGAGTCATCCTCTTCATGATCATCCTATCTGGTAATCTCAGCATA  
 ATTATTCTTATCAGAATTTCTTCTCAGCTCCATCATCCTATGTATTTCTTTCTGAGCCACTT  
 GGCTTTTGCTGACATGGCCTATTCATCTTCTGTGCACACCCAACATGCTTGAAACCTTCCTGG  
 TGGAGAGAAAATACAGTCTCCTACCTTGGATGTGCCATCCAGCTTGGTTCAGCGGCTTTCTT  
 TGCAACAGTGAATGCGTCCTTCTGGCTGCCATGGCCTATGACCGCTTTGTGGCAATTTGC  
 15 AGTCCACTGCTTTATTCAACCAAAATGTCCACACAAGTCAGTGTCCAGCTACTCTTAGTAG  
 TTTACATAGCTGGTTTTCTCATTGCTGTCTCCTATACTACTTCTTCTATTTTTTACTCTTCT  
 GTGGACCAAAATCAAGTCAATCATTTTTCTGTGATTTTCGCTCCCTTACTTGAACCTCTCCTGT  
 TCTGATATCAGTGTCTCCACAGTTGTTCTCTCATTTTCTTCTGGATCCATCATTGTGGTCAC  
 TGTGTGTGTATAGCCGCTCTGCTACATCTATATCCTCATCACCATCCTGAAGATGCGCTCCA  
 20 CTGAGGGGACCAACAAGGCCTTCTCCACCTGCACTTCCACCTCACTGTGGTTACCCTGTT  
 CTATGGGACCATTACCTTCATTTATGTGATGCCCAATTTTAGCTACTCAACTGACCCAGAAC  
 AAGGTGGTGTCTGTGTTGTACACAGTGGTGATTCCCATGTTGAACCCCTGATCTACAGCC  
 TCAGGAACAAGGAGATTAAGGGGGCTCTGAAGAGAGAGCTTGTAGAAAAATACTTTCTC  
 ATGATGCTTGTATTATTTAGTAGAACTTCAAATAATGATATTACATAG (SEQ ID NO: 62)

25

**AOLFR34 sequences:**

MLEGVEHLLLLLLTDVNSKELQSGNQTSVSHFILVGLHPPQLGAPLFLAFLVITYLLTVSGNG  
 LIILTVLVDIRLHRPMCLFLCHLSFLDMTISCAIVPKMLAGFLLGSRIISFGGCVIQLFSFHFLGCT  
 ECFLYTLMAYDRFLAICKPLHYATIMTHRVCSNLALGTWLGGTIHSFLQTSFVFRLPFCGPNRV  
 30 DYIFCDIPAMRLACADTAINELVTFADIGFLALTCFMLILTSYGYIVAAILRIPSADGRRNAFST  
 CAAHLTVVIVYVPCTFIYLRPCSQEPLDGVVAVFYTVITPLLSIHYTLCNKEMKAALQRLGG  
 HKEVQPH (SEQ ID NO: 63)

ATGTTAGAGGGTGTGAGCATCTCCTTCTGCTACTTCTTTTGACAGATGTGAACAGCAAGG  
 35 AACTGCAAAGTGGAACAGACTTCTGTGTCTCACTTCATTTTGGTGGGCCTGCACCAACC  
 ACCACAGCTGGGAGCGCCACTCTTCTTAGCTTTTCTTGTGCTATCTCCTCACTGTTTCTG  
 GAAATGGGCTCATCATCCTCACTGTCTTAGTGACATCCGGCTCCATCGTCCCATGTGCTT  
 GTTCTGTGTACCTCTCCTTCTTGGACATGACCAATTTCTTGTGCTATTGTCCCAAGATGC  
 TGGCTGGCTTTTCTTGGGTAGTAGGATATCTCCTTTGGGGCTGTGTAATCCAACTATTT  
 40 TCTTTCCATTTCTGGGCTGTAAGTGTCTTCTTTACACACTCATGGCTTATGACCGTTT  
 CCTTGCCATTTGTAAGCCCTTACACTATGCTACCATCATGACCCACAGAGTCTGTAACCTCCC  
 TGGCTTTAGGCACCTGGCTGGGAGGGACTATCCATTCACTTTTCCAAACAAGTTTGTATT  
 CCGGCTGCCCTTCTGTGGCCCCAATCGGGTCGACTACATCTTCTGTGACATTCTGCCATGC  
 TGCGTCTAGCCTGCGCCGATACGGCCATCAACGAGCTGGTCACCTTTGCAGACATTGGCTT  
 45 CCTGGCCCTCACCTGCTTCATGCTCATCCTCACTTCTATGGCTATATTGTAGCTGCCATCC  
 TGCGAATTCGCTCAGCAGATGGGCGCCGCAATGCCTTCTCACTTGTGCTGCCACCTCAC  
 TGTGTGCTATTGTTTACTATGTGCCCTGCACCTTCATTTACCTGCGGCCCTGTTTACAGGAGC  
 CCCTGGATGGGGTGGTAGCTGTCTTTACACTGTCTCACTCCCTTGCTTAACTCCATCATC  
 TACACACTGTGCAACAAAGAAATGAAGGCAGCATTACAGAGGCTAGGGGGCCACAAGGAA  
 50 GTGCAGCCTCACTGA (SEQ ID NO: 64)

**AOLFR35 sequences:**

MEPLNRTEVEFFLKGFSGYPALHLLFPLCSAMYLVLTLLGNTAIMAVSVLDIHLHTPVYFFLG  
 NLSTLDICYTPTFVPLMLVHLLSSRKTIISFAVCAIQMCLSLSTGSTECLLLAITAYDRYLAICQPL  
 55 RYHVLMSHRLCVLLMGAAWVLCLLKSVTEMVISMRLPFCGHHVVSHTCKILAVLKLACGNT  
 SVSEDFLLAGSILLPVPLAFICLSYLLILATILRVPSAARCKAFSTCLAHLAVVLLFYGTIIFMY

LKPKSKEAHISDEVFTVLYAMVTTMLNPTTYSLRNKEVKEAARKVWGRSRASR (SEQ ID NO: 65)

5 ATGGAGCCGCTCAACAGAACAGAGGTGTCCGAGTTCTTTCTGAAAGGATTTTCTGGCTACC  
CAGCCCTGGAGCATCTGCTCTTCCCTCTGTGCTCAGCCATGTACCTGGTGACCCCTCCTGGG  
GAACACAGCCATCATGGCGGTGAGCGTGCTAGATATCCACCTGCACACGCCCGTGTACTTC  
TTCCTGGGCAACCTCTCTACCCTGGACATCTGCTACACGCCACCTTTGTGCTCTGATGCT  
GGTCCACCTCCTGTATCCCGGAAGACCATCTCCTTTGCTGTCTGTGCCATCCAGATGTGTC  
10 TGAGCCTGTCCACGGGCTCCACGGAGTGCCTGCTACTGGCCATCACGGCCTATGACCGCTA  
CCTGGCCATCTGCCAGCCACTCAGGTACCACGTGCTCATGAGCCACCGGCTCTGCGTGCTG  
CTGATGGGAGCTGCCTGGGTCTCTGCCTCCTCAAGTCGGTGACTGAGATGGTCATCTCCA  
TGAGGCTGCCCTTCTGTGGCCACCACGTGGTCAGTCACCTCACCTGCAAGATCCTGGCAGT  
GCTGAAGCTGGCATGCGGCAACACGTGCGTCAGCGAAGACTTCCTGCTGGCGGGCTCCAT  
15 CCTGCTGCTGCCTGTACCCCTGGCATTCTGCTGCTGCTACTTGTCTATCCTGGCCACCA  
TCCTGAGGGTGCCCTCGGCCGCCAGGTGCTGCAAAGCCTTCTCCACCTGCTTGGCACACCT  
GGCTGTAGTGCTGCTTTTCTACGGCACCATCATCTTCATGTACTTGAAGCCCAAGAGTAAG  
GAAGCCACATCTCTGATGAGGTCTTACAGTCCTCTATGCCATGGTCACGACCATGCTGA  
ACCCACCATCTACAGCCTGAGGAACAAGGAGGTGAAGGAGGCCGCCAGGAAGGTGTGGG  
GCAGGAGTCGGGCCTCCAGGTGA (SEQ ID NO: 66)

20

**AOLFR36 sequences:**

MYLVTVLRNLLSILAVSSDSHPHTPMYFFLSNLCWADIGFTLATVPKMIVDMGSHSKVISYGG  
CLTQMSFLVLFACIVDMFLTVMAYDCFVAICRPLHYPVIVNPHLCVFFVLVSFFLSLLDSQLHS  
WIVLQFTFFKNVEISNFVCEPSQLKLASYDSVINSIFYDNTMFGFLPISGILLSYKIVPSILRIS  
25 SSDGKYKAFSACGCHLAVVCLFYGTGIGVYLTSAVAPPLRNGMVASVMYAVVTPMLNPFYIS  
LRNRDIQSALWRVCNKTVESHDLFHPFSCVVEKGQPHSIPTSANPAP (SEQ ID NO: 67)

30 ATGTATCTGGTCACGGTGCTGAGGAACCTGCTCAGCATCCTGGCTGTGAGCTCTGACTCCC  
ACCCACACACCCATGTACTTCTTCTCTCCAACTGTGCTGGGCTGACATCGGTTTCACC  
TTGGCCACGGTTCCCAAAATGATTGTGGACATGGGGTCGCATAGCAAAGTCATCTCTTATG  
GGGGCTGCCTGACACAGATGTCTTTCTTGGTACTTTTTGCATGTATAGTAGACATGTTCTT  
GACTGTGATGGCTTATGACTGCTTTGTAGCCATCTGTCGCCCTCTGCACTACCCAGTCATC  
GTGAATCCTCACCTCTGTGTCTTCTTCGTTTTGGTGCTCTTTTCTTAGCCTGTTGGATTCC  
35 CAGCTGCACAGTTGGATTGTGTTACAATTCACCTTCTTCAAGAATGTGGAAATCTCTAATT  
TTGTCTGTGAGCCATCTCAACTTCTCAAGCTTGCTCTTATGACAGCGTCATCAATAGCATA  
TTCATATATTTTGATAATACTATGTTTGGTTTTCTTCCCATTTTACGGGATCCTTTTGTCTTAC  
TATAAAATTGTCCCCTCCATTCTAAGGATTTTCATCATCAGATGGGAAGTACAAAGCCTTCT  
CAGCCTGTGGCTGTACCTGGCAGTTGTTTGCTTATTTATGGAACAGGCATTGGCGTGTA  
CCTGACTTCAGCTGTGGCACCACCCCTCAGGAATGGTATGGTGGCGTCAGTGATGTACGCT  
40 GTGGTCACCCCATGCTGAACCTTTTCATCTACAGCCTGAGAAACAGGGACATTCAAAGTG  
CCCTGTGGAGGGTGTGCAACAAACAGTCGAATCTCATGATCTGTTCCATCCTTTTTCTTG  
TGTGGTTGAGAAAGGGCAACCACATTCAATCCCTACATCTGCAAATCCTGCCCTTAG  
(SEQ ID NO: 68)

45 **AOLFR37 sequences:**

MEKANETSPVMGFVLLRLSAHPELEKTFVLLIMYLVILLGNGVLILVTILDSRLHTPMYFFLG  
NLSFLDICFTTSSVPLVLDSTLPQETISFSACAVQMAISFAMAGTECLLSMMAFDYVAICNP  
LRYSVIMSKAAYMPMAASSWAIGGAASVVHTSLAIQLPFCGDNVINHFTCEILAVLKLACADIS  
INVISMEVTNVIFLGVPLFISFSYVFHTTILRIPSAEGRKKVFSTCSAHLTVVIVFYGTLLFFMYG  
50 KPKSKDSMGADKEDLSDKLPLFYGVVTPMLNPIIYSLRNKDVKA AVRLLRPGKFTQ (SEQ ID  
NO: 69)

55 ATGGAAAAAGCCAATGAGACCTCCCCTGTGATGGGGTTCGTTCTCCTGAGGCTCTCTGCCC  
ACCCAGAGCTGGAAAAGACATTCTTCTGCTCATCCTGCTGATGTACCTCGTGATCCTGCT  
GGGCAATGGGGTCCTCATCCTGGTGACCATCCTTGACTCCCGCCTGCACACGCCCATGTAC  
TTCTTCTAGGGAACCTCTCCTTCTGACATCTGCTTCACTACCTCCTCAGTCCCACTGGT

CCTGGACAGCTTTTGGACTCCCCAGGAAACCATCTCCTTCTCAGCCTGTGCTGTGCAGATG  
 GCACTCTCCTTTGCCATGGCAGGAACAGAGTGCTTGCTCCTGAGCATGATGGCATTGATC  
 GCTATGTGGCCATCTGCAACCCCTTAGGTACTCCGTGATCATGAGCAAGGCTGCCTACAT  
 GCCCATGGCTGCCAGCTCCTGGGCTATTGGTGGTGTGCTTCCGTGGTACACACATCCTTG  
 5 GCAATTCAGCTGCCCTTCTGTGGAGACAATGTCAACCACTTCACCTGTGAGATTCTGG  
 CTGTTCTAAAGTTGGCCTGTGCTGACATTTCCATCAATGTGATCAGCATGGAGGTGACGAA  
 TGTGATCTTCTAGGAGTCCCGGTTCTGTTTCATCTCTTCTCCTATGTCTTCATCATACCA  
 CCATCCTGAGGATCCCCCTCAGCTGAGGGGAGGAAAAAGGTCTTCTCCACCTGCTCTGCCCCA  
 CCTCACCGTGGTGATCGTCTTCTACGGGACCTTATTCTTCATGTATGGGAAGCCTAAGTCT  
 10 AAGGACTCCATGGGAGCAGACAAAGAGGATCTTTCAGACAAACTCATCCCCCTTTTCTATG  
 GGGTGGTGACCCCGATGCTCAACCCCATCATCTATAGCCTGAGGAACAAGGATGTGAAGG  
 CTGCTGTGAGGAGACTGCTGAGACCAAAAGGCTTCACTCAGTGA (SEQ ID NO: 70)

**AOLFR38 sequences:**

15 MYLVTVLRLNLLILAVSSDSLHTPMCFFLSNLCWADIGFTSAMVPMKIVDMQSHSRVISYAGC  
 LTQMSFFVLFACIEDMLLTVMAYDRFVAICHPLHYPVIMNPHLGVLVLVSFFLSLLDSQLHSW  
 IVLQFTFFKNVEISNFVCDPSQLNLACSDSVINSIFYLDSIMFGFLPISGILLSYANNVPSILRISS  
 SDRKSKAFSTCGSHLAVVCLFYGTGIGVYLTSAVSPPPRNGVVASVMYAVVTPMLNPFYISLR  
 NRDIQSALWRLRSRTVESHDLLSQDLLHPFSCVGEKGQPH (SEQ ID NO: 71)

20 ATGTACCTGGTCACGGTGCTGAGGAACCTGCTCATCATCCTGGCTGTCAGCTCTGACTCCC  
 ACCTCCACACCCCCATGTGCTTCTTCTCTCCAACCTGTGCTGGGCTGACATCGGTTTCACC  
 TCGGCCATGGTTCCCAAGATGATTGTGGACATGCAGTCGCATAGCAGAGTCATCTCTTATG  
 CGGGCTGCCTGACACAGATGTCTTCTTGTCTTTTGCATGTATAGAAGACATGCTCCTG  
 25 ACAGTGATGGCCTATGACCGATTTGTGGCCATCTGTACCCCCCTGCACTACCCAGTCATCA  
 TGAATCCTCACCTTGGTGTCTTCTTAGTTTTGGTGTCTTTTCTCCTCAGCCTGTTGGATTCC  
 CAGCTGCACAGTTGGATTGTGTTACAATTCACCTTCTTCAAGAATGTGGAAATCTCCAATT  
 TTGTCGTGACCCATCTCAACTTCTCAACCTTGCTGTCTGACAGTGTATCAATAGCATA  
 TTCATATATTTAGATAGTATTATGTTTGGTTTTCTTCCCATTTACAGGGATCCTTTTGTCTTAC  
 30 GCTAACAAATGTCCCTCCATTCTAAGAATTCATCATCAGATAGGAAGTCTAAAGCCTTCT  
 CCACCTGTGGCTCTCACCTGGCAGTTGTTGCTTATTTATGGAACAGGCATTGGCGTGTA  
 CCTGACTTCAGCTGTGTCAACACCCCCAGGAATGGTGTGGTGGCATCAGTGATGTACGCT  
 GTGGTCACCCCATGCTGAACCTTTTCATCTACAGCCTGAGAAATAGGGACATTCAAAGTG  
 CCCTGTGGAGGCTGCGCAGCAGAACAGTCGAATCTCATGATCTGTTATCTCAAGATCTGCT  
 35 CCATCCTTTTTCTTGTGTGGGTGAGAAAGGTCAACCACATTAA (SEQ ID NO: 72)

**AOLFR39 sequences:**

40 MGVKNHSTVTEFLLSGLTEQABLQPLFLFLGIYTVTVVGNLSMISIIRLNRLHTPMYYFLSS  
 LSFLDFCYSSVITPKMLSGFLCRDRSISYSGCMIQLFFFCVVCVISECYMLAAMACDRYVAICSP  
 LYRVIMSPRVCSLLVAAVFSVGFTDAVIHGGCILRLSFCGSNIKHXYFCDIVPLIKLSCSSTYIDEL  
 LIFVIGGFNMVATSLTIISYAFILTSILRIHKKGRCKAFSTCSSHLTAVLMFYGSLMSMYLKPAS  
 SSSLTQEKVSSVFYTTVILMLNPLIYSLRNNEVRNALMKLLRRKISLSPG (SEQ ID NO: 73)

45 ATGGGTGTAAAAAACCATTCCACAGTGACTGAGTTTCTTCTTTCAGGATTAACCTGAACAAG  
 CAGAGCTTCAGCTGCCCCTCTTCTGCCTCTTCTTAGGAATTTACACAGTTACTGTGGTGGG  
 AAACCTCAGCATGATCTCAATTATTAGGCTGAATCGTCAACTTCATACCCCATGTAATAT  
 TTCCTGAGTAGTTTGTCTTTTTTAGATTCTGCTATTCTTCTGTCAATTACCCCTAAATGCT  
 ATCAGGGTTTTATGCAGAGATAGATCCATCTCCTATTCTGGATGCATGATTACAGCTGTTTT  
 TTTTCTGTGTTTGTGTTATTTCTGAATGCTACATGCTGGCAGCCATGGCCTGCGATCGCTAC  
 50 TTGGCCATCTGCAGCCCACTGCTCTACAGTGCTCATGCTGCCCTAGGGTCTGTTCTCTGC  
 TGGTGGCTGCTGTCTTCTCAGTAGGTTTCACTGATGCTGTGATCCATGGAGGTTGTATACT  
 CAGGTTGTCTTTCTGTGGATCAAACATCATTAACATTATTTCTGTGACATTGTCCCTCTTA  
 TTAACCTCTCCTGCTCCAGCACTTATATTGATGAGCTTTTGATTTTTGTCAATTGGTGGATTT  
 AACATGGTGGCCACAAGCCTAACAATCATTATTTTCATATGCTTTTATCCTCACCAGCATCCT  
 55 GCGCATCCACTCTAAAAAGGGCAGGTGCAAAGCGTTTAGCACCTGTAGCTCCACCTGACA  
 GCTGTTCTTATGTTTTATGGGTCTCTGATGTCCATGTATCTCAAACCTGCTTCTAGCAGTTC



ACTCACCAGGAGAAAGTATCCTCAGTATTTTATACCACTGTGATTCTCATGTTGAATCCC  
TTGATATATAGTCTGAGGAACAATGAAGTAAGAAATGCTCTGATGAAACTTTTAAGAAGA  
AAAATATCTTTATCTCCAGGATAA (SEQ ID NO: 74)

5 **AOLFR40 sequences:**

MSNATLLTAFILTGLPHAPGLDAPLFGIFLVVYVLTVLGNLLILLVIRVDSHLHTPMYYFLTNL  
FIDMWFSTVTVPKMLMTLVSPSGRTISFHSCVAQLYFFHFLGSTECFLYTVMSYDRYLAISYPL  
RYTNMMTGRSCALLATGTWLSGSLHSAVQILTFFHLPYCGPNQIQHYFCDAPPILKLACADTS  
ANEMVIFVNIGLVASGCFVLIVLSYVSIVCSILRIRTSEGRHRAFQTCASHCIVLFCFFGPGFLFIYL  
10 RPGSRDALHGVVAVFYTTLTPLFNPVVYTLRNEVKKALLKLKNGSVFAQGE (SEQ ID NO:  
75)

ATGTCCAACGCCACCCTACTGACAGCGTTTCATCCTCACGGGCCTTCCCCATGCCCCAGGGC  
TGGACGCCCCCTCTTTGGAATCTTCCTGGTGGTTTACGTGCTCACTGTGCTGGGGAACCT  
15 CCTCATCCTGCTGGTGATCAGGGTGGATTCTCACTCCACACCCCCATGTACTACTTCTCTCA  
CCAACCTGTCTTCAITGACATGTGGTTCTCCACTGTACGGGTGCCCAAATGCTGATGAC  
CTTGGTGTCCCCAAGCGGCAGGACTATCTCCTTCCACAGCTGCGTGGCTCAGCTCTATTTTT  
TCCACTTCTGGGGAGCACCGAGTGTTCCTCTACACAGTCATGTCCTATGATCGCTACCT  
GGCCATCAGTTACCGCTCAGGTACACCAACATGATGACTGGGCGCTCGTGTGCCCTCCTG  
20 GCCACCGGCACTTGGCTCAGTGGCTCTCTGCACTCTGCTGTCCAGACCATATTGACTTTCC  
ATTTGCCCTACTGTGGACCCAACCAGATCCAGCACTACTTCTGTGACGCACCGCCCATCCT  
GAAACTGGCCTGTGCAGACACCTCAGCCAACGAGATGGTCATCTTTGTGAATATTGGGCTA  
GTGGCCTCGGGCTGCTTTGTCTGATAGTGTCTCTATGTGTCCATCGTCTGTTCCATCCT  
GCGGATCCGCACCTCAGAGGGGAGGCACAGAGCCTTTCAGACCTGTGCCCTCCCACTGTATC  
25 GTGGTCTTTGCTTCTTTGGCCCTGGTCTTTTCATTTACCTGAGGCCAGGCTCCAGGGACGC  
CTTGCACTGGGGTTGTGGCCGTTTTCTACACCACGCTGACTCCTCTTTTCAACCCTGTTGTGT  
ACACCCTGAGAAACAAGGAGGTAAAGAAAGCTCTGTTGAAGCTGAAAAATGGGTCAGTAT  
TTGCTCAGGGTGAATAG (SEQ ID NO: 76)

30 **AOLFR41 sequences:**

MNPENWTQVTSFVLLGFPSSHLLIQFLVFLGLMVITYVTATGKLLIIVLSWIDQRLHIQMYFFLRN  
FSFLELLLVTVVVPKMLVVILTGDHTISFVSCIHSYLYFFLGTTDFLLAVMSLDYLAICRPLR  
YETLMNGHVCSQLVLASWLAGFLWVLCPTVLMASLPFCGPNIDHFFRDSWPLRLRLSCGDTH  
LLKLVAFMLSTLVLLGSLALTSVSYACILATVLRAPTAERRKAFSTCASHLTVVVVHYGSSIFLY  
35 IRMSEAQSKLLNKGASVLSCHITPLNPFIFTLRNDKVQQAALREALGWPRLTAVMKLRVTSQRK  
(SEQ ID NO: 77)

ATGAACCCTGAAAACCTGGACTCAGGTAACAAGCTTTGTCTTCTGGGTTTCCCCAGTAGCC  
ACCTCATACAGTTCTGCTGTTCTGGGGTTAATGGTGACCTACATTGTAACAGCCACAGG  
40 CAAGCTGCTAATTATTGTGCTCAGCTGGATAGACCAACGCCTGCACATACAGATGTACTTC  
TTCTGCGGAATTTCTCTTCTGGAGCTGTTGCTGGTAACCTGTTGTGGTTCCCAAGATGCT  
TGTCGTCATCCTCACGGGGGATCACACCATCTCATTTGTCAGCTGCATCATCCAGTCTTACC  
TCTACTTCTTTCTAGGCACCACTGACTTCTTCTCTTGGCCGTCATGTCTCTGGATCGTTAC  
CTGGCAATCTGCCGACCACTCCGCTATGAGACCCTGATGAATGGCCATGTCTGTTCCCAAC  
45 TAGTGCTGGCCTCCTGGCTAGCTGGATTCTCTGGGTCTTTGCCCACTGTCTCATGGCC  
AGCCTGCCTTTCTGTGGCCCCAATGGTATTGACCACTTCTTTCGTGACAGTTGGCCCTTGCT  
CAGGCTTTCTGTGGGGACACCCACCTGCTGAAACTGGTGGCTTTTCATGCTCTCTACGTTG  
GTGTTACTGGGCTCACTGGCTCTGACCTCAGTTTCTCTATGCCTGCATTCTTGCCACTGTTCT  
CAGGGCCCCTACAGCTGCTGAGCGAAGGAAAGCGTTTTCCACTGCGCCTCGCATCTTACA  
50 GTGGTGGTCATCATCTATGGCAGTTCCATCTTTCTCTACATTCTGATGTGAGAGGCTCAGTC  
CAAACCTGCTCAACAAAGGTGCCTCCGTCCTGAGCTGCATCATCACACCCTCTTGAACCA  
TTCATCTTCACTCTCCGCAATGACAAGGTGCAGCAAGCACTGAGAGAAGCCTTGGGGTGGC  
CCAGGCTCACTGCTGTGATGAAACTGAGGGTCACAAGTCAAAGGAAATGA (SEQ ID NO:  
78)

55

**AOLFR42 sequences:**

MNPANHSQVAGFVLLGLSQVWELRFVFFTVFSAVYFMTVVGNLLIVVIVTSDPHLHTTMYFLL  
 GNLSFLDFCYSSITAPRMLVDLLSGNPTISFGGCLTQLFFFHFIGGIKIFLLTVMAYDRYIAISQPL  
 HYTLIMNQTVCALLMAASWVGGFHSIVQIALTIQLPFCGPKLDNFYCDVPQLIKLACTDTFV  
 5 LELLMVSNNGLVTLMCFLVLLGSYTAALLVMLRSHSREGRSKALSTCASHIAVVTLIFVPCITYVY  
 TRPFRFTFMDKAVSVLYTIVTPMLNPAIYTLRNKEVIMAMKKLWRRKKDPIGPLEHRPLH  
 (SEQ ID NO: 79)  
  
 ATGAATCCAGCAAATCATTCCCAGGTGGCAGGATTTGTTCTACTGGGGCTCTCTCAGGTTT  
 10 GGGAGCTTCGGTTTGTCTTCTCACTGTTTTCTCTGCTGTGTATTTATGACTGTAGTGGGA  
 AACCTTCTTATTGTGGTCATAGTGACCTCCGACCCACACCTGCACACAACCATGTATTTCT  
 CTTGGGCAATCTTTCTTCTCGGACTTTTGCTACTCTTCCATCACAGCACCTAGGATGCTGG  
 TTGACTTGCTCTCAGGCAACCTACCATTTCCCTTTGGTGGATGCCTGACTCAACTCTTCTTC  
 TTCCACTTCATTGGAGGCATCAAGATCTTCTGCTGACTGTCTATGGCGTATGACCGCTACA  
 15 TTGCCATTTCCCAGCCCCTGCACTACACGCTCATTATGAATCAGACTGTCTGTGCACTCCTT  
 ATGGCAGCCTCCTGGGTGGGGGGCTTCATCCACTCCATAGTACAGATTGCATTGACTATCC  
 AGCTGCCATTCTGTGGGCCTGACAAGCTGGACAACCTTTTATTGTGATGTGCCTCAGCTGAT  
 CAAATTGGCCTGCACAGATACTTTGTCTTAGAGCTTTTAATGGTGTCTAACAATGGCCTG  
 GTGACCTGATGTGTTTTCTGGTGCTTCTGGGATCGTACACAGCACTGCTAGTCATGCTCC  
 20 GAAGCCACTCACGGGAGGGCCGAGCAAGGCCCTGTCTACCTGTGCCTCTCACATTGCTGT  
 GGTGACCTTAATCTTTGTGCCTTGCACTACGTCTATACAAGGCCCTTTTCGGACATCCCCA  
 TGGACAAGGCCGTCTCTGTGCTATACACAATTGTACCCCCATGCTGAATCCTGCCATCTA  
 TACCCTGAGAAACAAGGAAGTGATCATGGCCATGAAGAAGCTGTGGAGGAGGAAAAAGG  
 ACCCTATTGGTCCCCTGGAGCACAGACCCTTACATTAG (SEQ ID NO: 80)

25

**AOLFR43 sequences:**

MQKPQLLVPIIATSNGNLVHAAFYLLVGIPGLGPTIHFWLAFPLCFMYALATLGNLTIVLIIRVE  
 RRLHEPMYLFLAMLSTIDLVLSSITMPKMASLFLMGIQIEIFNICLAQMFLIHSAVESAVLLA  
 MAFDRFVAICHPLRHASVLTGCTVAKIGLSALTRGFVFFFLPFILKWLSCYQHTVTHSFCLHQ  
 30 DIMKLSCTDTRVNVVYGLFIILSVMGVDSLFIGFSYILILWAVLELSSRAALKAFNTCISHLCAV  
 LVFYVPLIGLSVVHRLGGPTSLHVVMMANTYLLLPPVVNPLVYGAKTKEICSRVLCMFSSQGGK  
 (SEQ ID NO: 81)

ATGCAGAAGCCCCAGCTCTTGGTCCCTATCATAGCCACTTCAAATGGAAATCTGGTCCACG  
 35 CAGCATACTTCCTTTTGGTGGGTATCCCTGGCCTGGGGCCTACCATACACTTTTGGCTGGCT  
 TTCCCACTGTGTTTTATGTATGCCTTGGCCACCCTGGGTAACCTGACCATTGTCCTCATCAT  
 TCGTGTGGAGAGGCGACTGCATGAGCCCATGTACCTCTTCTGGCCATGCTTTCCACTATT  
 GACCTAGTCCTCTCCTCTATCACCATGCCCAAGATGGCCAGTCTTTCTGTATGGGCATCCA  
 GGAGATCGAGTTCAACATTTGCCTGGCCAGATGTTCTTATCCATGCTGTGACCCGCTG  
 40 GAGTCAGCTGTCTGCTGGCCATGGCTTTTGACCGCTTTGTGGCCATTTGCCACCCATTGC  
 GCCATGCTTCTGTGCTGACAGGGTGTACTGTGGCCAAGATTGGACTATCTGCCCTGACCAG  
 GGGGTTTGTATTCTTCTTCCCACTGCCCTTCATCCTCAAGTGGTTGTCCTACTGCCAAACAC  
 ATACTGTACACACTCCTTCTGTCTGCACCAAGATATTATGAAGCTGTCTGTACTGACAC  
 CAGGGTCAATGTGGTTTATGGACTCTTCATCATCCTCTCAGTCATGGGTGTGGACTCTCTCT  
 45 TCATTGGCTTCTCATATATCCTCATCCTGTGGGCTGTTTTGGAGCTGTCTCTCGGAGGGCA  
 GCACTCAAGGCTTTCAACACCTGCATCTCCACCTCTGTGCTGTTCTGGTCTTCTATGTACC  
 CCTCATTTGGGCTCTCGGTGGTGCATAGGCTGGGTGGTCCCACCTCCCTCCTCATGTGGTT  
 ATGGCTAATACTACTTGTCTGCTACCACTGTAGTCAACCCCTTGTCTATGAGGCCAAGA  
 CCAAAGAGATCTGTTCAAGGGTCTCTGTATGTTCTCACAAGGTGGCAAGTGA (SEQ ID  
 50 NO: 82)

**AOLFR44 sequences:**

MSSCNFTHATFVLIGIPGLEKAHFWVGFPLLSMYVVMFNGNCIVVFIVRTERS LHAPMYLFLC  
 MLAADLALSTSTMPKILALFWFDSREISFEACLTQMFFIHLSAIESTILLAMAFDRYVAICHPL  
 55 RHAAVLNNTVTAQIGIVAVVRGSLFFFLPLLKRLAFCHSNVLSHSYCVHQDVMKLAYADTLP  
 NVVYGLTAILLVMGVDVMFISLSYFLIIRTVLQLPSKSERAKAFGTCVSHIGVVLAIFYVPLIGLS

VVHRFGNSLHPIVRVVMGDIYLLPVPINPIYGA TKQIRTRVLAMFKISCDKDLQAVGGK  
(SEQ ID NO: 83)

5 ATGAGTTCCTGCAACTTCACACATGCCACCTTTGTGCTTATTGGTATCCCAGGATTAGAGA  
AAGCCCATTTCTGGGTTGGCTTCCCCCTCCCTTCCATGTATGTAGTGGCAATGTTTGAAAC  
TGCATCGTGGTCTTCATCGTAAGGACGGAACGCAGCCTGCACGCTCCGATGTACCTCTTTC  
TCTGCATGCTTGCAGCCATTGACCTGGCCTTATCCACATCCACCATGCCTAAGATCCTTGCC  
CTTTTCTGGTTTGATTCCCGAGAGATTAGCTTTGAGGCCTGTCTTACCCAGATGTTCTTTAT  
10 TCATGCCCTCTCAGCCATTGAATCCACCATCCTGTGCTGGCCATGGCCTTTGACCGTTATGTGG  
CCATCTGCCACCCACTGCGCCATGCTGCAGTGCTCAACAATACAGTAACAGCCAGATTGG  
CATCGTGGCTGTGGTCCGCGGATCCCTCTTTTTTTTCCCACTGCCTCTGCTGATCAAGCGGC  
TGGCCTTCTGCCACTCCAATGTCCTCTCGCACTCCTATTGTGTCCACCAGGATGTAATGAA  
GTTGGCCTATGCAGACACTTTGCCAATGTGGTATATGGTCTTACTGCCATTCTGCTGGTC  
ATGGGCGTGGACGTAATGTTTCATCTCCTTGTCTATTTTCTGATAATACGAACGGTTCTGC  
15 AACTGCCTTCCAAGTCAGAGCGGGCCAAGGCCTTTGGAACCTGTGTGTACACATTGGTGT  
GGTACTCGCCTTCTATGTGCCACTTATTGGCCTCTCAGTGGTACACCGCTTTGGAACAGC  
CTTCATCCCATTTGTGCGTGTGTGTCATGGGTGACATCTACCTGCTGCTGCCTCCTGTCATCAA  
TCCCATCATCTATGGTGCCAAAACCAACAGATCAGAACACGGGTGCTGGCTATGTTCAAG  
ATCAGCTGTGACAAGGACTTGCAAGGCTGTGGGAGGCAAGTGA (SEQ ID NO: 84)

20

**AOLFR45 sequences:**

MLPSNITSTHPAVFLLVGIPGLEHLHAWISIPFCFAYTLALLGNCTLLFIIQADAALHEPMYLFLA  
MLATIDLVLSSSTLTPKMLAIFWFRDQEINFACLVQMFFLHSFSIMESAVLLAMAFDRYVAICKP  
LHYTTVLTGSLITKIGMAAVARA VTLMTPLPFLRRFHYCRGPVIAHCYCEHMAVVRACGDT  
25 SFNNIYGIAVAMFSVVDLLFVLSYVFILQAVLQLASQEARYKAFGTCVSHIGAILSTYTPVVIS  
SVMHRVARHAAPRVHILLAIFYLLFPPMVNPIYGVKTKQIREYVLSLFQRKNM (SEQ ID NO:  
85)

30 TGGAACAAGAGGTAATCTTTGCAGGTGGGATAGCACAGGTTGAACTCTAATCATATATA  
CTGTAGAAGGTATATATAGAAGGTGAAGAAGCCCTGTAAAAATTGACAAGGAGATTTCCA  
GGAGCCATGCTTCCCTCTAATATCACCTCAACACATCCAGCTGTCTTTTTGTGGTAGGAAT  
TCCTGGTTTGGAACACCTGCATGCCTGGATCTCCATCCCCTTCTGCTTTGCTTATACTCTGG  
CCCTGCTAGGCAACTGTACCCTTCTCTTCATTATCCAGGCTGATGCAGCCCTCCATGAACCC  
ATGTACCTCTTCTGGCCATGTTGGCAACCATTGACTTGGTTCTTTCTTCTACAACGCTGCC  
35 CAAAATGCTTGCCATATTCTGGTTCAGGGATCAGGAGATCAACTTCTTTGCCTGTCTGGTC  
CAGATGTTCTTCCCTCACTCCTTCTCCATCATGGAGTCAGCAGTGCTGCTGGCCATGGCCTT  
TGACCGCTATGTGGCCATCTGCAAGCCATTGCACTACACGACGGTCTGACTGGGTCCCTC  
ATCACCAAGATTGGCATGGCTGCTGTGGCCCGGGCTGTGACACTAATGACTCCACTCCCT  
TCCTGCTCAGACGCTTCCACTACTGCCGAGGCCAGTGATTGCCCATGCTACTGTGAACA  
40 CATGGCTGTGGTAAGGCTGGCGTGTGGGGACACTAGCTTCAACAATATCTATGGCATTGCT  
GTGGCCATGTTTAGTGTGGTGTGGACCTGCTCTTTGTTATCCTGTCTTATGCTTCATCCT  
TCAGGCAGTTCTCCAGCTTGCTCTCAGGAGGCCCGCTACAAAGCATTGTTGGGACATGTGTG  
TCTACATAGGTGCCATCCTGTCCACCTACACTCCAGTAGTCATCTCTTCAGTCATGCACCG  
TG TAGCCCGCCATGCTGCCCCCTCGTGTCCACATACTCCTTGCTATTTTCTATCTCCTTTTCC  
45 CACCCATGGTCAATCCTATCATATATGGAGTCAAGACCAAGCAGATTTCGTGAGTATGTGCT  
CAGTCTATTCCAGAGAAAGAACATGTAGATGGATAGTTCTCTTTTTTATCCCACTTGCCA  
AGTAATGAGAATGCTGGATTGGGGTTGAGGGGAAAAATCTAAATAGGAAAATTGCAGAGT  
ATCTTTGACAATTCTCTAGTATGATAAGGAAAAATGAGGTTTCATTCTCACAGATCTACGA  
GTCAGGTCAAACCAGGAGTGACCTATAGTCTGGTCTGATAGTAGAGGTTTGACCTTCCCA  
50 TTGTCATAGACTCATCACATGGCTAAGGAAGACAAACCTCTCAAAGTGGTATTGTAATCTG  
GGTGAAAGACAGTAGGACCTTTATTGGCTGAGATTGGCCCAAACAGCTGAGTC (SEQ ID  
NO: 86)

**AOLFR46 sequences:**

55 MNIKHCGWHMIHTWLNIREDDSDDFKNFIGIQGLSGNPHSTTSRMYFLCFCTSLLGFKVHVW  
SRLIXKLYMASPNNDSTAPVSEFLICFPNFQSWQHWLSLPLSLLFLLAMGANTLLITIQLEAS

LHQPLYYLLSLLSLLDIVLCLTVIPKVLAIWFDFLRSISFPACFLQMFIMNSFLTMESECTFMVMA  
YDRYVAICHPLRYPSTIDQFVARAVVFVIARNAFVSLPVMLSARLRYCAGNIKNKICNSLSVS  
KLSCDDITFNQLYQFVAGWTLLGSDLLIVISYSFILKVVLRIKAEGAVAKALSTCGSHFILIFFS  
TVLLVLVTNLARKRIPDPVILLNLHLLIPPALNPVYGVRTKEIKQGIQNLKRL (SEQ ID NO:  
5 87)

ATGAATATAAAACATTGTGGCTGGCATATGATACATACTTGGTTAAATATAAGGGAGGAT  
GATGACAGTGATTTTAAAAAATTTATTGGACAGATACAGGGCCTCAGTGGAAACCCACACT  
CTACTACGTCTAGAATGTACTTTTTATGTTTCTGTACTTCTCTACTAGGTTTTAAGGTACAC  
10 TGGGTCTCCAGATTGATCANGAACTTTACATATGGCATCTCCCAACAATGACTCCACTGCCC  
CAGTCTCTGAATTCCTCCTCATCTGCTTCCCAACTCCAGAGCTGGCAGCACTGGTTGTCT  
CTGCCCTCAGCCTTCTCTTCTCCTGGCCATGGGAGCTAACACCACCCTCCTGATCACCAT  
CCAGCTGGAGGCCTCTCTGCACCAGCCCCTGTACTACCTGCTCAGCCTCCTCTCCCTGCTGG  
ACATCGTGCTCTGCCTCACCGTCATCCCCAAGGTCCTGGCCATCTTCTGGTTTTGACCTCAGG  
15 TCGATCAGCTTCCCAGCCTGCTTCTCCAGATGTTTCATCATGAACAGTTTTTTGACCATGGA  
GTCCTGCACGTTTCATGGTCATGGCCTATGACCGTTATGTGGCCATCTGCCATCCATTGAGA  
TACCCGTCTATCATCACTGACCAGTTTGTGGCTAGGGCCGTGGTCTTTGTTATAGCCCGGA  
ATGCCCTTGTCTCTTCTCCTGTTCCCATGCTTCTGCCAGGCTCAGATACTGTGCAGGAAAC  
ATAATCAAGAACTGCATCTGCAGTAACCTGTCTGTGTCCAACTCTCTTGATGACATCA  
20 TTTCAATCAGCTCTACCAAGTTTGTGGCAGGCTGGACTCTGTTGGGCTCATCTTATCCTT  
ATTGTTATCTCCTATTCTTTTATATTGAAAGTTGTGCTTAGGATCAAGGCCGAGGGTGCTGT  
GGCCAAGGCCCTGAGCACGTGTGGTTCACCTTCATCCTCATCCTCTTCTTCAGCACAGTCC  
TGCTGGTTCTGGTCATCACTAACCTGGCCAGGAAGAGAATTCTCCAGATGTCCCCATCCT  
GCTCAACATCCTGCACCACCTCATTCCCCAGCTCTGAACCCCATGTTTATGGTGTGAGA  
25 ACCAAGGAGATCAAGCAGGGAATCCAAAACCTGCTGAAGAGGTTGTAA (SEQ ID NO: 88)

#### AOLFR47 sequences:

MSASNITLTHPTAFLLVGIPGLEHLHIWISIPFCLAYTLALLGNCTLLLIQADAALHEPMYLFLA  
MLAAIDLVLSSALPKMLAIFWFRDREINFFACLAQMFFLHSFSIMESAVLLAMAFDRYVAICK  
30 PLHYTKVLTGSLITKIGMAAVARAVTLMTPFLRLCFHYCRGPVIAHCYCEHMAVVRACGD  
TSFNNTYGLIIVAMFIVVLDLLLVILSYIFILQAVLLASQEARYKAFGTCVSHIGAILAFYTTVVIS  
SVMHRVARHAAPHVHILLANFYLLFPPMVNPIYGVKTKQIRESILGVFPRKDM (SEQ ID NO:  
89)

ATGTCAGCCTCCAATATCACCTTAACACATCCAACCTGCCTTCTTGTGGTGGGGATTCCAG  
GCCTGGAACACCTGCACATCTGGATCTCCATCCCTTTCTGCTTAGCATATACACTGGCCCTG  
CTTGAAACTGCACTCTCCTTCTCATCATCCAGGCTGATGCAGCCCTCCATGAACCCATGT  
ACCTCTTCTGGCCATGTTGGCAGCCATCGACCTGGTCCTTTCTCCTCAGCACTGCCAA  
ATGCTTGCCATATTCTGGTTCAGGGATCGGGAGATAAACTTCTTTGCCTGTCTGGCCCAGA  
40 TGTCTTCTTCACTCCTTCTCCATCATGGAGTCAGCAGTGCTGCTGGCCATGGCCTTTGAC  
CGCTATGTGGCTATCTGCAAGCCACTGCACTACACCAAGGTCCTGACTGGGTCCTCATCA  
CCAAGATTGGCATGGCTGCTGTGGCCCGGGCTGTGACACTAATGACTCCACTCCCCTTCT  
GCTGAGATGTTTCCACTACTGCCGAGGCCAGTGATCGCTCACTGCTACTGTGAACACATG  
GCTGTGGTGAGGCTGGCGTGTGGGGACACTAGCTTCAACAATATCTATGGCATCGCTGTGG  
45 CCATGTTTATTGTGGTGTGGACCTGCTCCTTGTATCCTGTCTTATATCTTTATCTTCAG  
GCAGTTCTACTGCTTGCCTCTCAGGAGGCCCGCTACAAGGCATTTGGGACATGTGTCTCTC  
ATATAGGTGCCATCTTAGCCTTCTACACAACCTGTGGTCATCTCTTCAGTCATGCACCGTGA  
GCCCGCCATGCTGCCCCTCATGTCCACATCCTCCTTGCCAATTTCTATCTGCTCTTCCCACC  
CATGGTCAATCCCATATCTATGGTGTCAAGACCAAGCAAATCCGTGAGAGCATCTTGGGA  
50 GTATTCCCAAGAAAGGATATGTAG (SEQ ID NO: 90)

#### AOLFR48 sequences:

MMVDPNGNESSATYFILIGLPGLEEAQFWLAFPLCSLYLIAVLGNLTITYIVRTEHSLHEPMYIFL  
CMLSGIDILISTSSMPKMLAIFWFNSTTIQFDACLLQMFIAHSLSGMESTVLLAMAFDRYVAICH  
55 PLRHATVLTLPRTKIGVAAVVRGAALMAPLPVFIKQLPFCRSNLSHSYCLHQDVMKLACDDI  
RVNVVYGLIVISAIGLDSLISFSYLLILKTVLGLTREAAKAFGTCVSHVCAVFIFYVPFIGLSM

VHRFSKRRDSPLPVILANIYLLVPPVLNPVYGVKTKRILRLRFHVATHASEP (SEQ ID NO: 91)

5 ATGATGGTGGATCCCAATGGCAATGAATCCAGTGCTACATACTTCATCCTAATAGGCCTCC  
CTGGTTTAGAAGAGGCTCAGTTCTGGTTGGCCTTCCCATTGTGCTCCCTCTACCTTATTGCT  
GTGCTAGGTAACCTTGACAATCATCTACATTGTGCGGACTGAGCACAGCCTGCATGAGCCCA  
TGTATATATTTCTTTGCATGCTTTCAGGCATTGACATCCTCATCTCCACCTCATCCATGCCC  
AAAATGCTGGCCATCTTCTGGTTCAATTCCACTACCATCCAGTTTGATGCTTGTCTGCTACA  
GATGTTTGGCATCCACTCCTTATCTGGCATGGAATCCACAGTGCTGCTGGCCATGGCCTTTT  
10 GACCGCTATGTGGCCATCTGTCAACCACTGCGCCATGCCACAGTACTTACGTTGCCTCGTG  
TCACCAAAATTGGTGTGGCTGCTGTGGTGGGGGGGCTGCACTGATGGCACCCCTTCCTGT  
CTTCATCAAGCAGCTGCCCTTCTGCCGCTCCAATATCCTTTCCCATTCCTACTGCCTACACC  
AAGATGTCATGAAGCTGGCCTGTGATGATATCCGGGTCAATGTCGTCTATGGCCTTATCGT  
CATCATCTCCGCCATTGGCCTGGACTCACTTCTCATCTCCTTCTCATATCTGCTTATTCTTA  
15 AGACTGTGTTGGGCTTGACACGTGAAGCCCAGGCCAAGGCATTTGGCACTTGCGTCTCTCA  
TGTGTGTGCTGTGTTTATATTCTATGTACCTTTCATTGGATTGTCCATGGTGCATCGCTTTA  
GCAAGCGGCGTGACTCTCCGCTGCCCGTCATCTTGGCCAATATCTATCTGCTGGTTCCTCCT  
GTGCTCAACCCAATTGTCTATGGAGTGAAGACAAAGGAGATTGACAGCGCATCCTTCGA  
CTTTTCCATGTGGCCACACACGCTTCAGAGCCCTAG (SEQ ID NO: 92)

20

**AOLFR49 sequences:**

MLTFHNVCSVPSSFVLTGIPGLES�HVWLSIPFGSMYLVAVVGNVTILAVVKIERSLHQPMYFF  
LCMLAAIDLVLSTSTIPKLLGIFWFGACDIGLDA CLGQMFLIHC FATVESGIFLAMAFDRYVAIC  
NPLRHSMVLTYTVVGRGLVSLRGVLYIGPLPLMRLRLPLYKTHVISHSYCEHMAVVALTC  
25 GDSRVNNVYGLSIGFLVLILDSVAIAASYVMIFRAVMGLATPEARLKT LGTCASHLCAILIFYVP  
IAVSSLIHRFGQCVPPPVTLLANFYLLIPPILNPVYAVRTKQIRESLLQIPRIEMKIR (SEQ ID  
NO: 93)

30 ATGCTCACTTTTCATAATGTCTGCTCAGTACCCAGCTCCTTCTGGCTCACTGGCATCCCAGG  
GCTGGAGTCCCTACACGCTGGCTCTCCATCCCCCTTGGCTCCATGTACCTGGTGGCTGTG  
GTGGGGAATGTGACCATCCTGGCTGTGGTAAAGATAGAACGCAGCCTGCACCAGCCCATG  
TACTTTTTCTTGTGCATGTTGGCTGCCATTGACCTGGTTCTGTCTACTTCCACTATACCCAA  
ACTTCTGGGAATCTTCTGGTTCGGTGCTTGTGACATTGGCCTGGACGCCTGCTTGGGCCAA  
ATGTTCTTATCCACTGCTTTGCCACTGTTGAGTCAGGCATCTTCCTTGCCATGGCTTTTGA  
35 TCGCTACGTGGCCATCTGCAACCCACTACGTCATAGCATGGTGCTCACTTATACAGTGGTG  
GGTGGTTTGGGGCTTGTCTCTCCTCCGGGGTGTCTCTACATTGGACCTCTGCCTCTGAT  
GATCCGCTGCGGCTGCCCTTTATAAAACCCATGTTATCTCCACTCCTACTGTGAGCAC  
ATGGCTGTAGTTGCCTTGACATGTGGCGACAGCAGGGTCAATAATGTCTATGGGCTGAGC  
ATCGGCTTTCTGGTGTGATCCTGGACTCAGTGGCTATTGCTGCATCCTATGTGATGATTTT  
40 CAGGGCCGTGATGGGGTTAGCCACTCCTGAGGCTAGGCTTAAACCCCTGGGGACATGCGC  
TTCTCACCTCTGTGCCATCCTGATCTTTTATGTTCCCATTTGCTGTTTCTTCCCTGATTACCG  
ATTTGGTCAGTGTGTGCCTCCTCCAGTCCACACTCTGCTGGCCAACCTTCTATCTCCTCATTC  
CTCCAATCCTCAATCCCATTGTCTATGCTGTTGCGACCAAGCAGATCCGAGAGAGCCTTCT  
CCAAATACCAAGGATAGAAATGAAGATTAGATGA (SEQ ID NO: 94)

45

**AOLFR50 sequences:**

MNLSFFSFLLKSLIMALSNSSWRLPQPSFFLVGIPGLEESQHWIALPLGILYLLALVGNVTILFI  
WMDPSLHQSMYLFSLMLAAIDLVASSTAPKALAVLLVRAQEIGYTVCLIQMFTHAFSSMES  
GVLVAMALDRYVAICHPLHHSTILHPGVIGHIGMVVLRGLLLIPFLILLRKLIFCQATIGHAY  
50 CEHMAVVKLACSETTVNRAYGLTVALLVVGLDVLAIGVSYAHILQAVLKVPNEARLKAFST  
CGSHVCVILVFYIPGMFSFLTHRFGHVPHHVHVLAILYRLVPPALNPLVYRVKTKQIHQ  
(SEQ ID NO: 95)

55 ATGAATTTGGATTCTTTTTCTCTTTCCTCCTCAAGTCATTGATAATGGCACTTAGCAATTC  
CAGCTGGAGGCTACCCAGCCTTCTTTTTCTCTGGTAGGAATTCCGGGTTTAGAGGAAAGC  
CAGCACTGGATCGCACTGCCCTGGGCATCCTTTACCTCCTTGCTCTAGTGGGCAATGTTA

CCATTCTCTTCATCATCTGGATGGACCCATCCTTGACCAATCTATGTACCTCTTCTGTCC  
 ATGCTAGCTGCCATCGACCTGGTTGTGGCCTCCTCCACTGCACCCAAAGCCCTTGCACTGC  
 TCCTGGTTTCGTGCCCAAGAGATTGGTTACACTGTCTGCCTGATCCAGATGTTCTTACCCAT  
 GCATTCTCCTCCATGGAGTCAGGGGTACTTGTGGCCATGGCTCTGGATCGCTATGTAGCCA  
 5 TTGTACACCCCTTGACCATTCACAACTCTGCATCCAGGGGTCATAGGGCACATCGGAAT  
 GGTGGTGCTGGTGCAGGGATTACTACTCCTCATCCCCCTCCTCATTCTGTTGCGAAACTT  
 ATCTTCTGCCAAGCCACCATCATAGGCCATGCCTATTGTGAACATATGGCTGTTGTGAAC  
 TTGCCTGCTCAGAAACCACAGTCAATCGAGCTTATGGGCTGACTGTGGCCTTGCTTGTGGT  
 TGGGCTGGATGTCCTGGCCATTGGTGTTCCTATGCCACATTCTCCAGGCAGTGTGAAG  
 10 GTACCAGGAAATGAGGCCCGACTTAAGGCCTTTAGCACATGTGGCTCTCATGTTGTGTCA  
 TCCTGGTCTTCTATATCCCGGGAATGTTCTCCTCCTCACTCACCGCTTTGGTCATCATGTA  
 CCCCATCACGTCCATGTTCTTCTGGCCATACTGTATCGCCTTGTGCCACCTGCACTCAATCC  
 TCTTGTCTATAGGGTGAAGACCCAGAAGATCCACCAGTGA (SEQ ID NO: 96)

15 **AOLFR51 sequences:**

MCQQILRDCILLIHLHCINRKKVSLVMLGPAYNHTMETPASFLLVGIPGLQSSHLWLAISLSAM  
 YIALLGNTIIVTAIWMSTRHEPMYCFLCVLAAVDIVMASSVVPKMVSIFCSGDSSISFSACFTQ  
 MFFVHLATAVETGLLLTMAFDTRYVAICKPLHYKRILTPQVMLGMSMAITIRAIATPLSWMVS  
 HLPFCGSNVVHVSCEHIALARLACADPVPSSLYSLIGSSLMVGS DVAFIAASYILILKAVFGLSS  
 20 KTAQLKALSTCGSHVGMALYLPGMASIYAAWLGQDVVPLHTQVLLADLYVIIPATLNPITY  
 GMRTKQLRERIWSYLMHVLFDHNSLGS (SEQ ID NO: 97)

ATGTGTCAACAAATCTTACGGGATTGCATTCTTCTCATACATCATTTGTGCATTAACAGGA  
 AAAAAGTCTCACTTGTGATGCTGGGTCCAGCTTATAACCACACAATGGAAACCCCTGCCTC  
 25 CTTCCTCCTTGTGGGTATCCCAGGACTGCAATCTTACATCTTTGGCTGGCTATCTCACTGA  
 GTGCCATGTACATCATAGCCCTGTTAGGAAACACCATCATCGTGACTGCAATCTGGATGGA  
 TTCCACTCGGCATGAGCCCATGTATTGCTTTCTGTGTGTTCTGGCTGCTGTGGACATTGTTA  
 TGGCCTCCTCGGTGGTACCCAAGATGGTGAGCATCTTCTGCTCAGGAGACAGCTCAATCAG  
 CTTIAGTGCTTGTTCCTCAGATGTTTTTGTCCACTTAGCCACAGCTGTGGAGACGGGG  
 30 CTGCTGCTGACCATGGCTTTTGACCGCTATGTAGCCATCTGCAAGCCTCTACACTACAAGA  
 GAATTCTCACGCCTCAAGTGATGCTGGGAATGAGTATGGCCATCACCATCAGAGCTATCAT  
 AGCCATAACTCCACTGAGTTGGATGGTGAGTCATCTACCTTTCTGTGGCTCCAATGTGGTT  
 GTCCACTCCTACTGTGAGCACATAGCTTTGGCCAGGTTAGCATGTGCTGACCCCGTGCCCA  
 GCAGTCTCTACAGTCTGATTGGTTCTCTCTTATGGTGGGCTCTGATGTGGCCTTCATTGCT  
 35 GCCTCCTATATCTTAATTCTCAAGGCAGTATTTGGTCTCTCCTCAAAGACTGCTCAGTTGAA  
 AGCATTAAAGCACATGTGGCTCCCATGTGGGGGTTATGGCTTTGTACTATCTACCTGGGATG  
 GCATCCATCTATGCGGCCTGGTTGGGGCAGGATGTAGTGCCCTTGACACCCCAAGTCTGC  
 TAGCTGACCTGTACGTGATCATCCCAGCCACCTTAAATCCCATCATCTATGGCATGAGGAC  
 CAAACAACTGCGGGAGAGAATATGGAGTTATCTGATGCATGTCCTCTTTGACCATTCCAAC  
 40 CTGGGTTTCATGA (SEQ ID NO: 98)

**AOLFR52 sequences:**

MLGPAYNHTMETPASFLLVGIPGLQSSHLWLAISLSAMYITALLGNTLIVTAIWMSTRHEPMY  
 CFLCVLAAVDIVMASSVVPKMVSIFCSGDSSISFSACFTQMFFVHLATAVETGLLLTMAFDTRYV  
 45 AICKPLHYKRILTPQVMLGMSMAVTIRAVTFMTPLSWMMNHLFPFCGSNVVHVSCKHIALAR  
 LACADPVPSSLYSLIGSSLMVGS DVAFIAASYILILRAVFDLSSKTAQLKALSTCGSHVGMALY  
 YLPGMASIYAAWLGQDIVPLHTQVLLADLYVIIPATLNPITYGMRTKQLLEGIWSYLMHFLFDH  
 SNLGS (SEQ ID NO: 99)

ATGCTGGGTCCAGCTTACAACCACACAATGGAAACCCCTGCCTCCTTCTCCTTGTGGGTA  
 TCCCAGGACTGCAATCTTACATCTTTGGCTGGCTATCTCACTGAGTGCCATGTACATCAC  
 AGCCCTGTTAGGAAACACCCCTCATCGTGACTGCAATCTGGATGGATTCCACTCGGCATGAG  
 CCCATGTATTGCTTTCTGTGTGTTCTGGCTGCTGTGGACATTGTTATGGCCTCCTCCGTGGT  
 ACCCAAGATGGTGAGCATCTTCTGCTCGGGAGACAGCTCCATCAGCTTTAGTGCTTGTTC  
 55 ACTCAGATGTTTTTTGTCCACTTAGCCACAGCTGTGGAGACGGGGCTGCTGCTGACCATGG  
 CTTTGTACCGCTATGTAGCCATCTGCAAGCCTCTACACTACAAGAGAATTCTCACGCCTCA

AGTGATGCTGGGAATGAGTATGGCCGTCACCATCAGAGCTGTCACATTCATGACTCCACTG  
 AGTTGGATGATGAATCATCTACCTTTCTGTGGCTCCAATGTGGTTGTCCACTCCTACTGTAA  
 GCACATAGCTTTGGCCAGGTTAGCATGTGCTGACCCCGTGCCAGCAGTCTCTACAGTCTG  
 ATTGGTTCTCTCTTATGGTGGGCTCTGATGTGGCCTTCATTGCTGCCTCCTATATCTTAAT  
 5 TCTCAGGGCAGTATTTGATCTCTCCTCAAAGACTGCTCAGTTGAAAGCATTAAAGCACATGT  
 GGCTCCCATGTGGGGGTTATGGCTTTGTACTATCTACCTGGGATGGCATCCATCTATGCGG  
 CCTGGTTGGGGCAGGATATAGTGCCCTTGACACACCAAGTGTGCTAGCTGACCTGTACGT  
 GATCATCCCAGCCACTTTAAATCCCATCATCTATGGCATGAGGACCAAACAATTGCTGGAG  
 10 GGAATATGGAGTTATCTGATGCACCTTCTTTGACCACTCCAACCTGGGTTTCATGA (SEQ  
 ID NO: 100)

**AOLFR54 sequences:**

MSDSNLSNDNHLPTFFLTGIPGLEAAHFVIAIPFCAMYLVALVGNAALILVIAMDNALHAPMY  
 LFLCLLSLTDLALSSTTVPKMLAILWLHAGEISFGGCLAQMFVHSIYALESSILLAMAFDRYVA  
 15 ICNPLRYTTILNHAVIGRIGFVGLFRSVAIVSPFILLRRLPYCGHRVMTHTYCEHMGARLACA  
 NITVNIVYGLTVALLAMGLDSILIAISYGFIHLAVFHLPSHDAQHKALSTCGSHIGIILVFYIPAFF  
 SFLTHRFHGHEVPKHVHIFLANLYVLVPPVLNPILYGARTKEIRSRLKLLHLGKTSI (SEQ ID  
 NO: 101)

20 ATGTCAGATTCCAACCTCAGTGATAACCATCTTCCAGACACCTTCTTCTTAACAGGGATCC  
 CAGGGCTGGAGGCTGCCACTTCTGGATTGCCATCCCTTTCTGTGCCATGTATCTTGTAGC  
 ACTGGTTGGAAATGCTGCCCTCATCTGGTCATTGCCATGGACAATGCTCTTCATGCACCT  
 ATGTACCTCTTCTCTGCCTTCTCTCACTCACAGACCTGGCTCTCAGTCTCACCCTGTGCC  
 CAAGATGCTGGCCATTTTGTGGCTCCATGCTGGTGAGATTTCCTTTGGTGGATGCCCTGGCC  
 25 CAGATGTTTTGTGTCCATTCTATCTATGCTCTGGAGTCCTCGATTCTACTTGCCATGGCCTT  
 TGATAGGTATGTGGCTATCTGTAACCCATTAAGGTATACAACCATTCTCAACCATGCTGTC  
 ATAGGCAGAATTGGCTTTGTTGGGCTATTCCGTAAGTGTGGCTATTGTCTCCCCCTTCATCTT  
 CTTGCTGAGGCGACTCCCCTACTGTGGTCACCGTGTGATGACACACACATACTGTGAGCAT  
 ATGGGCATCGCCCGACTGGCCTGTGCCAACATCACTGTCAATATTGTCTATGGGCTAACTG  
 30 TGGCTCTGCTGGCCATGGGACTGGATTCCATTCTCATTGCCATTTCTATGGCTTTATCCTC  
 CATGCAGTCTTTCACCTTCCATCTCATGATGCCAGCACAAAGCTCTGAGTACCTGTGGCT  
 CCCACATTGGCATCATCCTGGTTTTCTACATCCCTGCCTTCTTCTCCTTCCCTACCCACCGC  
 TTTGGTCAACCACGAAGTCCCCAAGCATGTGCACATCTTTCTGGCTAATCTCTATGTGCTGG  
 TGCCTCCTGTACTCAATCCTATTCTCTATGGAGCTAGAACCAAGGAGATTGCGAGTCGACT  
 35 TCTAAAACTGCTTCACCTGGGGAAGACTTCAATATGA (SEQ ID NO: 102)

**AOLFR57 sequences:**

MSFQVITYMYFLHWTMEKSNNSTLFILLGFSQNKNIIEVLFCVLFVLCYIAIWMGNLLIMISITCTQ  
 LIHQPMYFFLNYSLSDLCTYSTVTPKLMVDLLAERKTISYNNCMQLFTTHFFGGIEIFLTGM  
 40 AYDRYVAICKPLHYTHMSROKCNTHIVCCTGGFIHSASQFLLTIFVPFCGPNEIDHYFCDVYPLL  
 KLACSNHIMIGLLVIANSGLIALVTFVLLLSYVFILYTRAYSERRSKALATCSSHVIVVVLFF  
 APALFIYIRPVTTFSEDKVFAFYTHAPMFNPLIYTLRNTMKNAMRKVWCCQILLKRNQLF  
 (SEQ ID NO: 103)

45 ATGTCATTTTCAGGTGACTTATATGTTCTATCTACACTGGACCATGGAAAAAGCAATAATA  
 GCACITTTGTTTATTCTCTTGGGGTTTTCCCAAATAAAGAACATTGAAGTCCTCTGCTTTGTA  
 TTATTTTTGTTTTGCTACATTGCTATTTGGATGGGAAACTTACTCATAATGATTTCTATCAC  
 GTGCACCCAGCTCATTACCAACCCATGATTTCTTCTCAATTACCTCTCACTCTCCGACC  
 TTTGCTACACATCCACAGTGACCCCCAAATTAATGGTTGACTTACTGGCAGAAAGAAAGAC  
 50 CATTTCTATAATAACTGTATGATACAACCTCTTACCACCCATTTTTTTGGAGGCATAGAGA  
 TCTTCATTCTCACAGGGATGGCCTATGACCGCTATGTGGCCATTTGCAAGCCCCTGCACTA  
 CACCATTATTATGAGCAGGCAAAAGTGTAACACAATCATCATAGTTTGTGTACTGGGGGA  
 TTTATACATTCTGCCAGTCAGTTTCTTCTCACCATTCTTGTACCATTTGTGGCCCAAATGA  
 GATAGATCACTACTTCTGTGATGTGTATCCTTTGCTGAAATTGGCCTGTTCTAATATACACA  
 55 TGATAGGTCTCTTAGTCATTGCTAATTCAGGCTTAATTGCTTTGGTGACATTTGTTGTCTTG  
 TTGTTGTCTTATGTTTTTATATTGTATACCATCAGAGCATACTCTGCAGAGAGACGCAGCA

AAGCTCTTGCCACTTGTAGTTCTCATGTAATTGTTGTGGTCCTGTTTTTGTCTCCTGCATTG  
TTCATTTACATTAGACCGGTCAACACATTCTCAGAAAGATAAAGTGTTTGCCCTTTTTTATAC  
CATCATTGCTCCCATGTTCAACCCTCTCATATACACGCTGAGAAACACAGAGATGAAGAAC  
GCCATGAGGAAAGTGTGGTGTGTCAAATACTCCTGAAAAGAAATCAACTTTTCTGA (SEQ  
5 ID NO: 104)

**AOLFR58 sequences:**

MFSMTTEALNNFALGCTNLLMTMIPQIDLKQIFLCPNCRLYMIPVGAFIFSLGNMQNQSFVTEF  
VLLGLSQPNVQEIIVFVFLFVYIATVGGNMLIVVTILSSPALLVSPMYFFLGFLSFLDACFSSVI  
10 TPKMIVDSLYVTKTISFEGCMMQLFAEHFFAGVEVIVLTAMAYDRYVAICKPLHYSSIMNRRL  
CGILMGVAWTGGLLHSMIQLFTFQLPFCGPNVINHFMCPLYLLELACTDTHIFGLMVVINS  
FICIINFSLLLVSYAVILLSLRTHSSEGRWKALSTCGSHIAVVILFFVPCIFVYTRPPSAFSLDKMA  
AIFYIILNPLLNPLIYTFRNKEVKQAMRRIWNRLMVVSDEKENIKL (SEQ ID NO: 105)

15 ATGTTCTCAATGACAACAGAAGCACTCAATAATTTGCACTTGGATGTACCAACTTGTTAA  
TGACTATGATACCAACAAATTGATCTGAAGCAAATTTTCCTTTGTCCTAATTGCAGACTATA  
CATGATCCCTGTTGGAGCTTTTCATCTTTTCCTTGGGAAACATGCAAAACCAAAGCTTTGTA  
ACTGAGTTTGTCTCCTCTGGGACTTTACAGAATCCAAATGTTTCAGGAAATAGTATTTGTTG  
TATTTTTGTTTGTCTACATTGCAACTGTTGGGGGCAACATGCTAATTGTAGTAACCAATTCTC  
20 AGCAGCCCTGCTCTTCTGGTGTCTCCTATGTACTTCTTCTTGGGCTTCCTGTCTTCTCTGGA  
TGCCTGCTTCTCATCTGTCATCACCCCAAAGATGATTGTAGACTCCCTCTATGTGACAAAA  
ACCATCTCTTTTGAAGGCTGCATGATGCAGCTCTTTGCTGAACACTTCTTTGCTGGGGTGG  
AGGTGATTGTCTCACAGCCATGGCCTATGATCGTTATGTGGCCATTTGCAAGCCCTTGCA  
TTACTCTTCTATCATGAACAGGAGGCTCTGTGGCATTCTGATGGGGGTAGCCTGGACAGGG  
25 GGCCTCTTGCAATCCATGATACAAATCTTTTACTTTCCAGCTTCCCTTTTGTGGCCCCAA  
TGTCATCAATCACTTTATGTGTGACTTGTACCCGTTACTGGAGCTTGCTGCACTGATACTC  
ACATCTTTGGCCTCATGGTGGTCAACAGTGGGTTTATCTGCATCATAAACTTCTCCTTG  
TTGCTTGTCTCCTATGCTGTCTCTTGTCTCTCTGAGAACACACAGTTCTGAAGGGCGCTG  
GAAAGCTCTCTCCACCTGTGGATCTCACATTGCTGTTGTGATTTTGTCTTTGTCCCATGCA  
30 TATTTGTATATACACGACCTCCATCTGCTTTTCCCTTGACAAAATGGCGGCAATATTTTAT  
ATCATCTTAAATCCCTTGCTCAATCCTTTGATTTACACTTTCAGGAATAAGGAAGTAAAC  
AGGCCATGAGGAGAATATGGAACAGACTGATGGTGGTTTCTGATGAGAAAGAAAATATTA  
AACTTTAA (SEQ ID NO: 106)

**AOLFR59 sequences:**

MGDWNNSDAVEPIFILRGFPGLEYVHSWLSILFCLAYLVAFMGNVTILSVTWIESSLHQPMMYYFI  
SILAVNDLGMSTLPTMLAVLWLDAPETQASACYAQLFFIHTFTFLESSVLLAMAFDRFVAICH  
PLHYPTILTNSVIGKIGLACLLRSLGVLPPTLLLRHYHYCHGNALSHAFCLHQDVLRLSCTDA  
RNTSIYGLCVVIATLGVDSIFILLSYVLIINTVLDIASREEQLKALNTCVSHICVLIFFVPVIGVS  
40 MVHRFGKHLSPIVHILMADIYLLPVLNPIVYSVRTKQIRLGILHKFVLRRRF (SEQ ID NO:  
107)

ATGGGAGACTGGAATAACAGTGATGCTGTGGAGCCCATATTTATCCTGAGGGGTTTTCTCTG  
GACTGGAGTATGTTTATTCTTGGCTCTCCATCCTCTTCTGTCTTGCATATTTGGTAGCATTT  
45 ATGGGTAATGTTACCATCCTGTCTGTCAATTTGGATAGAATCCTCTCTCCATCAGCCCATGTA  
TTACTTTATTTCCATCTTAGCAGTGAATGACCTGGGGATGTCCCTGTCTACACTTCCACCA  
TGCTTGCTGTGTTATGGTTGGATGCTCCAGAGATCCAGGCAAGTGCTTGCTATGCTCAGCT  
GTTCTTCATCCACACATTACATTCTTGGAGTCCCTCAGTGTTGCTGGCCATGGCCTTTGACC  
GTTTTGTTGCTATCTGCCATCCACTGCACTACCCACCATCCTCACCAACAGTGTAATTGGC  
50 AAAATTGGTTTGGCCTGTTTGCTACGAAGCTTGGGAGTTGTAATTTCCACACCTTTGCTACT  
GAGACACTATCACTACTGCCATGGCAATGCCCTCTCTACGCCTTCTGTTTGCACCAGGAT  
GTTCTAAGATTATCCTGTACAGATGCCAGGACCAACAGTATTTATGGGCCTTGTGTAGTCA  
TTGCCACACTAGGTGTGGATTCAATCTTCATACCTTTCTTATGTTCTGATTCTTAATACT  
GTGCTGGATATTGCATCTCGTGAAGAGCAGCTAAAGGCACTCAACACATGTGTATCCCAT  
55 TCTGTGTGGTGCTTATCTTCTTTGTGCCAGTTATTGGGGTGTCAATGGTCCATCGCTTTGGG  
AAGCATCTGTCTCCCATAGTCCACATCCTCATGGCAGACATCTACCTTCTTCTCCCCCAGT



CCTTAACCCTATTGTCTATAGTGTGAGAACAAAGCAGATTTCGTCTAGGAATTCTCCACAAG  
TTTGTCTTAAGGAGGAGGTTTTAA (SEQ ID NO: 108)

**AOLFR60 sequences:**

5 MFLPNDTQFHPSSFLLLGIPGLETLHIWIGFPFCAVYMIALIGNFTILLVIKTDSSLHQPMFYFLA  
MLATTDVGLSTATIPKMLGIFWINLRGIIFEAQLTQMFFIHNFTLMESAVLVAMAYDSYVAICN  
PLQYSAILTNKVVSIVGLGVFVRALIFVIPSILLILRLPFCGNHVIPHTYCEHMGHLASCAIKINI  
IYGLCAICNLVFDITVIALSYVHILCAVRLPHEPRLSLSTCGSHVCVILAFYTPALFSFMTHC  
FGRNVPRYIHILLANLYVVVPPMLNPVIYGVRTKQIYKCVKKILLQEQGMEKEEYLIHTRF  
10 (SEQ ID NO: 109)

ATGTTCCCTTCCCAATGACACCCAGTTTCACCCCTCCTCCTTCTGTTGCTGGGGATCCCAGG  
ACTAGAAACACTTCACATCTGGATCGGCTTTCCCTTCTGTGCTGTGTACATGATCGCACTC  
ATAGGGAACCTTCACTATTCTACTTGTGATCAAGACTGACAGCAGCCTACACCAGCCCAGT  
15 TCTACTTCTGGGCCATGTTGGCCACCAGTGTGGGTCTCTCAACAGCTACCATCCCTAA  
GATGCTTGGAACTTCTGATCAACCTCAGAGGGATCATCTTTGAAGCCTGCCTCACCCAG  
ATGTTTTTTATCCACAACCTTCACTTATGGAGTCAGCAGTCCTTGTGGCAATGGCTTATG  
ACAGCTATGTGGCCATCTGCAATCCACTCCAATATAGCGCCATCCTCACCAACAAGGTTGT  
TTCTGTGATTGGTCTTGGTGTGTTTGTGAGGGCTTTAATTTTCGTCAATCCCTCTATACTTC  
20 TTATATTGCGGTTGCCCTTCTGTGGGAATCATGTAATTCCCCACACCTACTGTGAGCACAT  
GGGCTTGTCTCATCTATCTTGTGCCAGCATCAAAATCAATATTATTATGGTTTATGTGCCA  
TTTGTAATCTGGTGTGTTGACATCACAGTCATTGCCCTCTCTTATGTGCATATTCTTTGTGCT  
GTTTTCCGTCTTCTACTCATGAGCCCCGACTCAAGTCCCTCAGCACATGTGGTTCACATGT  
GTGTGTAATCCTTGCCTTCTATACACCAGCCCTCTTTTCTTTATGACTCATTGCTTTGGCC  
25 GAAATGTGCCCCGCTATATCCATATACTCTAGCCCAATCTCTATGTTGTGGTGCCACCAAT  
GCTCAATCCTGTATATATGGAGTCAGAACCAAGCAGATCTATAAATGTGTAAAGAAAAT  
ATTATTGCAGGAACAAGGAATGGAAAAGGAAGAGTACCTAATACATACGAGGTTCTGA  
(SEQ ID NO: 110)

30 **AOLFR61 sequences:**

MSINTSYVEITTFVLVGMPLGLEIAHIWISIPICSMYLIAILGNGTILFIKTEPSLHGPMYYFLSML  
AMSDLGLSLSSLPTVLSIFLNPETSSSACFAQEFFIHGFSVLESSVLLIMSFDRFLAIHNPLRYT  
SILTTVRVAQIGIVFSFKSMLLVLPFPFTLRSLRYCKKNQLSHSYCLHQDVMKLACSDNRIDVY  
GFFGALCLMVDFILIAVSYTLILKTVPGIASKKEBELKALNTCVSHICAVIIFYLPINLAVVHFRFAG  
35 HVSPLINVLMANVLLLVPPLMKPIVYCVKTKQIRVRVAKLCQWKI (SEQ ID NO: 111)

ATGTCCATTATCAACACATCATATGTTGAAATCACACCTTCTTCTTGGTTGGGATGCCAG  
GGCTAGAAATATGCACACATCTGGATCTCTATCCCCATCTGCAGCATGTATCTTATTGCTATT  
CTAGGAAATGGCACCATTCTTTTATCATCAAGACAGAGCCCTCCTTGCATGGGCCCAGT  
40 ACTATTTTCTTTCCATGTTGGCTATGTCAGACTTGGGTTTGTCTTTATCATCTCTGCCCACT  
GTGTTAAGCATCTTCCGTGTTCAATGCCCTGAAACTTCTTCTAGTGCCTGCTTTGCCAGGA  
ATTCTTCATTGATGATTCTCAGTACTGGAGTCCTCAGTCCTCCTGATCATGTCAATTTGATA  
GATTCCTAGCCATCCACAATCCTCTGAGATACACCTCAATCCTGACAACTGTCAGAGTTGC  
CCAAATAGGGATAGTATTCTCCTTTAAGAGCATGCTCCTGGTTCTTCCCTTCCCTTTCACTT  
45 TAAGAAGCTTGAGATATTGCAAGAAAAACCAATTATCCCATTCCCTACTGTCTCCACCAGGA  
TGTCATGAAGTTGGCCTGTTCTGACAACAGAATTGATGTTATCTATGGCTTTTTTGGAGCA  
CTCTGCCTTATGGTAGACTTTATTCTCATTGCTGTGTCTTACACCCTGATCCTCAAGACTGT  
ACCGGGAATTGCATCCAAAAGGAGGAGCTTAAGGCTCTCAATACTTGTGTTTCACACATC  
TGTGCAAGTATCATCTTCTACCTGCCATCATCAACCTGGCCGTTGTCCACCGCTTTGCCGG  
50 GCATGTCTCTCCCTCATTAAATGTTCTCATGGCAAATGTTCTCCTACTTGTACCTCCGCTGA  
TGAAACCAATTGTTTATTGTGTAATAAATAACAGATTAGAGTGAGAGTTGTAGCAAAATT  
GTGTCAATGGAAGATTTAA (SEQ ID NO: 112)

**AOLFR62 sequences:**

55 MFYHNKSIFHPVTFFLIGIPLEDHFMWISGPFCSVYLVALLGNAITLLVIKVEQTLREPMFYFL  
AILSTIDLALSATSVPRMLGIFWFDABEINYGACVAQMFLIHAFTGMEAEVLLAMAFDRYVAIC

APLHYATILTSVLVVGISMCIIVIRPVLLTLPVMVYLIYRLPFCQAHIAHSYCEHMGIAKLSCGNIRI  
 NGIYGLFVVVSFFVLNLVLIGISYVYILRAVFRLPASHDAQLKALSTCGAHVGVICVFYIPSVFSFLT  
 HRFHQIPGYIHILVANLYLIIPPSLNPITYGVRTKQIRERVLYVFTKK (SEQ ID NO: 113)

- 5 ATGTTTTATCACAACAAGAGCATATTTACCCAGTCACATTTTTCTCATTGGAATCCCAGG  
 TCTGGAAGACTTCCACATGTGGATCTCCGGGCCTTTCTGCTCTGTTTACCTTGTGGCTTTGC  
 TGGGCAATGCCACCATTCTGCTAGTCATCAAGGTAGAACAGACTCTCCGGGAGCCCATGTT  
 CTAATTCCTGGCCATTCTTTCCACTATTGATTTGGCCCTTTCTGCAACCTCTGTGCCTCGCA  
 TGCTGGGTATCTTCTGGTTTGATGCTCAGGAGATTAACATGGAGCTTGTGTGGCCAGAT  
 10 GTTCTGATCCATGCCITCACTGGCATGGAGGCTGAGGTCTTACTGGCTATGGCTTTTGAC  
 CGTTATGTGGCCATCTGTGCTCCACTACATTACGCAACCATCTTGACATCCCTAGTGTGGT  
 GGGCATTAGCATGTGCATTGTAATTCGTCCTCGTTTACTTACACTTCCCATGGTCTATCTTA  
 TCTACCGCCTACCCTTTGTGAGGCTCACATAATAGCCCATTCCTACTGTGAGCACATGGG  
 CATTGCAAAATGTCTGTGGAACATTCTGATCAATGGTATCTATGGGCTTTTTGTAGTTT  
 15 CTTTCTTTGTTCTGAACCTGGTGCTCATTGGCATCTCGTATGTTTACATTCTCCGTGCTGTC  
 TTCCGCCTCCCATCACATGATGCTCAGCTAAAAGCCCTAAGCACGTGTGGCGCTCATGTTG  
 GAGTCATCTGTGTTTCTATATCCCTTCAGTCTTCTCTTCCCTTACTCATCGATTTGGACAC  
 CAAATACCAGGTTACATTACATTCTTGTGCAATCTCTATTTGATTATCCCACCTCTCT  
 CAACCCCATCATTTATGGGGTGAGGACCAACAGATTGAGAGCGAGTGCTCTATGTTTTT  
 20 ACTAAAAAATAA (SEQ ID NO: 114)

**AOLFR63 sequences:**

- MSIINTSYVEITTFVLVGMPLGLEAHTWISIPICSMYLIAILNGNTILFIKTEPSLHEPMYYFLSML  
 AMSDLGLSLSSLPTVLSIFLNAPEISSNACFAQEFFIHGFSVLESSVLLIMSFDRLAIHNPLRYTS  
 25 ILTTVRVAQIGIVFSFKSMMLVLPFPFTLRNLRYCKKNQLSHSYCLHQDVMKLACSDNRIDVIY  
 GFFGALCLMVDFILIAVSYTLLIKTVLGIASKKEQLKALNTCVSHICAVIIFYPINLAVVHRFAR  
 HVSPLINVLMANVLLLVPPLTNPIVYCVKTKQIRVRVVAKLQQRKI (SEQ ID NO: 115)

- ATGTCCATTATCAACACATCATATGTTGAAATCACACCTTCTTCTTGGTTGGGATGCCAG  
 30 GGCTAGAATATGCACACATCTGGATCTCTATCCCCATCTGCAGCATGTATCTTATTGCTATT  
 CTAGGAAATGGCACCATTCTTTTATCATCAAGACAGAGCCCTCCTTGCATGAGCCCATGT  
 ACTATTTTCTTTCCATGTTGGCTATGTCAGACTGGGTTTGTCTTTATCATCTCTGCCCCACT  
 GTGTTAAGCATCTTCTGTTCAATGCTCCTGAAATTTATCCAATGCCTGCTTTGCCAGGA  
 ATTCCTCATTCATGGATTCTCAGTACTGGAGTCCTCAGTCCTCCTGATCATGTCATTTGATA  
 35 GATTCCTAGCCATCCACAACCCTCTGAGATACACCTCAATCCTGACAACTGTCAGAGTTGC  
 CCAAATAGGGATAGTATTCTCCTTTAAGAGCATGCTCCTGGTTCTTCCCTTCCCTTTCACTT  
 TAAGAAACTTGAGATATTGCAAGAAAAACCAATTATCCCATTCCTACTGTCTCCACCAGGA  
 TGTCATGAAGTTGGCCTGTTCTGACAACAGAATTGATGTTATCTATGGCTTTTGGAGCA  
 CTCTGCCTTATGGTAGACTTTATTCTCATTGCTGTGTCTTACACCCTGATCCTCAAGACTGT  
 40 ACTGGGAATTGCATCCAAAAGGAGCAGCTTAAGGCTCTCAATACTTGTGTTTACACATC  
 TGTGCAGTGATCATCTTCTACCTGCCCATCATCAACCTGGCCGTTGTCCACCGCTTGGCCG  
 GCATGTCTCTCCCTCATTAATGTTCTCATGGCAAATGTTCTCCTACTTGTACCTCCACTGA  
 CGAACCCAATTGTTTATTGTGTAATAAATAACAGATTAGAGTGAGAGTTGTAGCAAAATT  
 GTGTCAACGGAAGATTTAA (SEQ ID NO: 116)

45

**AOLFR64 sequences:**

- MTILLNSSLQRATFFLTGFQGLEGLHGWISIPFCFIYLTIVLGNLTILHVICTDATLHGPMYYFLG  
 MLAVTDLGLCLSTLPTVLGIFWFDTREIGIPACFTQLFFIHTLSSMESSVLLSMSIDRSVAVCNPL  
 HDSTVLT PACIVKMGLSSVLSALLILPLPFLKRFQYCHSHVLAHAYCLHLEIMKLACSSIIVN  
 50 HIYGLFVVACTVGVDSLLIFLSYALILRTVLSIASHQERLRALNTCVSHICAVLLFYIPMIGLSLV  
 HRFGEHLPRVVHLFMSYVYLLVPPLMNPPIYSIKTKQIRQRIKKFQFIKSLRCFWKD (SEQ ID  
 NO: 117)

- ATGACAATTCTTCTTAATAGCAGCCTCCAAAGAGCCACTTTCTTCTGACGGGCTTCCAAG  
 55 GTCTAGAAGGTCTCCATGGCTGGATCTCTATTCCCTTCTGCTTCATCTACCTGACAGTTATC  
 TTGGGGAACCTCACCATTCTCCACGTCATTGTACTGATGCCACTCTCCATGGACCCATGT

ACTATTTCTTGGGCATGCTAGCTGTACAGACTTAGGCCTTTGCCTTTCCACACTGCCCACT  
 GTGCTGGGCATTTTCTGGTTTGATACCAGAGAGATTGGCATCCCTGCCTGTTTCACTCAGC  
 TCTTCTTCATCCACACCTTGTCTTCAATGGAGTCATCAGTTCTGTTATCCATGTCCATTGAC  
 CGCTCCGTGGCCGTCTGCAACCCACTGCATGACTCCACCGTCTGACACCTGCATGTATTG  
 5 TCAAGATGGGGCTAAGCTCAGTGCTTAGAAGTGCTCTCCTCATCCTCCCTTGCCATTCCCTC  
 CTGAAGCGCTTCCAATACTGCCACTCCCATGTGCTGGCTCATGCTTATTGTCTTCACCTGGA  
 GATCATGAAGCTGGCCTGCTCTAGCATCATTGTCAATCACATCTATGGGCTCTTTGTTGTG  
 GCCTGCACCGTGGGTGTGGACTCCCTGCTCATCTTTCTCTCATACGCCCTCATCCTTCGCAC  
 CGTGCTCAGCATTGCCTCCCACCAGGAGCGACTCCGAGCCCTCAACACCTGTGTCTCTCAT  
 10 ATCTGTGCTGTACTGCTCTTCTACATCCCCATGATTGGCTTGTCTCTTGTGCATCGCTTTGG  
 TGAACATCTGCCCCGCGTTGTACACCTCTTCATGTCTATGTGTATCTGCTGGTACCACCCC  
 TTATGAACCCCATCATCTACAGCATCAAGACCAAGCAAATTCGCCAGCGCATCATTAAAGAA  
 GTTTCAGTTTATAAAGTCACTTAGGTGTTTTTGAAGGATTAA (SEQ ID NO: 118)

15 **AOLFR65 sequences:**

MAGRMSTSNHTQFHPSSFLLLGIPIGLEDVHIWIGVPPFFVYLVALLGNTALLFVIQTEQSLHEPM  
 YYFLAMLDSIDLGLSTATIPKMLGIFWFNTKEISFGGCLSHMFFIHFHTAMESIVLVAMAFDRYI  
 AICKPLRYTMILTSKIIISLIAGI AVLRSYLMVVPVLFLLRLPFCGHRIPHTYCEHMGARLACAS  
 IKVNIRFGLGNISLLLLDVILILSYVRILYAVFCLPSWEARLKALNTCGSHIGVILAFFTPAFFSFL  
 20 THRFHGNIPQYIHILANLYVVVPPALNPVTYGVRTKQIRERVLRIFLKTNH (SEQ ID NO: 119)

ATGGCAGGAAGAATGTCTACGTCTAATCACACCCAGTTCCATCCTTCTTCATTCCCTACTGCT  
 GGGTATCCCAGGGCTAGAAGATGTGCACATTTGGATTGGAGTCCCTTTTTCTTTGTGTAT  
 CTTGTTGCACTCCTGGGAAACACTGCTCTCTTGTGTTGTGATCCAGACTGAGCAGAGTCTCC  
 25 ATGAGCCTATGTACTACTTCCCTGGCCATGTTGGATTCCATTGACCTGGGCTGTCTACAGC  
 CACCATCCCCAAAATGTTGGGCATCTTCTGGTTCAATACCAAAGAAATATCTTTTGGAGGC  
 TGCCTTTCTCACATGTTCTTCATCCATTTCTTCACTGCTATGGAGAGCATTGTGTTGGTGGC  
 CATGGCCTTTGACCGCTACATTGCCATTTGCAAACCTCTTCGGTACACCATGATCCTCACCA  
 GCAAAATCATCAGCCTCATTGCAGGCATTGCTGTCTGAGGAGCCTGTACATGGTTGTTCC  
 30 ACTGGTGTCTCTCCTTCTGAGGCTGCCCTTCTGTGGGCATCGTATCATCCCTCATACTTATT  
 GTGAGCACATGGGCATTGCCCCGTCTGGCCTGTGCCAGCATCAAAGTCAACATTAGGTTTGG  
 CCTTGGCAACATATCTCTCTTGTACTGGATGTTATCCTTATTATTCTCTCCTATGTCAGGA  
 TCCTGTATGCTGTCTTCTGCCTGCCCTCCTGGGAAGCTCGACTCAAAGCTCAACACCTGCT  
 GGTCTCATATTGGTGTATCTTACGCTTTTTTACACCAGCATTTTTTTCATTCTTGACACA  
 35 TCGTTTTGGCCATAATATCCCACAGTATATACATATTATATTAGCCAACCTGTATGTGGTTG  
 TCCCACCAGCCCTCAATCCTGTAATCTATGGAGTCAGGACAAAGCAGATTGAGAGAGAG  
 TGCTGAGGATTTTTCTCAAGACCAATCACTAA (SEQ ID NO: 120)

**AOLFR66 sequences:**

40 MSFLNGTSLTPASFILNGIPGLEDVHLWISFPLCTMYSIAITGNFGLMYLIYCDEALHRPMYVFL  
 ALLSFTDVLMTSTLPNTLFILWFNLKEIDFKACLAQMFFVHTFTGMESGVLMMLALDHCVAI  
 CFPLRYATILTNSVIAKAGFLTFLRGVMLVIPSTFLTKRLPYCKGNVIPHTYCDHMSVAKISCGN  
 VRVNAIYGLIVALLIGGFILCITISYTMILQAVVSLSSADARQKAFSTCTAHFCAIVLTYVPAFF  
 TFFTHHFGGHTIPLHIIIMANLYLLMPPTMNPVYGVKTRQVRESVIRFFLKGDNSHNF (SEQ  
 45 ID NO: 121)

ATGTCATTTCTAAATGGCACCAGCCTAACTCCAGCTTCATTCATCCTAAATGGCATCCCTG  
 GTTTGGAAGATGTGCATTTGTGGATCTCCTTCCCACTGTGTACCATGTACAGCATTGCTATT  
 ACAGGGAACCTTCGGCCTTATGTACCTCATCTACTGTGATGAGGCCTTACACAGACCTATGT  
 50 ATGCTCTCCTTGGCCTTCTTCCCTTCACAGATGTGCTCATGTGCACCAGCACCTTCCCAAC  
 ACTCTCTTCATATTGTGGTTTAACTCAAGGAGATTGATTTTAAAGCCTGCCTCGCCAGAT  
 GTTCTTTGTGCACACCTTCACAGGGATGGAGTCTGGGGTGCTCATGCTATGGCCCTGGAC  
 CACTGTGTGGCCATCTGCTTCCCTCTGCGTTATGCCACCATCCTCACTAATTCAGTCATTGTC  
 TAAAGCTGGGTTCCCTCACTTTTCTTAGGGGTGTGATGCTTGTATCCCTTCCACTTTCTCA  
 55 CCAAGCGCCTTCCATACTGCAAGGGCAACGTCATACCCACACCTACTGTGACCACATGTC  
 TGTGGCCAAGATATCTTGTGGTAATGTCAGGGTTAACGCCATCTATGGTTTGATAGTTGCC

CTGCTGATTGGGGGCTTTGATATCCTGTGCATTACAATCTCCTACACTATGATTCTTCAAGC  
 AGTTGTGAGTCTATCATCAGCAGATGCTCGACAGAAGGCCTTCAGCACCTGCACTGCCAC  
 TTCTGTGCCATAGTCTCACCTATGTTCCAGCCTTCTTTACCTTCTTTACACACCATTTTGG  
 GGGACACACCATTCCTCTACACATACATATTATTATGGCTAATCTCTACCTACTAATGCCTC  
 5 CCACAATGAACCCTATTGTGTATGGGGTGAAAACCAGGCAGGTACGAGAAAGTGTCTATTA  
 GGTTCCTTCTTAAGGGAAAGGACAATTCTCATAACTTTTAA (SEQ ID NO: 122)

**AOLFR67 sequences:**

MSGDNSSSLTPGFFILNGVPGLEATHIWISLPFCFMYIIA VVGNCGLICLISHEEALHRPMYYFLA  
 10 LLSFTDVTLCCTMVPNMLCIFWFNLKEIDFNACLAQMFFVHMLTGMESGVMLMALDRYVAI  
 CYPLRYATILTNPVIAKAGLATFLRNVMLIPFTLLTKRLPYCRGNFIPHTYCDHMSVAKVSCGN  
 FKVNAIYGLMVALLIGVFDICISVSYTMILQAVMSLSSADARHKAFSTCTSHMCSIVITYVAAF  
 FTFFTHRFVGHNPNIHIIIVANLYLLLPTMNPVIVGVKTKQIQEGVIKFLLDGDKVSFTYDK  
 (SEQ ID NO: 123)

15 ATGTCCTGGGGACAACAGCTCCAGCCTGACCCCAGGATTCTTTATCTTGAATGGCGTTCTCTG  
 GGCTGGAAGCCACACACATCTGGATCTCCCTGCCATTCTGCTTTATGTACATCATTTGCTGTC  
 GTGGGGAAGTGTGGGCTCATCTGCCTCATCAGCCATGAGGAGGCCCTGCACCGGCCCATGT  
 ACTACTTCTGGCCCTGCTCTCCTTCACTGATGTACCTTGTGCACCAACCATGGTACCTAAT  
 20 ATGCTGTGCATATTCTGGTTCAACCTCAAGGAGATTGACTTTAACGCCTGCCTGGCCCAGA  
 TGTTTTTTGTCCATATGCTGACAGGGATGGAGTCTGGGGTGTCTCATGCTCATGGCCCTGGA  
 CCGCTATGTGGCCATCTGCTACCCCTTACGCTATGCCACCATCCTTACCAACCCTGTCATCG  
 CCAAGGCTGGTCTTGCCACCTTCTTGAGGAATGTGATGCTCATCATCCATTCACTCTCCTC  
 ACCAAGCGCCTGCCCTATTGCCGGGGGAACCTTCATCCCCCACACCTACTGTGACCATATGT  
 25 CTGTGGCCAAGGTATCCTGTGGCAATTCAAGGTCAATGCTATTTATGGTCTGATGGTTGC  
 TCTCTGATTGGTGTGTTTGATATCTGCTGTATCTCTGTATCTTACACTATGATTTTGCAGG  
 CTGTTATGAGCCTGTCATCAGCAGATGCTCGTCACAAAGCCTTCAGCACCTGCACATCTCA  
 CATGTGTTCCATTGTGATCACCTATGTTGCTGCTTTTTTCACTTTTTTCACTCATCGTTTTGT  
 AGGACACAATATCCCAAACCACATACATCATCGTGGCCAACCTTTATCTGCTACTGCCT  
 30 CCTACCATGAACCCAATTGTTTATGGAGTCAAGACCAAGCAGATTCAAGGAAGGTGTAATTA  
 AATTTTTACTTGGAGACAAGGTTAGTTTTACCTATGACAAATGA (SEQ ID NO: 124)

**AOLFR68 sequences:**

MTTHRNDTLSTEASDFLLNCFVRSPSWQHWLSLPLSLLFLLAVGANTLLMTIWLEASLHQPL  
 35 YYLLSLLSLLDIVLCLTVIPKVLTFWFDLRPISFPACFLQMYIMNCF LAMESCTFMVMAYDRY  
 VAICHPLRPSIITDHFVKAAMFILTRNVMLTLPILSAQLRYCGRNVIENCICANMSVSRLSC  
 DDVTINHL YQFAGGWTL LGSDDLIFLSYTFILRAVRLKAEGAVAKALSTCGSHFMLILFFSTIL  
 LVFVLTHVAKKVVSPDVPVLLNVLHVIPAALNPIHVGVRTQEIKQGMQRLLKKGC (SEQ ID  
 NO: 125)

40 ATGACAACACACCGAAATGACACCCTCTCCACTGAAGCTTCAGACTTCCTCTTGAATTGTT  
 TTGTCAGATCCCCCAGCTGGCAGCACTGGCTGTCCCTGCCCTCAGCCTCCTTTTCTCTTG  
 GCCGTAGGGGCCAACACCAACCCTCCTGATGACCATCTGGCTGGAGGCCCTCTCTGCACCAAGC  
 CCCTGTACTACCTGCTCAGCCTCCTCTCCCTGCTGGACATCGTGCTCTGCCTCACTGTCATC  
 45 CCCAAGGTCCTGACCATCTTCTGGTTTGACCTCAGGCCCATCAGCTTCCCTGCCTGCTTCTC  
 CCAGATGTACATCATGAATTGTTTCTAGCCATGGAGTCTTGCACATTTCATGGTCATGGCC  
 TATGATCGTTATGTAGCCATCTGCCACCCACTGAGATATCCATCAATCATCACTGATCACTT  
 TGATGTC AAGGCTGCCATGTTTATTTTGACCAGAAATGTGCTTATGACTCTGCCCATCCCC  
 ATCCTTTT CAGCAAACTCCGTTATTGTGGAAGAAATGTCATTGAGAACTGCATCTGTGCCA  
 50 ATATGTCTGTTTCCAGACTCTCCTGCGATGATGTCACCATCAATCACCTTTACCAATTTGCT  
 GGAGGCTGGACTCTGCTAGGATCTGACCTCATCCTTATCTTCTCTCTACACCTTCATTCT  
 GCGAGTGTGCTGAGACTCAAGGCAGAGGGTGCCGTGGCAAAGGCCCTAAGCACATGTGG  
 CTCCCACTTCATGCTCATCTCTTCTT CAGCACCATCCTTCTGGTTTTTGTCTTACACATGT  
 GGCTAAGAAGAAAGTCTCCCTGATGTGCCAGTCTTGCTCAATGTTCTCCACCATGTCATT  
 55 CCTGCAGCCCTTAACCCCATCATTTACGGGGTGAGAACCCAAGAAATTAAGCAGGGAATG  
 CAGAGGTTGTTGAAGAAAGGGTGCTAA (SEQ ID NO: 126)

**AOLFR69 sequences:**

- MSYSIYKSTVNIPLSHGTVVHSFCHNMNCNFMHIFKFLVDFNMKNVTEVTLFVLKGFTDNLELQ  
 TIFFFLFLAIYLFITLMGNLGLILVVIRDSQLHKPMYYFLSMLSSVDACYSSVITPNMLVDFTTKN  
 5 KVISFLGCVAQVFLACSFGTTECFLLAAMAYDRYVAIYNPLLYSVMSPRVYVIMPLINASYVAGI  
 LHATHTVATFSLSFSGANEIRRVFCIDPPLLAISYSDTHTNQLLLFYFVGSIELVTILIVLISYGLIL  
 LAILKMYSAEGRRKVFSTCGAHLTGVSIIYGTILFMYVRPSSSYASDHDMIVSIFYTIVIPLLNPV  
 IYSLRNKDVKDSMKKMFgKNQVINKVYFHTKK (SEQ ID NO: 127)
- 10 ATGTCGTACAGTATATACAAGAGCACAGTTAACATCCCCTTGAGTCATGGTGTGTTTCATT  
 CTTTTGTGCATAATATGAACTGTAACCTTATGCATATCTTCAAGTTTGTCTAGATTTCAAC  
 ATGAAGAATGTCACTGAAGTTACCTTATTTGTAAGGCTTACAGACAACTTGAAC  
 TGCAGACTATCTTCTTCTCTGTTCTAGCAATCTACCTCTTCACTCATGGGAAATTTA  
 GGACTGATTTTGTGCTCATTAGGGATTCCCAGCTCCACAAACCCATGTACTATTTTCTGA  
 15 GTATGTTGTCTTCTGTGGATGCCTGCTATTCCTCAGTTATTACCCCAAATATGTTAGTAGAT  
 TTTACGACAAAGAATAAAGTCATTTTCATTCCTTGGATGTGTAGCACAGGTGTTTCTGCTT  
 GTAGTTTGTGAACACAGAATGCTTTCTCTTGGCTGCAATGGCTTATGATCGCTATGTAGC  
 CATCTACAACCTCTCCTGTATTCACTGAGCATGTCAACCCAGAGTCTACATGCCACTCATC  
 AATGCTTCCTATGTTGCTGGCATTTTACATGCTACTATACATACAGTGGCTACATTTAGCCT  
 20 ATCCTTCTGTGGAGCCAATGAAATTAGGCGTGTCTTTGTGATATCCCTCCTCTCCTTGCTA  
 TTTCTTATTTCTGACACTCACACAAACAGCTTCTACTCTTCTACTTTGTGGGCTCTATCGAG  
 CTGGTCACTATCCTGATTGTTCTGATCTCCTATGTTTGAATCTGTTGGCATTCTGAAGAT  
 GTATTCTGCTGAAGGGAGGAGAAAAGTCTTCTCCACATGTGGAGCTCACCTAACTGGAGT  
 GTCAATTTATTATGGGACAATCCTCTTCATGTATGTGAGACCAAGTTCCAGCTATGCTTCG  
 25 GACCATGACATGATAGTGTCAATATTTTACACCATTGTGATTCCTTGTGAATCCCGTCAT  
 CTACAGTTTGAGGAACAAAGATGTAAAAGACTCAATGAAAAAATGTTTGGGAAAAATCA  
 GGTTATCAATAAAGTATATTTTCATACTAAAAAATAA (SEQ ID NO: 128)

**AOLFR70 sequences:**

- 30 MDSTFTGYNLVNLQVKTEMKDLSSGLDIYRNPLKNKTEVTMFI LTGFTDDFELQVFLFFFAI  
 YLFTLIGNLGLVVLVIEDSWLHNP MYFLSVLSFLDACYSTVVT PKMLVNFLAKNKSISFIGCA  
 TQMLLFVTFGTTECFLLAAMAYDHYVAIYNPLLYSVMSPRVYVPLITASVYAGILHATHIVA  
 TFLSFCGSNEIRHVFCIDPPLLAISCSDTHTNQLLLFYFVGSIEIVTILIVLISCDFILLSILKMHS  
 KGRQKAFSTCGSHLTGVTIYHGTLVS YMRPSSSYASDHDIIVSIFYTIVIPKLNPIIYSLRNKEVK  
 35 KAVKKMLKL VYK (SEQ ID NO: 129)
- ATGGACTCCACTTTACAGGCTATAACCTTTATAACCTGCAAGTAAAACTGAAATGGACA  
 AGTTGTGCATCAGGTTTGGATATATACAGGAATCCACTGAAGAACAAGACTGAAGTCACCA  
 TGTTTATATTGACAGGCTTACAGATGATTTTGTAGCTGCAAGTCTTCCTATTTTACTATTT  
 40 TTTGCAATCTATCTCTTACCTTGATAGGCAATTTAGGGCTGGTTGTGTTGGTCATTGAGG  
 ATTCTGGCTCCACAACCCCATGTATTATTTCTTAGTGTTTATCATTCTTGGATGCTTGC  
 TATTCTACAGTTGTCACTCCAAAAATGTTGGTCAATTTCTGGCAAAAAATAAATCCATTT  
 CATTTATCGGATGTGCAACACAGATGCTTCTTTTGTACTTTTGGAACTACAGAATGTTTT  
 CTCTGGCTGCAATGGCTTATGATCACTATGTAGCCATCTACAACCTCTCCTGTATTCACT  
 45 GAGCATGTCAACCCAGAGTCTATGTCCACTCATCACTGCTTCTACGTTGCTGGCATTTTAC  
 ATGCTACTATACATATAGTGGCTACATTTAGCCTGTCCTTCTGTGGATCCAATGAAATTAG  
 GCATGTCTTTTGTGATATGCCTCCTCTCCTTGCTATTTCTTGTCTGACACTCACACAAACC  
 AGCTTCTACTCTTCTACTTTGTGGGTTCTATTGAGATAGTCACTATCCTGATTGTCTCATT  
 TCCTGTGATTTTATTCTGTTGTCCATTCTGAAGATGCATTCTGCTAAGGGAAGGCAAAAGG  
 50 CCTTCTCTACATGTGGCTCTCACCTAAGTGGAGTGACAATTTATCATGGAACAATCTCGTC  
 AGTTATAGACCAAGTTCCAGCTATGCTTACAGACCATGACATCATAGTGTCAATATTTT  
 ACACAATTGTGATTCCCAAGTTGAATCCCATCATCTATAGTTTGAGGAACAAAGATAA  
 AAAGGCAGTGAAGAAAATGTTGAAATTGGTTTACAAATGA (SEQ ID NO: 130)

**AOLFR71 sequences:**

MGRNNTNVPDFILTGLSDSEEVQMALFILFLIYLITMLGNVGMILIRLDLQLHTPMYFFLTH  
LSFIDLSYSTVITPKTLANLLTSNYISFMGCFAQMFFVFLGAAECFLSSMAYDRYVAICSPLRY  
PVIMSKRLCCALVTGPYVISFINSFVN VVWMSRLHFCDNSNVVRHFFCDTSPILALSCMDTYDIEI  
5 MIHILAGSTLMVSLITISASYVSILSTILKINSTSGKQKALSTCASHLLGVITIFYGTMIFTYILKPRK  
SYSLGRDQVASVFYTTIVPMLNPLIYSLRNKEVKNALIRVMQRRQDSR (SEQ ID NO: 131)

ATGGGTAGAAGAAATAACACAAATGTGCCTGACTTCATCCTTACGGGACTGTCAGATTCTG  
AAGAGGTCCAGATGGCCCTCTTTATACTATTTCTCCTGATATACCTAATTACTATGCTGGGC  
10 AATGTGGGGATGATATTGATAATCCGCCTGGACCTCCAGCTTCACACTCCCATGTATTTTT  
TCCTTACTCACTTGTCATTTATTGACCTCAGTTACTCAACTGTCATCACACCTAAAACCTTA  
GCGAACTTACTGACTTCCAATAATTTCTTTCATGGGCTGCTTTGCCAGATGTTCTTTTT  
TGTCTTCTTGGGAGCTGCTGAATGTTTTCTTCTCTCATCAATGGCCTATGATCGCTACGTAG  
CTATCTGCAGTCTCTACGTTACCCAGTTATTATGTCCAAAAGGCTGTGTTGCGCTCTTGTC  
15 ACTGGGCCCTATGTGATTAGCTTTATCAACTCCTTTGTCAATGTGGTTTGGATGAGCAGAC  
TGCATTTCTGCGACTCAAATGTAGTTCGTCACTTTTTCTGCGACACGTCTCCAATTTAGCT  
CTGTCCTGCATGGACACATACGACATTGAAATCATGATACACATTTTAGCTGGTTCCACCC  
TGATGGTGTCCCTTATCACAAATATCTGCATCCTATGTGTCCATTCTCTCTACCATCCTGAAA  
ATTAATTCCACTTCAGGAAAGCAGAAAGCTTTGTCTACTTGTGCCTCTCATCTCTTGGGAG  
20 TCACCATCTTTTATGGAAGTATGATTTTACTTATTTAAACCAAGAAAGTCTTATTCTTTG  
GGAAGGGATCAAGTGGCTTCTGTTTTTATACTATTGTGATTCCCATGCTGAATCCACTCAT  
TTATAGTCTTAGAAACAAAGAGTTAAATAATGCTCTCATTAGAGTCATGCAGAGAAGACA  
GGACTCCAGGTAA (SEQ ID NO: 132)

**AOLFR72 sequences:**

MAPENFTRVTEFILTVSSCPQLPLFLVFLVLYGLTMAGNLGITLTSVDSRLQTPMYFFLQHL  
ALINLGNSTVIAPKMLINFLVKKKTTSFYECATQLGGFLFFIVSEVIMLALMACDRYVAICNPLL  
YMVVVSRRLLCLLVSLTYLYGFSTAIVVSSYVFSVSYCSSNIINHFCNPNPLALSCSDTYLPE  
TVVFISAATNVVGSLLIVLSYFNIVLSILKICSSEGRKKAFSTCASHMMAVTIFYGTLLFMYVQP  
30 RSNHSLDTHDKMASVFYTLVIPMLNPLIYSLRNKDVKTALQRFMTNLCYSFKTM (SEQ ID NO:  
133)

ATGGCTCCTGAAAATTTACCAGGGTCACTGAGTTTATTCTTACAGGTGTCTCTAGCTGTC  
CAGAGCTCCAGATTCCCCTCTTCTGGTCTTTCTGGTGCTCTATGGGCTGACCATGGCAGG  
35 GAACCTGGGCATCATCACCTCACCAGTGTTGACTCTCGACTTCAAACCCCCATGTACTTTT  
TCCTGCAACATCTGGCTCTCAATTAATCTTGGTAACTCTACTGTCAATTGCCCTAAAATGCTG  
ATTAACTTTTTAGTAAAGAAGAAAACCTACCTCATTCTATGAATGTGCCACCCAACCTGGGAG  
GGTTCITGTTCTTTATTGTATCGGAGGTAATCATGCTGGCTTTGATGGCCTGTGACCGCTAT  
GTGGCTATTTGTAAACCTCTGCTGTACATGGTGGTGGTGTCTCGCGGCTCTGCCTCCTGCT  
40 GGTCTCCCTCACATACCTCTATGGCTTTTCTACAGCTATTGTGGTTTCATCTTATGTATTCT  
CTGTGCTTATTGCTCTTCTAATATAATCAATCATTTTTTACTGTGATAATGTTCTCTGTTA  
GCATTATCTTGCTCTGATACTTACTTACCAGAAACAGTTGTCTTTATATCTGCAGCAACAA  
ATGTGGTTGGTTCCTTGATTATAGTTCTAGTATCTTATTTCAATATTGTTTGTCTATTTTA  
AAAATATGTTTCATCAGAAGGAAGGAAAAAGCCTTTTCTACCTGTGCTTCACATATGATGG  
45 CAGTCACAATTTTTTATGGGACATTGCTATTCATGTATGTGCAGCCCCGAAGTAACCATTC  
ATTGGATACTGATGATAAGATGGCTTCTGTGTTTTACACGTTGGTAATTCCTATGCTGAAT  
CCCTTGATCTACAGCCTGAGGAATAAGGATGTGAAGACTGCTCTACAGAGATTTCATGACA  
AATCTGTGCTATTCTTTAAAACAATGTAA (SEQ ID NO: 134)

**AOLFR73 sequences:**

MNHVVKHNTAVTKVTEFILMGITDNPGLQAPLFLFLIYLVTVIGNLGMVILTYLDSKLHTP  
MYFFLRHLSITDLGYSTVIAPKMLVNFIVHKNTISYNWYATQLAFFEIFIISSELFILSAMAYDRYV  
AICKPLLYVIMAELVWVVLVIVPYLYSTFVSLFTIKLFKLSFCGNSIISFYCDCIPLMSILCSDT  
NELELILIFSGCNLLFSLIVLISYMFILVAILRMNSRKGRYKAFSTCSSHLTVVIMFYGTLLFIYL  
55 QPKSSH TLADKMASVFYTLIPMLNPLIYSLRNKEVKDALKRTLNRFKIPI (SEQ ID NO: 135)

ATGAATCATGTGGTAAAAACACAATCACACGGCAGTGACCAAGGTGACTGAATTTATTCTCA  
 TGGGGATTACAGACAACCCTGGGCTGCAGGCTCCACTGTTTGGACTCTTCCTCATCATATA  
 TCTGGTCACAGTGATAGGCAATCTGGGCATGGTTATCTTGACCTACTTGGACTCCAAGCTA  
 CACACCCCCATGTACTTTTTCCTTAGACATTTGTCAATCACTGATCTTGGTTACTCCACTGT  
 5 CATTGCCCGAAGATGTTAGTAAACTTCATAGTGCACAAAAACACAATTTCTTACAATTGG  
 TATGCCACTCAGCTAGCATTCTTTGAGATTTTCATCATCTCTGAGCTCTTTATTCTATCAGC  
 AATGGCCTATGATCGCTACGTAGCCATCTGTAAACCTCTTCTGTACGTGATCATCATGGCA  
 GAGAAAGTACTTTGGGTGCTGGTAATTGTTCCCTATCTCTATAGCACGTTTGTGTCACTATT  
 10 TCTCACAATTAAGTTATTTAAACTGTCTTCTGTGGCTCAAACATAATCAGCTATTTTTACT  
 GTGACTGTATCCCTCTGATGTCCATACTCTGTTCTGACACAAATGAATTAGAATTAATAAT  
 TTTGATCTTCTCAGGCTGTAATTTGCTCTTCTCCCTCTCAATTGTTCTCATATCCTACATGTT  
 TATTCTAGTGGCCATTCTCAGAATGAACTCAAGGAAAGGGAGGTACAAAGCCTTCTCCACC  
 TGTAGCTCTCATCTGACAGTGGTGATCATGTTCTATGGGACATTGTTATTTATTACTTGCA  
 ACCCAAGTCCAGTCATACTTTGGCTATTGATAAAATGGCCTCAGTGTTTTATACCTGTTG  
 15 ATTCCTATGCTGAATCCGTTGATCTACAGCCTAAGGAACAAAGAAGTAAAAGATGCTCTAA  
 AGAGAACTTTAACCAATCGATTCAAAATTTCCATTAA (SEQ ID NO: 136)

**AOLFR74 sequences:**

MEQHNLTTVNEFILTGITDIAELQAPLFLFLMIYVISVMGNLGMIVLTKLDSRLQTPMYFFLRH  
 20 LAFMDLGYSTTVGPKMLVNFVVDKNIISYYFCATQLAFFLVFIGSELFILSAMSVDLYVAICNPL  
 LYTVIMSRRVCQVLVAIPYLYCTFISLLVTIKIFLSFCGYNVISHFYCDLPLPLLLCSNTHBIELI  
 ILFAAIDLISLLIVLLSYLLLVAILRMNSAGRQKAFSTCGAHLTVVIVFYGTLLFMYVQPKSSH  
 SFDTDKVASIFYTLVIPMLNPLIYSLRNKDVKYALRRTWNNLCNIFV (SEQ ID NO: 137)

25 ATGGAACAACACAATCTAACAACGGTGAATGAATTCATTCTTACGGGAATCACAGATATC  
 GCTGAGCTGCAGGCACCATTATTTGCATTGTTCTCATGATCTATGTGATCTCAGTGATGG  
 GCAATTTGGGCATGATTGTCCTCACCAGTTGGACTCCAGGTTGCAAAACCCTATGTACTT  
 TTTTCTCAGACATCTGGCTTTTCATGGATCTTGGTTATTCAACAACCTGTGGGACCCAAAATG  
 TTAGTAAATTTTGTGTGGATAAGAATATAATTTCTTATTATTTTTGTGCAACACAGCTAGC  
 30 TTTCTTTCTTGTGTTTATTGGTAGTGAACTTTTATTCTCTCAGCCATGTCCTACGACCTCT  
 ATGTGGCCATCTGTAACCCCTCTGCTATACACAGTAATCATGTACGAAGGGTATGTCAGGT  
 GCTGGTAGCAATCCCTTACCTCTATTGCACATTCATTCTCTTCTAGTCACCATAAAGATTT  
 TTACTTTATCCTTCTGTGGCTACAACGTCATTAGTCATTTCTACTGTGACAGCTCTCCCTTG  
 TTACCTTTGCTTTGTTCAAATACACATGAAATTGAATTGATAATTCTGATCTTTGCAGCTAT  
 35 TGATTTGATTTTCATCTCTTCTGATAGTTCTTTTATCTTACCTGCTCATCCTTGTAGCCATTCT  
 CAGGATGAATTCTGCTGGCAGACAAAAGGCTTTTTCTACCTGTGGAGCCCACCTGACAGTG  
 GTCATAGTGTCTATGGGACTTTGCTTTTCATGTACGTGCAGCCCAAGTCCAGTCATTCCCT  
 TGACACTGATAAAGTGGCTTCCATATTTTACACCCTGGTTATCCCCATGTTGAATCCCTTGA  
 40 TCTATAGTTTACGAAACAAAGATGTAAAATATGCCCTACGAAGGACATGGAATAAATTATG  
 TAATATTTTTGTTTAA (SEQ ID NO: 138)

**AOLFR75 sequences:**

MEGKNQTNISEFLLLGFSWQQQVLLFALFLCLYLTGLFGNLLILLAIGSDHCLHTPMYFFLA  
 NLSLVDLCLPSATVPKMLLNITQTQTISYPGCLAQMYFCMMFANMDNELLTVMAYDRYVAI  
 45 CHPLHYSTMALRLCASLVAAPWVIAILNPLLHTLMMALHLFCSDNVIIHFFCDINSLPLSCSD  
 TSLNQLSVLATVGLIFVPSVCIIVSYILIVSAVMKVPSAQGKLKAFSTCGSHLALVILFYGANT  
 GVYMSPLSNHSTEKDSAASVIFMVVAPVLNPFYISLRNNELKGTLLKTLRPGAVAHACNPSTL  
 GGRGGWIMRSGDRDHPG (SEQ ID NO: 139)

50 ATGGAAGGGAAAAATCAAACCAATATCTCTGAATTTCTCCTCCTGGGCTTCTCAAGTTGGC  
 AACACAGCAGGTGCTACTCTTTGCACTTTTCTGTGCTCTATTTAACAGGGCTGTTTGGA  
 AACTTACTCATCTTGCTGGCCATTGGCTCGGACTCACTGCCTTCACACACCCATGTATTTCTT  
 CCTTGCCAATCTGTCTTGGTAGACCTCTGCCTTCCCTCAGCCACAGTCCCCAAGATGCTAC  
 TGAACATCCAAACCCAAACCCAAACCATCTCCTATCCCGGCTGCCTGGCTCAGATGTATTT  
 55 CTGTATGATGTTTGCCAATATGGACAATTTTCTTCTCACAGTGATGGCATATGACCGTTAC  
 GTGGCCATCTGTCACCCCTTTACATTACTCCACCATTATGGCCCTGCGCCTCTGTGCCTCTCT

GGTAGCTGCACCTTGGGTCATTGCCATTTTGAACCTCTCTTGCACACTCTTATGATGGCCC  
ATCTGCACTTCTGCTCTGATAATGTTATCCACCATTTCTTCTGTGATATCAACTCTCTCCTC  
CCTCTGTCCTGTTCCGACACCAAGTCTTAATCAGTTGAGTGTCTGGCTACGGTGGGGCTGA  
TCTTTGTGGTACCTTCAGTGTGTATCCTGGTATCCTATATCCTCATTGTTTCTGCTGTGATG  
5 AAAGTCCCTTCTGCCCCAAGGAAAACTCAAGGCTTCTCTACCTGTGGATCTCACCTTGCCTT  
GGTCATTCTTTTCTATGGAGCAAACACAGGGGTCTATATGAGCCCCTTATCCAATCACTCT  
ACTGAAAAAGACTCAGCCGCATCAGTCATTTTTATGTTGTAGCACCTGTGTTGAATCCAT  
TCATTTACAGTTTAAGAAACAATGAACTGAAGGGGACTTTAAAAAAGACCCTAAGCCGGC  
CGGGCGCGGTGGCTCAGCCTGTAATCCAGCACTTTGGGAGGCCGAGGCGGGTGGATCA  
10 TGAGGTCAGGAGATCGAGACCATCCTGGCTAA (SEQ ID NO: 140)

**AOLFR76 sequences:**

MENNTEVSEFILLGLTNAPELQVPLFIMFTLIYLITLTGNLGMILLLDSHLHTPMYFFLSNLSLA  
GIGYSSAVTPKVLTGLLIEDKAISYSACAAQMFFCAVFATVENYLLSSMAYDRYAAVCNPLHY  
15 TTTMTTRVCACLAIGCYVIGFLNASIQIGDTFRLSFCMSNVIIHFFCDKPAVITLTCSEKHISELIL  
VLISFNVFFALLVTLISYLFILITILKRHTGKGYQKPLSTCGSHLIAIFLYITVIIMYIRPSSSHSM  
DTDKIASVFYTMIPMLSPIVYTLRNKDVKNAFMKVVEKAKYSLDSVF (SEQ ID NO: 141)

ATGGAGAATAATACAGAGGTGAGTGAATTCATCCTGCTTGGTCTAACCAATGCCCCAGAA  
20 CTACAGGTTCCCCTCTTTATCATGTTTACCCTCATCTACCTCATCACTCTGACTGGGAACCT  
GGGGATGATCATATTAATCCTGCTGGACTCTCATCTCCACACTCCCATGTACTTTTTTCTCA  
GTAACCTGTCTCTTGCAGGCATTGGTTACTCCTCAGCTGTCACTCCAAAGGTTTTAACTGG  
GTTGCTTATAGAAGACAAAGCCATCTCCTACAGTGCCTGTGCTGCTCAGATGTTCTTTTGT  
GCAGTCTTTGCCACTGTGGAAAATTACCTCTTGTCTCAATGGCCTATGACCGCTACGCAG  
25 CAGTGTGTAACCCCTACATTATACCACCACCATGACAACACGTGTGTGCTTGTCTGGC  
TATAGGCTGTTATGTCATTGGTTTTCTGAATGCTTCTATCCAAATTGGAGATACATTTTCGCC  
TCTCTTTCTGCATGTCCAATGTGATTTCATCACTTTTTCTGTGACAAACCAGCAGTCATTACT  
CTGACCTGCTCTGAGAAACACATTAGTGAGTTGATTCTTGTCTTATATCAAGTTTAAATGT  
CTTTTTTGCACITCTTGTACCTTGATTTCCTATCTGTTTCATATTGATCACCACTTCTTAAGAG  
30 GCACACAGGTAAGGGATACCAGAAGCCTTTATCTACCTGTGGTTCTCACCTCATTGCCATT  
TTCTTATTTTATATAACTGTCATCATCATGTACATACGACCAAGTTCAGTCATTCCATGGA  
CACAGACAAAATTGCATCTGTGTTCTACACTATGATCATCCCCATGCTCAGTCCTATAGTCT  
ATACCCTGAGGAACAAAGAGCGTGAAGAATGCATTTCATGAAGGTTGTTGAGAAGGCAAAAT  
ATTCTCTAGATTCAAGTCTTTTAA (SEQ ID NO: 142)

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**AOLFR77 sequences:**

MGDVNQSVASDFILVGLFSHSGSRQLLFSLVAVMVFVIGLLGNTVLLFLIRVDSRLHTPMYFLLS  
QLSLFDIGCPMVTIPKMASDFLRGEGATSYGGGAAQIFFLTLMGVAEGVLLVLMSYDRYVAVC  
QPLQYPVLMRRQVCLLMGSSWVGVNLASIQTSITLHFPYCASRIVDHFFCEVPALLKLSCA  
40 DTCAYEMALSTSGVLILMLPLSLIATSYGHVLQAVLSMRSEEARHKAVTTCSSHITVVGLFYGA  
AVFMYMVP CAYHSPQQDNVVSFLFYSLVPTLNPLIYSLRNPEVWMALVKVLSRAGLRQMC  
(SEQ ID NO: 143)

ATGGGGGATGTGAATCAGTCGGTGGCCTCAGACTTCATTCTGGTGGGCCTCTTCAGTCACT  
45 CAGGATCACGCCAGCTCCTCTTCTCCCTGGTGGCTGTATGTTTGTATAGGCCTTCTGGGC  
AACACCGTTCTTCTCTTCTTGATCCGTGTGGACTCCCGGCTCCACACACCCATGTACTTCCT  
GCTCAGCCAGCTCTCCCTGTTTGACATTGGCTGTCCCATGGTCACCATCCCCAAGATGGCA  
TCAGACTTTCTGCGGGGAGAAGGTGCCACCTCCTATGGAGGTGGTGCAGCTCAAATATTCT  
TCCTCACACTGATGGGTGTGGCTGAGGGCGTCTGTTGGTCTCATGTCTTATGACCGTTA  
50 TGTTGCTGTGTGCCAGCCCTGCAGTATCCTGTACTTATGAGACGCCAGGTATGTCTGCTG  
ATGATGGGCTCCTCCTGGGTGGTGTGCTCAACGCCTCCATCCAGACCTCCATCACCC  
TGCATTTTCCCTACTGTGCCTCCCGTATTGTGGATCACTTCTTCTGTGAGGTGCCAGCCCTA  
CTGAAGCTCTCCTGTGCAGATACCTGTGCCTACGAGATGGCGCTGTCCACCTCAGGGGTGC  
TGATCCTAATGCTCCCTCTTTCCCTCATCGCCACCTCCTACGGCCACGTGTTGCAGGCTGTT  
55 CTAAGCATGCGCTCAGAGGAGGCCAGACACAAGGCTGTCACCACCTGCTCCTCGCACATCA  
CGGTAGTGGGGCTCTTTTATGGTGCCGCGGTGTTTCATGTACATGGTGCCTTGCGCCTACCA



CAGTCCACAGCAGGATAACGTGGTTTCCCTCTTCTATAGCCTTGTCACCCCTACACTCAAC .  
 CCCCTTATCTACAGTCTGAGGAATCCGGAGGTGTGGATGGCTTTGGTCAAAGTGCTTAGCA  
 GAGCTGGACTCAGGCAAATGTGCTGA (SEQ ID NO: 144)

5 **AOLFR78 sequences:**

MSPDGNHSSDPTEFVLAGLPNLNSARVELFSVFLVYLLNLTGNVLIVGVVRADTRLQTPMYF  
 FLGNLSCLLEILLTSVTPKMLSNFLSRQHTISFAACITQFYFYFFLGASEFLLAVMSADRYLAICH  
 PLRYPLLMMSGAVCFRVALACWVGGLVPVLGPTVAVALLPFCKQGAVVQHFFCDSGPLLRAC  
 TNTKKLEETDFVLASLVVSSLLITAVSYGLIVLAVLSIPSASGRQKAFSTCTSHLIVVTLFYGSAI  
 10 FLYVRPSQSGSVDTNWAVTVITFVTPLLNPFYIALRNEQVKEALKDMFRKVVAGVLGNLLLD  
 KCLSEKAVK (SEQ ID NO: 145)

ATGAGTCCTGATGGGAACACAGTAGTGATCCAACAGAGTTCGTCCTGGCAGGGCTCCCA  
 AATCTCAACAGCGCAAGAGTGGAATTATTTTCTGTGTTTCTTCTGTCTATCTCCTGAATCT  
 15 GACAGGCAATGTGTTGATTGTGGGGGTGGTAAGGGCTGATACTCGACTACAGACCCCTAT  
 GTACTTCTTCTGGGTAACCTGTCCTGCCTAGAGATACTGCTCACTTCTGTCATCTTCCAA  
 AGATGCTGAGCAATTTCTCTCAAGGCAACACACTATTTCTTTGCTGCTATGTATCACCCA  
 ATTCTATTTCTACTTCTTCTCGGGGCTCCGAGTTCTTACTGTTGGCTGTCATGCTGCGG  
 ATCGCTACCTGGCCATCTGTCATCCTCTGCGCTACCCCTTGCTCATGAGTGGGGCTGTGTG  
 20 CTTTCGTGTGGCCTTGGCCTGCTGGGTGGGGGGACTCGTCCCTGTGCTTGGTCCCACAGTG  
 GCTGTGGCCTTGCTTCTTCTGTAAAGCAGGGTGCTGTGGTACAGCACTTCTTCTGCGACA  
 GTGGCCCACTGCTCCGCCTGGCTTGACCAACACCAAGAAGCTGGAGGAGACTGACTTTGT  
 CCTGGCCTCCCTCGTCATTGTATCTTCTTGTGATCACTGCTGTGTCTACGGCCTCATTG  
 TGCTGGCAGTCCTGAGCATCCCCTCTGCTTCAGGCCGTCAGAAGGCCTTCTCTACCTGTAC  
 25 TCCCCACTTGATAGTGGTGACCTCTTCTATGGAAGTGCCATTTTCTCTATGTGCGGCCAT  
 CGCAGAGTGGTTCTGTGGACACTAACTGGGCAGTGACAGTAATAACGACATTTGTGACAC  
 CACTGTTGAATCCATTCTATGCTTACGTAATGAGCAAGTCAAGGAAGCTTTGAAGGA  
 CATGTTTAGGAAGGTAGTGGCAGGCGTTTTAGGGAATCTTTTACTTGATAAATGTCTCAGT  
 GAGAAAGCAGTAAAGTAA (SEQ ID NO: 146)

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**AOLFR79 sequences:**

MTPGELALASGNHTPVTKFILOQFSNYPDLQELLFGAILLIYAITVVGNLGMMLIFTDSHLQSP  
 MYFFLNVL SFLDICYSVVPKLLVNFLVSDKSISFEGCVVQLAFFVHVTAESFLLASMA YDR  
 FLAICQPLHYGSIMTRGTCLQLVAVSYAFGGANS AIQTGNVFALPFCGPNQLTHYYCDIPLLH  
 35 LACANTATARVVLVFSALVTLPAAVILTSYCLVLVAIGRMRSVAGREKDLSTCASHFLAIAI  
 FYGTVVFTYVQPHGSTNNTNGQVVSFYTHIIPMLNPFYSLRNKEVK GALQRKLQVNIFPG  
 (SEQ ID NO: 147)

ATGACACCTGGAGAACTAGCCCTTGCCAGTGCGCAACCACACCCCAAGTTCATCT  
 40 TGCAGGGATTCTCCAATTATCCAGACCTCCAGGAGCTTCTCTTCGGAGCCATCTGCTCAT  
 CTATGCCATAACAGTGGTGGGCAACTTGGGAATGATGGCACTCATCTTCACAGACTCCCAT  
 CTCCAAAGCCCAATGTATTTCTTCTCAATGTCCTCTCGTTTCTTGATATTTGTIACCTTCT  
 GTGGTCACACCTAAGCTCTTGGTCAACTTCTGCTCTGACAAGTCCATCTCTTTTGAGG  
 GCTGTGTGGTCCAGCTCGCCTTCTTTGTAGTGCATGTGACAGCTGAGAGCTTCTGCTGGC  
 45 TCCATGGCCTATGACCGCTTCTAGCCATCTGTCAACCCCTCCATTATGGTTCTATCATGA  
 CCAGGGGGACCTGTCTCCAGCTGGTAGCTGTGCTCATGCAATTTGGTGGAGCCAACTCCGC  
 TATCCAGACTGGAAATGTCTTTGCCCTGCCTTTCTGTGGGCCCAACCAGCTAACACACTAC  
 TACTGTGACATACCACCCCTTCTCCACCTGGCTTGTGCCAACACAGCCACAGCAAGAGTGG  
 TCCTCTATGTCTTTCTGCTCTGGTCACCCCTTCTGCCTGCTGCAGTCATTCTCACCTCCTACT  
 50 GCTTGGTCTTGGTGGCCATTGGGAGGATGCGCTCAGTAGCAGGGAGGGAGAAGGACCTCT  
 CCACTTGTGCCTCCCACTTTCTGGCCATTGCCATTTTCTATGGCACTGTGGTTTTACCTAT  
 GTTCAGCCCCATGGATCTACTAACAATACCAATGGCCAAGTAGTGTCCGTCTTCTACACCA  
 TCATAATTCCCATGCTCAATCCCTTCTATAGCCTCCGCAACAAGGAGGTGAAGGGCGC  
 TCTGCAGAGGAAGCTTCAGGTCAACATCTTTCCCGGCTGA (SEQ ID NO: 148)

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**AOLFR80 sequences:**

MEGINKTAKMQFFFRPSPDPEVQMLIFVFLMMYLTSLGGNATIAVIVQINHSLHTPMYFFLA  
 NLAVLEIFYTSSITPLALANLLSMGKTPVSITGCGTQMFFVFLGGADCVLLVVMAYDRFIAICH  
 PLRYRLIMSWSLCVELLVGSVLGFLSLPLTLIFHLPFCHNDEIYHFYCDMPAVMRLACADTR  
 5 VHKTALYIISFIVLSIPLSLISISYVFIVVAILRIRSAEGRQQAYSTCSSHILVLLQYGCTSFYILSPS  
 SSYSPEMGRVVSVAYTFITPILNPLIYSLRNKELKDALRKALRKF (SEQ ID NO: 149)

ATGGAAGGAATAAATAAAACTGCAAAGATGCAGTTTTTCTTTCGTCCATTCTCACCTGACC  
 CTGAGGTCCAGATGCTGATTTTTGTGGTCTTCCTGATGATGTATCTGACCAGCCTCGGTGG  
 10 AAATGCTACAATTGCAGTCATTGTTGAGATCAATCATTCCCTCCACACCCCCATGTACTTTT  
 TCCTGGCTAATCTGGCAGTTCTAGAAATCTTCTATACATCTTCCATCACCCCCATTGGCCTTG  
 GCAAACCTCCTTTCAATGGGCAAAACTCCTGTTTCCATCACGGGATGTGGCACCCAGATGT  
 TTTTCTTTGTCTTCTTGGGTGGGGCTGATTGTGTCTGCTGGTAGTCATGGCTTATGACCGG  
 TTTATAGCGATCTGTCACCTCTGCGATACAGGCTCATCATGAGCTGGTCTTGTGTGTGG  
 15 AGCTGCTGGTAGGCTCCTTGGTGTGCTGGGGTTCTGTTGTCACTGCCACTCACCATTTTAATC  
 TTCCATCTCCCATTTCTGCCACAATGATGAGATCTACCATTCTACTGTGACATGCCTGCAGT  
 CATGCGCCTGGCTTGTGCAGACACACGCGTTCACAAGACTGCTCTGTATATCATCAGCTTC  
 ATCGTCCTTAGCATCCCCCTCTCATTGATCTCCATCTCCTATGTCTTCATCGTGGTAGCCAT  
 TTTACGGATCCGGTCAGCAGAAAGGGCGCCAGCAAGCCTACTCTACCTGCTCTTCTCACATC  
 20 TTAGTGGTCTCCTGCAGTATGGCTGCACCAGCTTTATATACTTGTCCCCCAGTTCCAGCTA  
 CTCTCCTGAGATGGGCCGGGTGGTATCTGTGGCCTACACATTTATCACTCCCATTTTAAAC  
 CCCTTGATCTATAGTTGAGGAACAAGGAACTGAAAGATGCCCTAAGGAAAGCATTGAGA  
 AAATTCTAG (SEQ ID NO: 150)

**AOLFR81 sequences:**

MGVKNHSTVTEFLLSGLTEQAEQLPLFCLFLGIYTVTVVGNLSMISIRLNRLHTPMYYFLSS  
 LSFLDFCYSSVITPKMMKLWMESHLPVETRPSRPMMSNQTLVTEFILQGFSEHPEYRVFLFSCF  
 LFLYSGALTGNVLITLITFNPGLHAPMYFFLLNLATMDIICTSSIMPKALASLVSEESSISYGGC  
 30 MAQLYFLTWAASSELLLLTVMAYDRYAAICHPLHYSSMMSKVFCGLATAVWLLCAVNTAIH  
 TGLMLRLDFCGPNVHHFFCEVPPLLLSCSSTYVNGVMIVLADAFYGIVNFMLTIASYGFIVSSI  
 LKVKTAWGRQKAFSTCSSHLTVVCMYYTAVFYAYISPVSGYSAGKSKLAGLLYTVLSPTLNPL  
 IYTLRNKEVKAALRKLPFFRN (SEQ ID NO: 151)

ATGAAGCTGTGGATGGAGAGTCACCTGATAGTCCCAGAAACCCGTCCCAGCCCAAGGATG  
 35 ATGAGTAACCAGACGTTGGTAACCGAGTTCATCCTGCAGGGCTTTTCGGAGCACCCAGAAT  
 ACCGGGTGTTCTTATTCAGCTGTTTCTCTCTCTACTCTGGGGCCCTCACAGGTAATGTC  
 CTCATCACCTTGCCATCACGTTCAACCTGGGCTCCACGCTCCTATGTACTTTTTCTTACT  
 CAACTTGGCTACTATGGACATTATCTGCACCTCTTCCATCATGCCCAAGGCGCTGGCCAGT  
 CTGGTGTGCGGAAGAGAGCTCCATCTCCTACGGGGGCTGCATGGCCAGCTCTATTTCTCA  
 40 CGTGGGCTGCATCCTCAGAGCTGCTGCTCCTCACGGTCATGGCCTATGACCGGTACGCAGC  
 CATCTGCCACCCGCTGCATTACAGCAGCATGATGAGCAAGGTGTTCTGCAGCGGGCTGGCC  
 ACAGCCGTGTGGCTGCTCTGCGCCGTCAACACGGCCATCCACACGGGGCTGATGCTGCGCT  
 TGGATTTCTGTGGCCCCAATGTCATTATCCATTTCTTCTGCGAGGTCCCTCCCCTGCTGCTT  
 CTCTCCTGCAGCTCCACCTACGTCAACGGTGCATGATTGTCTGGCGGATGCTTTCTACG  
 45 GCATAGTGAACCTCCTGATGACCATCGCGTCTATGGCTTCATCGTCTCCAGCATCCTGAA  
 GGTGAAGACTGCCTGGGGGAGGCAGAAAGCCTTCTCCACCTGCTCTTCCCACCTCACCGTG  
 GTGTGCATGTATTACACCGCTGTCTTCTACGCCTACATAAGCCCGGTCTCTGGCTACAGCG  
 CAGGGAAGAGCAAGTTGGCTGGCCTGCTGTACACTGTGCTGAGTCTACCCTCAACCCCT  
 CATCTATACTTTGAGAAACAAGGAGGTCAAAGCAGCCCTCAGGAAGCTTTTCCCTTTCTTC  
 50 AGAAATTAA (SEQ ID NO: 152)

**AOLFR82 sequences:**

MQLNNNVTEFILLGLTQDPFWKKIVFVFLRLYLGTLLGNLLIISVKASQALKNPMFFFLFYLSL  
 SDTCLSTSIAPRMIVDALLKKTTSIFSECMIQVFSSHVFGCLEIFILITAVDRYVDICKPLHYMTII  
 55 SQWVCGVLMVAWVVGSCVHSLVQIFLALSPLFCGPNVINHCFLDLQPLLKQACSETYVVNLLI

VNSNGAICAVSYVMLIFSIVIFLHSLRNHSAEVIKKALSTCVSHIIVVILFFGPCIFMYTCPATVFP  
MDKMIAVFYTVGTSTFLNPVIYTLKNTBVKSAMRKLWSKKLITDDKR (SEQ ID NO: 153)

5 ATGCAACTGAATAATAATGTGACTGAGTTCATTCTGCTTGGATTGACACAGGATCCTTTTT  
GGAAGAAAATAGTGTGTTATTTTTTTCGCTCTCTACTTGGGAACACTGTTGGGTAATTT  
GCTAATCATTATTAGTGTCAAGGCCAGCCAGGCACTTAAGAACCCAATGTTCTTCTTCCTT  
TTCTACTTATCTTTATCTGATACTTGCCTCTCTACTTCCATAGCCCCCTAGAATGATTGTGGA  
TGCCCTTTTGAAGAAGACAACCTATCTCCTTCAGCGAGTGCATGATCCAAGTCTTTTCATCC  
CATGTCTTTGGCTGCCTGGAGATCTTCATCCTCATCCTCACGGCTGTTGACCGCTATGTGGA  
10 CATCTGTAAGCCCCCTGCACTACATGACCATCATAAGCCAGTGGGTCTGTGGTGTGTTGATG  
GCTGTGGCCTGGGTGGGATCCTGTGTGCATTCTTTAGTTCAGATTTTCTTGCCCTGAGTTT  
GCCATTCTGTGGCCCCAATGTGATCAATCACTGTTTCTGTGACTTGCAGCCCTTGTTGAAA  
CAAGCCTGTTTCAGAAACCTATGTGGTTAACCTACTCCTGGTTTCCAATAGTGGGGCCATTT  
GTGCAGTGAGTTATGTGCTGCTAATATTCTCCTATGTGCTCTTCTGCAATTCTCTGAGAAAC  
15 CACAGTGCTGAAGTGATAAAGAAAGCACTTTCACATGTGTCTCCACATCATTGTGGTCA  
TCTTGTTCTTTGGACCTTGCATATTTATGTACACATGCCCTGCAACCGTATTCCCCATGGAT  
AAGATGATAGCTGTATTTTATACAGTTGGAACATCTTTTCTCAACCTGTGATTTACACGCT  
GAAGAATACAGAAGTGAAAAGTGCCATGAGGAAGCTTTGGAGCAAGAAATTGATCACAGA  
TGACAAAAGATAA (SEQ ID NO: 154)

20

**AOLFR83 sequences:**

MGNWTAADVTEFVLLGFSLSRVELELLLVLLLPFTLLGNLLIISTVLSCSRLHTPMYFFLCNL  
SILDILFTSVISPKVLANLGSRDKTISFAGCITQCYFYFFLGTVEFLLTVMSYDRYATICPLRYT  
TIMRPSVCIGTVVFSWVGFLSVLFPTILISQLPFCGSNIINHFFCDSGPLLALACADTTAIELMDF  
25 MLSSMVLCCIVLVAYSITYIILTIVRIPSASGRKKAFNTCASHLTIVIPSGITVFYIYVTPSQKEYL  
EINKIPLVLSSVVTPLNPFYTLRNDTVQGVLRDVWVRVGRVFEKRMRAVLRSLSSNKDHQ  
GRACSSPPCVYSVKLQC (SEQ ID NO: 155)

30 ATGGGTAACTGGACTGCAGCGGTGACTGAGTTTGTCTGCTGGGGTTTTCCCTGAGCAGGG  
AGGTGGAGCTGCTGCTCCTGGTGCTCCTGCTGCCACGTTCCCTGCTGACTCTTCTGGGGAA  
CCTGCTCATCATCTCCACTGTGCTGTCTGCTCCCGCTCCACACCCCCATGTACTTCTTCT  
TGTGCAACCTCTCTATCCTGGACATCCTCTTACCTCAGTCATCTCTCCAAAAGTGTGGCC  
AACTTAGGATCTAGGGATAAAACCATCTCCTTTGCCGGATGTATCACCCAGTGCTATTTCT  
ACTTTTTCTTGGGCACAGTTGAGTTCCTCCTGCTGACGGTCATGTCCTATGACCGTTATGCC  
35 ACCATCTGCTGCCCCCTGCGGTACACCACCATCATGAGACCTTCTGTCTGCATTGGGACCG  
TTGTATTCTCTTGGGTGGGAGGCTTCCCTGTCTGTGCTCTTTCCAACCATCCTCATCTCCAG  
CTGCCCTTCTGTGGCTCCAATATCATTAACCACCTTCTTCTGTGACAGTGGACCCCTGTGCG  
CCTGGCCTGTGCAGACCACTGCCATCGAGCTGATGGATTTTATGCTTTCTTCCATGGTC  
ATCCTCTGCTGCATAGTCTCCTGCTGGCCTATTCTTACGTACATCATCTTGACCATAGTGC  
40 CATTCTTCTGCAAGTGGAAGGAAGAGGCCCTTTAATACCTGTGCTTCCACCTGACCATA  
GTCATCATTCCTAGTGGCATCACTGTGTTTATCTATGTGACTCCCTCCAGAAAGAATATCT  
GGAGATCAACAAGATCCCTTTGGTTCTGAGCAGTGTGGTGACTCCATTCCTCAACCCCTTT  
ATATATACTCTGAGGAATGACACAGTGCAGGGAGTCTCAGGGATGTGTGGGTGAGGGTT  
CGAGGAGTTTTTGAAGAGAGGATGAGGGCAGTGCTGAGAAGCAGATTATCCTCCAACAAA  
45 GACCACCAAGGAAGGGCTTGCTCTTCTCCACCATGTGTCTATTCTGTAAAGCTCCAGTGTT  
AG (SEQ ID NO: 156)

**AOLFR85 sequences:**

50 MGAKNNVTEFVLFGLFESREMQHTCFVFFLFHVLTVLGNLLVIITINARKTLKSPMYFFLSQL  
SFADICYPSTIPKMIADTFVEHKIISFNGCMTQLFSAHFFGGTEIFLLTAMAYDRYVAICRPLHY  
TAIMDCRCKGGLLAGASWLAGFLHSILQTLTVQLPFCGPNEIDNFFCDVHPLLKLACADTYMV  
GLIVVANSGMISLASFFILIIISYVILLNLRSQSSDDRKA VSTCGSHVITVLLVLMPPMFMYIRPS  
TTLAADKLILFNIVMPPLLNPLIYTLRNDVKNAMRKLFRVKRSLGEK (SEQ ID NO: 157)

55 ATGGGTGCCAAGAACAATGTGACTGAGTTTGTGTTTATTTGGCCTTTTTGAGAGCAGAGAGA  
TGCAGCATACATGCTTTGTGGTATTCTTCTCTTTCATGTGCTCACTGTCTGCGGGAACCTT

CTGGTCATCATCACCATCAATGCTAGAAAGACCTGAAGTCTCCCATGTATTTCTTCCTGA  
 GCCAGTTGTCTTTTGCTGACATATGTTATCCATCCACTACCATAACCAAGATGATTGCTGAC  
 ACTTTTGTGGAGCATAAGATCATCTCCTTCAATGGCTGCATGACCCAGCTCTTTTCTGCCCCA  
 CTTCTTTGGTGGCACTGAGATCTTCTCCTTACAGCCATGGCCTATGACCGCTATGTGGCC  
 5 ATCTGTAGGCCCTGCACTACACAGCCATCATGGATTGCCGGAAGTGTGGCCTGCTAGCGG  
 GGGCCTCCTGGTTAGCTGGCTTCTGCATTCCATCCTGCAGACCCTCCTCACGGTTCAGCTG  
 CCTTTTGTGGGCCCAATGAGATAGACAACTTCTTCTGTGATGTTTCATCCCCTGCTCAAGTT  
 GGCCTGTGCAGACACCTACATGGTAGGTCTCATCGTGGTGGCCAACAGCGGTATGATTTCT  
 TTAGCATCCTTTTTATCCTTATCATTTCCTATGTTATCATCTTACTGAACCTAAGAAGCCA  
 10 GTCATCTGAGGACCGGCGTAAGGCTGTCTCCACATGTGGCTCACACGTAATCACTGTCCTT  
 TTGGTTCTCATGCCCCCATGTTTCATGTACATTCGTCCCTCCACCACCCTGGCTGCTGACAA  
 ACTTATCATCCTCTTTAACAATTGTGATGCCACCTTTGCTGAACCCCTTTGATCTATACACTAA  
 GGAACAACGATGTGAAAAATGCCATGAGGAAGCTGTTTAGGGTCAAGAGGAGCTTAGGGG  
 AGAAGTGA (SEQ ID NO: 158)

15

**AOLFR86 sequences:**

MQLVLLLMFLLVFIGNTAPAFSVTLESMDIPQNITEFFMLGLSQNSEVQRVLFVVFLLIYVVTV  
 GNMLIVVTTTSSPTLASPVYFFLANLSFIDTFYSSSMAPKLIADSLYEGRTISYECMAQLFGAHF  
 LGGVEIILLTVMAYDRYVAICKPLHNTTIMTRHLCAMLVGVAWLGGFLHSLVQLLLVLWLPFC  
 20 GPNVINHFACDLYPLLEVACTNTYVIGLLVVANSGLICLLNFLMLAASYIVILYSLRSHSADGRC  
 KALSTCGAHFIVVALFFVPCIFTYVHPFSTLPIDKNMALFYGILTPMLNPLIYTLRNEEVKNAMR  
 KLFTW (SEQ ID NO: 159)

ATGCAATTAGTTCATTACTTATGTTTCTCCTTGTCTTTATAGGCAATACTGCACCTGCATT  
 25 CTCAGTGACCTTGGAATCTATGGACATACCACAAAATATCACAGAATTTTTCATGCTGGGG  
 CTCTCACAGAACTCAGAGGTACAGAGAGTTCTCTTTGTGGTCTTTTGTGCTGATCTATGTGG  
 TCACGGTTTGTGGCAACATGCTCATTGTGGTCACTATCACCTCCAGCCCCACGCTGGCTTC  
 CCCTGTGTATTTTTTCTGGCCAACCTATCCTTTATTGACACCTTTTATTCTTCTTCTATGGC  
 TCCTAAACTCATTGCTGACTCATTGTATGAGGGGAGAACCATCTCTTATGAGTGCTGCATG  
 30 GCTCAGCTCTTTGGAGCTCATTTTTTTGGGAGGTGTTGAGATCATTCTGCTCACAGTGATGG  
 CTTATGACCGCTATGTGGCCATCTGTAAGCCCTGCACAATACTACCATCATGACCAGGCA  
 TCTCTGTGCCATGCTTGTAGGGGTGGCTTGGCTTGGGGGCTTCTGCATTTCATTGGTTTCAG  
 CTCTCCTGGTCCTTTGGTTGCCCTTCTGTGGGGCCCAATGTGATCAATCACTTTGCCTGTGA  
 CTTGTACCCTTTGCTGGAAGTTGCCTGCACCAATACGTATGTCATTGGTCTGCTGGTGGTT  
 35 GCCAACAGTGGTTTAATCTGCCTGTTGAACTTCCTCATGCTGGCTGCCTCCTACATTGTCAT  
 CCTGTACTCCTTGAGGTCCACAGTGCAGATGGGAGATGCAAAGCCCTCTCCACCTGTGGA  
 GCCCACTTCATTGTTGTTGCCTTGTCTTTGTGCCCTGTATATTTACTTATGTGCATCCATTT  
 TCTACTTTACCTATAGACAAAAATATGGCATTATTTTATGGTATTCTGACACCTATGTTGAA  
 40 TCCACTCATTTATACCCTGAGAAATGAAGAGGTAAAAAATGCCATGAGAAAGCTCTTTACA  
 TGGTAA (SEQ ID NO: 160)

**AOLFR87 sequences:**

MNNIAQLSLGFIDLGPSVLQKIILTKIILLFKMYVSNCPCAIHRKINYPNTKLDFEQVNNITEFI  
 LLGLTQNAEAQKLLFAVFTLIYFLTMVDNLIVVTTTSPALDSPVYFFLSFFSFIDGCSSTMAP  
 45 KMIFDLLTEKKTISFSGCMTQLFVEHFFGGVEIILLVVMAYDCYVAICKPLYLITMNRQVCGL  
 LVAMAWVGGFLHALIQMLLIVWLPFCGPNVIDHFICDLFPLKLSCTDTHVFGFLVAANSGLM  
 CMLIFSILITSYVLILCSQRKALSTCAFHITVVVLFFVPCILVYLRPMITFPIDKAVSVFYTVVTPM  
 LNPLIYTLRNTTEVKNAMKQLWSQIHWGNLDCD (SEQ ID NO: 161)

ATGAATAACATAGCTCAACTTAGTCTTGGGTTTATAGATTTAGGGATTCCATCAGTGTTAC  
 AGAAAATAATCCTGACCAAAATTATTTTATTGTTCAAATGTATGTGTCAAATTGCAATCC  
 TTGTGCTATTACAGAAAAATCAATTATCCAAATACCAAATGGATTTGAGCAAGTGAAC  
 AACATAACGGAATTCATCTTGGCTTGGCCTGACACAGAACGCAGAGGCACAGAACTCTTGT  
 TTGCTGTGTTTACACTCATCTACTTCTCACCATGGTAGACAACCTAATCATTGTGGTGACA  
 55 ATCACCACCAGCCCAGCCCTGGACTCCCCCGTGTATTTTTTCTGTCTTTCTTTCTTTCAT  
 AGATGGCTGCTCCTCTTCTACCATGGCCCCCAAAATGATATTTGACTTACTCACTGAAAAAG

AAAACTATTTCTTCAGTGGGTGCATGACCCAGCTCTTTGTAGAACATTTCTTTGGGGGAG  
 TTGAGATCATTCTGCTCGTGGTGATGGCCTATGACTGCTATGTGGCCATCTGCAAGCCCCCT  
 GTACTACCTGATCACAATGAACAGGCAGGTATGTGGCCTCCTGGTGGCCATGGCATGGGTC  
 GGGGGATTTCTTCACGCTCTGATTCAAATGCTTTTAAATAGTCTGGCTGCCCTTCTGTGGCCC  
 5 CAATGTCATTGACCATTTCATCTGTGACCTTTTCCCTCTGCTAAAACTCTCCTGCACTGACA  
 CTCACGCTCTTTGGACTCTTTGTTGCCGCCAACAGTGGGCTGATGTGTATGCTCATTTTTTCT  
 ATTCTTATTACCTCTTACGTCCTAATCCTCTGCTCACAGCGGAAGGCTCTCTACCTGCGC  
 CTTCCATATCACTGTAGTCGTCCTATTCTTTGTTCCCTGTATATTGGTGTACCTTCGACCCA  
 TGATCACCTTCCCTATTGATAAAGCTGTGTCTGTGTTTTATACTGTGGTAACACCCATGTTA  
 10 AACCCTTTAATCTACACCTCAGAAACACAGAGGTGAAAAATGCCATGAAGCAGCTCTGG  
 AGCCAAATAATCTGGGGTAACAATTTGTGTGATTAG (SEQ ID NO: 162)

**AOLFR88 sequences:**

MWQKNQTSLADFILEGLFDDSLTHLFLFSLTMVVFLIAVSGNTLTILLICIDPQLHTPMYFLLSQ  
 15 LSLMDLMHVSTILKMATNYLSGKKSISFVGCATQHFLYLCLGGAECFLAVMSYDRYVAICH  
 PLRYAVLMNKKVGLMMAVMSWLGASVNSLIHMAILMHFPFCGPRKVYHFYCEFPVVKLV  
 GDITVYETTVYISSILLLLPIFLISTSYVFILQSVIQMRSSGSKRNAFATCGSHLTVVSLWFGACIFS  
 YMRPRSQCTLLQNKVGSVFYSIITPTLNSLIYTLRNKDVAKALRRVLRDVTQCIQRLQLWLP  
 RV (SEQ ID NO: 163)

20 ATGTGGCAGAAGAATCAGACCTCTCTGGCAGACTTCATCCTTGAGGGGCTCTTCGATGACT  
 CCCTTACCCACCTTTTCTTTCTCCTTGACCATGGTGGTCTTCCTTATTGCGGTGAGTGGC  
 AACACCCTCACCATTCTCCTCATCTGCATTGATCCCCAGCTTCATACACCAATGTATTTCTCT  
 GCTCAGCCAGCTCTCCCTCATGGATCTGATGCATGTCTCCACAATCATCCTGAAGATGGCT  
 25 ACCAACTACCTATCTGGCAAGAAATCTATCTCCTTTGTGGGCTGTGCAACCCAGCACTTCC  
 TCTATTTGTGTCTAGGTGGTGTGAATGTTTTCTCTTAGCTGTCTATGACCGCTAT  
 GTTGCCATCTGTCTCACTGCGCTATGCTGTGCTCATGAACAAGAAGGTGGGACTGATGA  
 TGGCTGTCTATGTCATGGTTGGGGGCATCCGTGAACCTCCCTAATTCACATGGCGATCTTGAT  
 GCACTTCCCTTTCTGTGGGCCTCGGAAAGTCTACCACTTCTACTGTGAGTTCCCAGCTGTTG  
 30 TGAAGTTGGTATGTGGCGACATCACTGTGTATGAGACCACAGTGTACATCAGCAGCATTCT  
 CCTCCTCCTCCCATCTTCTGATTTCTACATCCTATGTCTTCATCCTTCAAAGTGTCAATCA  
 GATGCGCTCATCTGGGAGCAAGAGAAATGCCTTTGCCACTGTGGCTCCCACCTCACGGTG  
 GTTCTCTTTGGTTTGGTGCCTGCATCTTCTCTACATGAGACCCAGGTCCCAGTGCACCTCT  
 ATTGCAGAACAAAGTTGGTTCTGTGTTCTACAGCATCATTACGCCACATTGAATTCTCTG  
 35 ATTTATACTCTCCGAATAAAGATGTAGCTAAGGCTCTGAGAAGAGTGCTGAGGAGAGAT  
 GTTATCACCCAGTGCATTCAACGACTGCAATTGTGGTTGCCCCGAGTGTAG (SEQ ID NO:  
 164)

**AOLFR89 sequences:**

40 MLDPSISSHTLYLHSLFPQGLRKGMWQKNQTSLADFILEGLFDDSLTHLFLFSLTMVVFLIAVS  
 GNTLTILLICIDPQLHTPMYFLLSQLSLMDLMHVSTILKMATNYLSGKKSISFVGCATQHFLYL  
 CLGGAECFLAVMSYDRYVAICHPLRYAVLMNKKVGLMMAVMSWLGASVNSLIHMAILMHF  
 PFCGPRKVYHFYCEFPVVKLVCGDITVYETTVYISSILLLLPIFLISTSYVFILQSVIQMRSSGSK  
 RNAFATCGSHLTVVSLWFGACIFS YMRPRSQCTLLQNKVGSVFYSIITPTLNSLIYTLRNKDVA  
 45 KALRRVLRDVTQCIQRLQLWLP (SEQ ID NO: 165)

ATGCTGGACCCAGTATTTCCAGTCACACTCTTTATCTCCACTCTCTGTTTCCTCAGGGATT  
 GAGAAAGGGGACAATGTGGCAGAAGAATCAGACCTCTCTGGCAGACTTCATCCTTGAGGG  
 50 GCTCTTCGATGACTCCCTTACCCACCTTTTCTTTCTCCTTGACCATGGTGGTCTTCCTTAT  
 TGCGGTGAGTGGCAACACCCTCACCATTCTCCTCATCTGCATTGATCCCCAGCTTCATACA  
 CCAATGTATTTCTGCTCAGCCAGCTCTCCCTCATGGATCTGATGCATGTCTCCACAACCAT  
 CCTGAAGATGGCTACCAACTACCTATCTGGCAAGAAATCTATCTCCTTTGTGGGCTGTGCA  
 ACCAGCACTTCCCTCTATTTGTGTCTAGGTGGTGTGAATGTTTTCTCTTAGCTGTCATGTC  
 CTATGACCGCTATGTTGCCATCTGTCTCACTGCGCTATGCTGTGCTCATGAACAAGAAG  
 55 GTGGGACTGATGATGGCTGTCTATGTTGGGGGCATCCGTGAACCTCCCTAATTCACA  
 TGGCGATCTTGATGCACTTCCCTTTCTGTGGGCCTCGGAAAGTCTACCACTTCTACTGTGA

GTTCCCAGCTGTTGTGAAGTTGGTATGTGGCGACATCACTGTGTATGAGACCACAGTGTAC  
 ATCAGCAGCATTCTCCTCCTCCTCCCATCTTCTGATTCTACATCCTATGTCTTCATCCTT  
 CAAAGTGTCAATCAGATGCGCTCATCTGGGAGCAAGAGAAATGCCTTTGCCACTTGTGGCT  
 CCCACCTCACGGTGGTTTCTCTTTGGTTTGGTGCCTGCATCTTCTCCTACATGAGACCCAGG  
 5 TCCAGTGCACCTCTATTGCAGAACAAAGTTGGTTCTGTGTTCTACAGCATCATTACGCCCA  
 CATTGAATTCTCTGATTTATACTCTCCGGAATAAAGATGTAGCTAAGGCTCTGAGAAGAGT  
 GCTGAGGAGAGATGTTATCACCCAGTGCATTCAACGACTGCAATTGTGGTTGCCCCGAGTG  
 TAG (SEQ ID NO: 166)

10 **AOLFR90 sequences:**

MFSMTTEALNNFALGCTNLLMTMIPQIDLKQIFLCPNCRLYMIPVGAFIFSLGNMQNQSFVTEF  
 VLLGLSQNPVQEIIVFVFLFVYIATVGGNMLIVVTILSSPALLVSPMYFFLGFLSFLDACFSSVI  
 TPKMIVDSLIVTKTISFEGCMMQLFAEHFFAGVEVIVLTAMAYDRYVAICKPLHYSSIMNRRL  
 CGILMGVAWTGGLLHSMIQLFTFQLPFCGPNVINHFMCPLYLLELACTDTHIFGLMVVINS  
 15 FICTINFSLLLVSAYAVILLSLRTHSSEGRWKALSTCGSHIAVVILFFVPCIFVYTRPPSAFSLDKMA  
 AIFYIILNPLLNPLIYTFRNKEVKQAMRRIWNRMLMVVSDEKENIKL (SEQ ID NO: 167)

ATGTTCTCAATGACAACAGAAGCACTCAATAATTTTGCACCTGGATGTACCAACTTGTAA  
 TGACTATGATACCAAAATTGATCTGAAGCAAATTTTCTTTGTCCTAATTGCAGACTATA  
 20 CATGATCCCTGTTGGAGCTTTTCATCTTTTCTTGGGAAACATGCAAAACCAAAGCTTTGTA  
 ACTGAGTTTGTCTCCTGCGGACTTTACAGAATCCAAATGTTGAGGAAATAGTATTTGTTG  
 TATTTTGTGTTGTCTACATTGCAACTGTTGGGGGCAACATGCTAATTGTAGTAACCAATTCTC  
 AGCAGCCCTGCTCTTCTGGTGTCTCCTATGTAATCTTCTTGGGCTTCTGCTTCTCCTGGA  
 TCGGTGCTTCTCATCTGTCTATCACCCTAAAGATGATTGTAGACTCCCTCTATGTGACAAAA  
 25 ACCATCTCTTTTGAAGGCTGCATGATGCAGCTCTTTGCTGAACACTTCTTTGCTGGGGTGG  
 AGGTGATTGTCTCACAGCCATGGCCTATGATCGTTATGTGGCCATTTGCAAGCCCTTGCA  
 TTAATCTTCTATCATGAACAGGAGGCTCTGTGGCATTCTGATGGGGGTAGCCTGGACAGGG  
 GGCCTCTTGCAATCCATGATACAAATCTTTTACTTTCCAGCTTCCCTTTTGTGGCCCCAA  
 TGTCTATCAATCACTTTATGTGTGACTTGTACCCGTTACTGGAGCTTGCCTGCACTGATACTC  
 30 ACATCTTTGGCCTCATGGTGGTCATCAACAGTGGGTTTATCTGCATCATAAACTTCTCCTTG  
 TTGCTTGTCTCCTATGCTGTCTATCTGCTCTCTCTGAGAACACACAGTTCTGAAGGGCGCTG  
 GAAAGCTCTCTCCACCTGTGGATCTCACATTGCTGTTGTGATTTTGTCTTTGTCCCATGCA  
 TATTTGTATATACAGACCTCCATCTGCTTTTCCCTTGACAAAATGGCGGCAATATTTAT  
 ATCATCTTAAATCCCTTGGCTCAATCTTTGATTTACACTTTCAGGAATAAGGAAGTAAAC  
 35 AGGCCATGAGGAGAATATGGAACAGACTGATGGTGGTTTCTGATGAGAAAGAAAATATTA  
 AACTTTAA (SEQ ID NO: 168)

**AOLFR91 sequences:**

MGNWSTVTEITLIAFPALLEIRISLFFVVLVVTYTLTATGNITISLIWIDHRLQTPMYFFLSNLSFL  
 40 DILYTTVITPKLLACLLEKTIISFAGCMIQTYFYFFLGTVEFILLAVMSFDRYMAICDPLHYTVI  
 MNSRACLLLVLCWVGAFSLVLFPTIVVTRLPYCRKEINHFFCDIAPLLQVACINTHLIEKINFL  
 SALVILSSLAFTTGSYVYIISTILRIPSTQGRQKAFSTCASHITVVSIAHGSNIFVYVRPNQNSSLD  
 YDKVA AVLITVVTPLNPFYSLRNEKVQEVLRVNRIMTLIQRKT (SEQ ID NO: 169)

ATGGGAAACTGGAGCACTGTGACTGAAATCACCTAATTGCCTTCCCAGCTCTCCTGGAGA  
 TTCGAATATCTCTCTTCGTGGTTCTTGTGGTAACTTACACATTAACAGCAACAGGAAACAT  
 CACCATCATCTCCCTGATATGGATTGATCATCGCCTGCAAACTCCAATGTACTTCTCTCA  
 GTAATTTGTCTTTCTGGATATCTTATACACCACTGTCATTACCCCAAAGTTGTTGGCCTGC  
 CTCCTAGGAGAAAGAGAAAACCATATCTTTTGTGTTGTCATGATCCAAACATATTTCTACT  
 50 TCTTTCTGGGGACGGTGGAGTTTATCTCTTGGCGGTGATGTCTTTGACCGCTACATGGC  
 TATCTGCGACCCACTGCACTACACGGTCATCATGAACAGCAGGGCCTGCCTTCTGCTGGTT  
 CTGGGATGCTGGGTGGGAGCCTTCTGTCTGTGTTTCCAACCATTTGATGTGACAAGGC  
 TACCTTACTGTAGGAAAGAAATTAATCATCTTCTTCTGTGACATTGCCCTCTTCTTCAAGGTG  
 GCCTGTATAAATACTCACCTCATTGAGAAGATAAACTTTCTCCTCTCTGCCCTTGTCTATCCT  
 55 GAGCTCCCTGGCATTCACTACTGGGTCTACGTGTACATAATTTCTACCATCCTGCGTATCC  
 CCTCCACCCAGGGCCGTCAGAAAGCTTTTCTACCTGTGCTTCTCACATCACTGTTGTCTCC

ATTGCCACGGGAGCAACATCTTTGTGTATGTGAGACCCAATCAGAACTCCTCACTGGATT  
ATGACAAGGTGGCCGCTGTCCTCATCACAGTGGTGACCCCTCTCCTGAACCCCTTTATCTA  
CAGCTTGAGGAATGAGAAGGTACAGGAAGTGTGAGAGAGACAGTGAACAGAATCATGAC  
CTTGATACAAAGGAAAACCTTGA (SEQ ID NO: 170)

5

**AOLFR92 sequences:**

MRNGTVITEFILLGFPVIQGLQTPLFIAFLTYILTLAGNGLIATVWAEPRLOIPMYFFLCNLSFLE  
IWYTTITVIPKLLGTFVVARVVICMSCLLQAFFHFVGTTEFLILTIMSFDRYLTCNPLHPTIM  
TSKLCLQLALSSWVVGFTIVFCQTMILLIQLPFCGNNVISHFYCDVGPSLKAACIDTSILELLGVIA  
TILVIPGSLLFNMISSYIYLSAILRIPSATGHQKTFSTCASHLTVVSLLYGAVLFMYLRPTAHSSFK  
INKVSVLNTILTPLLNPFIYTIRNKEVKGALRKAMTCPKTGHAK (SEQ ID NO: 171)

10

ATGAGAAATGGCACAGTAATCACAGAATTCATCCTGCTAGGCTTTCCTGTTATCCAAGGCC  
TACAAACACCTCTCTTTATTGCAATCTTTCTCACCTACATATTAACCCCTGCAGGCAATGGG  
CTTATTATTGCCACTGTGTGGGCTGAGCCCAGGCTACAAATCCAATGTACTTCTCCTTTG  
TAACCTGTCTTTCTTAGAAATCTGGTACACCACCACAGTCATCCCCAAACTGCTAGGAACC  
TTTGTAGTGGCAAGAACAGTAATCTGCATGTCCTGCTGCCTGCTGCAGGCCTTCTTCCACT  
TCTTCGTGGGCAACCACCGAGTTCCTGATCCTCACTATCATGTCTTTTGACCGCTACCTCACC  
ATCTGCAATCCCTTCAACCACCCACCATCATGACCAGCAAACTCTGCCTGCAGCTGGCCC  
TGAGCTCCTGGGTGGTGGGCTTACCATTGTCTTTTGTGACACGATGCTGCTCATCCAGTT  
GCCATTCTGTGGCAATAATGTTATCAGTCATTTCTACTGTGATGTTGGGCCCAGTTGAAA  
GCCGCTGCATAGACACCAGCATTTTGGAACTCCTGGGCGTCATAGCAACCATCCTTGTGA  
TCCCAGGGTCACTTCTCTTTAATATGATTTCTTATATCTACATTCTGTCCGCAATCCTACGA  
ATTCCTTCAGCCACTGGCCACCAAAAGACTTCTCTACCTGTGCCTCGCACCTGACAGTTGT  
CTCCCTGCTCTACGGGGCTGTTCTGTTCATGTACCTAAGACCCACAGCACACTCCTCCTTTA  
AGATTAATAAGGTGGTGTCTGTGCTAAATACTATCCTCACCCCCCTTCTGAATCCCTTTATT  
TATACTATTAGAAACAAGGAGGTGAAGGGAGCCTTAAGAAAGGCAATGACTTGCCCAAAG  
ACTGGTCATGCAAAGTAA (SEQ ID NO: 172)

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**AOLFR93 sequences:**

MLMNYSSATEFYLLGFPSEELHHILFAIFFFFYLVTLMGNTVIIMIVCVDKRLQSPMYFFLGHIL  
SALEILVTTIIVPVMWGLLLPGMQTYLSACVVQLFLYLAVGTTEFALLGAMAVDRYVAVCN  
PLRYNIIMNRHTCNFVVLVSWVFGFLFQIWPVYVMFQLTYCKSNVNNFFCDRGQLKLSCN  
NTLFTEFILFLMAVFLFGSLIPTVSNAYIISTILKIPSSSGRRKSFSTCASHFTCVVIGYGSCFLY  
VKPKQTQAADYNWVVSMLMVSVVTPLNPFIFTLRNDKVIEALRDGVKRCCQLFRN (SEQ ID  
NO: 173)

35

ATGTTGATGAATTACTCTAGTGCCACTGAATTTTATCTCCTTGGCTTCCCTGGCTCTGAAGA  
ACTACATCATATCCTTTTTGCTATATTCTTCTTTTCTACTTGGTGACATTAATGGGAAACA  
CAGTCATCATCATGATTGTCTGTGTGGATAAACGCTCTGCAGTCCCCCATGTATTTCTTCTC  
GGCCACCTCTCTGCCCTGGAGATCCTGGTCACAACCATAATCGTCCCCGTGATGCTTTGGG  
GATTGCTGCTCCCTGGGATGCAGACAATATATTTGTCTGCCTGTGTTGTCCAGCTCTTCTTG  
TACCTTGCTGTGGGGACAACAGAGTTCGCATTACTTGGAGCAATGGCTGTGGACCGTTATG  
TGGCTGTCTGTAAACCCTCTGAGGTACAACATCATTATGAACAGACACACCTGCAACTTTGT  
GGTTCTTGTGTCTATGGGTGTTTGGGTTTCTTTTTTCAAATCTGGCCGGTCTATGTCATGTTT  
AGCTTACTTACTGCAATCAAATGTGGTGAACAATTTTTTTTGTGACCGAGGGCAATTGCT  
CAAATATCCTGCAATAATACTCTTTTACGGAGTTTATCCTCTTCTTAATGGCTGTTTTTG  
TTCTCTTTGGTTCTTTGATCCCTACAATTGTCTCCAACGCCTACATCATCTCCACCATTTCTC  
AAGATCCCGTCATCCTCTGGCCGGAGGAAATCCTTCTCCACTTGTGCCTCCCACTTCACTG  
TGTTGTGATTGGCTACGGCAGCTGCTTGTCTCTACGTGAAACCCAAGCAAACGCAGGCA  
GCTGATTACAATTGGGTAGTTCCCTGATGGTTTCAGTAGTAACCTCCTTTCCTCAATCCTTT  
CATCTTCAACCTCCGGAATGATAAAGTCATAGAGGCCCTTCGGGATGGGGTGAAACGCTGC  
TGTCAACTATTAGGAATTAG (SEQ ID NO: 174)

50

**AOLFR94 sequences:**

METWVNQSYTDGFFLLGIFSHSTADLVLFVSVMAVFTVALCGNVLLIFLIYMDPHLHTPMYFF  
 LSQSLMDLMLVCTNVPKMAANFLSGRKSISFVGCIGLQGLFVCLVGSEGLLLGLMAYDRYVA  
 ISHPLHYPILMNQRVCLQITGSSWAFGIIDGLIQMVVVMNFPYCGLRKVNHHFCEMLSLLKLAC  
 5 VDTSLFEKVIFACCVFMLLPFSIIVASYAHILGTVLQMHSQAQWKKALATCSSHLTAVTLFYG  
 AAMFIYLRPRHYRAPSHDKVASIFYTVLTPMLNPLIYSLRNREVMGALRKGLDRCRIGSQH  
 (SEQ ID NO: 175)

ATGGAGACGTGGGTGAACCAGTCCTACACAGATGGCTTCTTCTCTTAGGCATCTTCTCCC  
 10 ACAGTACTGCTGACCTTGTCTCTTCTCCGTGGTTATGGCGGTCTTCACAGTGGCCCTCTGT  
 GGAATGTCTCTCATCTTCTCATCTACATGGACCCTCACCTTCACACCCCATGTACTT  
 CTTCTCAGCCAGCTCTCCCTCATGGACCTCATGTTGGTCTGTACCAATGTGCCAAAGATG  
 GCAGCCAACTTCTGTCTGGCAGGAAGTCCATCTCTTTGTGGGCTGTGGCATACAAATG  
 GCCTCTTTGTCTGTCTTGTGGGATCTGAGGGGCTCTTGTCTGGGACTCATGGCTTATGACCG  
 15 CTATGTGGCCATTAGCCACCCACTTCACTATCCCATCCTCATGAATCAGAGGGTCTGTCTCC  
 AGATTACTGGGAGCTCCTGGGCCTTTGGGATAATCGATGGCTTGATCCAGATGGTGGTAGT  
 AATGAATTTCCCCTACTGTGGCTTGAGGAAGGTGAACCATTTCTTCTGTGAGATGCTATCC  
 TTGTTGAAGCTGGCCTGTGTAGACACATCCCTGTTTGAGAAGGTGATATTTGCTTGTGTG  
 TCTTCATGCTTCTCTTCCCATCTCCATCATCGTGGCCTCCTATGCTCACATTCTAGGGACT  
 20 GTGCTGCAAATGCACCTCTGCTCAGGCCTGGAAAAAGGCCCTGGCCACCTGCTCTCTCCACC  
 TGACAGCTGTACCCCTCTTCTATGGGGCAGCCATGTTTCATCTACCTGAGGCCTAGGCACTA  
 CCGGGCCCCCAGCCATGACAAGGTGGCCTCTATCTTCTACACGGTCTTACTCCCATGCTC  
 AACCCCTCATTTACAGCTTGAGGAACAGGGAGGTGATGGGGGCACTGAGGAAGGGGCTG  
 GACCGCTGCAGGATCGGCAGCCAGCACTGA (SEQ ID NO: 176)

25

**AOLFR95 sequences:**

MLGSKPRVHLYILPCASQQVSTMGDRGTSNHSEMTDFILAGFRVRPELHILLFLLFLFVYAMILL  
 GNVGMMTIIMTDPRLNTPMYFFLGNLSFIDLFYSSVIEPKAMINFWSENKISFAGCVAQLFLFA  
 LLIVTEGFLLAAMAYDRFIAICNPLLYSVQMSTRCTQLVAGSYFCGCISSVIQTSMTFTLSFCAS  
 30 RAVDHFYCDRPLQRLSCSDLFIHRMISFSLSCMILPTIIVIVSYMYIVSTVLKIHSTEGHKKAFST  
 CSSHLGVVSVLYGAVFFMYLTPDRFPELSKVASLCYSLVTPMLNPLIYSLRNKDVQEALKKFLE  
 KKNIL (SEQ ID NO: 177)

ATGCTAGGATCCAAACCAAGAGTTCATTTGTATATTTTGCCCTGTGCCTCTCAACAGGTTTC  
 35 TACCATGGGTGACAGGGGAACAAGCAATCACTCAGAAATGACTGACTTCATTCTTGCAGG  
 CTTCAGGGTACGCCCAGAGCTCCACATTCTCCTCTTCTGCTATTTTTGTTTGTATGCCA  
 TGATCCTTCTAGGGAATGTTGGGATGATGACCATTATTATGACTGATCCTCGGCTGAACAC  
 ACCAATGATTTTTTCTAGGCAATCTCTCCTCATTTGATCTTTTCTATTCTATCTGTTATGA  
 ACCCAAGCTATGATCAACTTCTGGTCTGAAAAACAAGTCTATCTCCTTTGACGGCTGTGTG  
 40 GCCCAGCTCTTTCTCTTTGCCCTCCTCATTGTGACTGAGGGATTTCTCCTGGCGGCCATGGC  
 TTATGACCGCTTTATTGCCATCTGCAACCCTCTGCTCTACTCTGTTCAAATGTCCACACGTC  
 TGTGTACTCAGTTGGTGGCTGGTTCCTATTTTTGTGGCTGCATTAGCTCAGTTATTACAGCT  
 AGCATGACATTTACTTTATCTTTTGGCGCTTCTCGGGCTGTTGACCACTTTTACTGTGATTC  
 TCGCCCACTTCAGAGACTGTCCTGTTCTGATCTCTTTATCCATAGAATGATATCTTTTTCT  
 45 TATCATGTATTATTATCTTGCCTACTATCATAGTCATTATAGTATCTTACATGTATATTGTG  
 TCCACAGTTCTAAAGATACATTCTACTGAGGGACATAAGAAGGCCTTCTCCACCTGCAGCT  
 CTCACCTGGGAGTTGTGAGTGTGCTGTATGGTGTCTTCTTTTATGTATCTCACTCCTGAC  
 AGATTTCTGAGCTGAGTAAAGTGGCATCCTTATGTTACTCCCTAGTCACTCCCATGTTGA  
 ATCCTTTGATTTACTCTCTGAGGAACAAAGATGTCCAAGAGGCTCTAAAAAAATTTCTAGA  
 50 GAAGAAAAATATTATTCTTTGA (SEQ ID NO: 178)

**AOLFR96 sequences:**

MICENHTRVTEFILLGFTNNPEMQVSLFIFFLAIYTVTLLGNFLIVTVTSVDLALQTPMYFFLQN  
 LSLLEVCFTLVMPKMLVDLVSPRKIISFVGCQTQMYFFFFFGSSECFLLSMMA YDRFVAICNP  
 55 LHYSVIMNRSCLLWMAIGSWMSGVPVSMQLQTAWMMALPFCGPNAVDFHFFCDGPPVLKLVTV  
 DTTMYEMQALASTLLFIMFPFCLILVSYTRIITILRMSSATGRQKAFSTCSSHLIVVSLFYGTASL



TYLRPKSNQSPESKLVSLSYTVITPMLNPIIYGLRNNEVKGAVKRTTQKVLQKLDVF (SEQ ID NO: 179)

5 ATGATCTGTGAAAATCACACCAGAGTCACTGAATTTATTCTTCTTGGTTTTACAAACAACC  
CCGAGATGCAAGTTTCCCTCTTTATTTTTTCTGGCCATTTATACAGTCACTTTGTTGGGC  
AACTTTCTTATTGTACAGTTACCAGTGTGGATCTCGCACTTCAAACACCCATGTACTTCTT  
TCTTCAAATCTGTCACTTCTGAAGTATGTTTCACCTTGGTTATGGTGCCAAAATGCTTG  
TAGATCTAGTGTCCCCAAGGAAAATTATCTCTTTTGTGGGCTGTGGTACCCAGATGTACTT  
10 CTTCTTCTTCTTGGCAGTTCTGAATGTTTCTTCTCTCCATGATGGCTTATGATCGCTTTGT  
GGCCATCTGTAAACCCTCTCCATTATTAGTCATAATGAACAGGTCCCTATGCTTGTGGATG  
GCCATAGGCTCTTGGATGTCCGGTGTTCCTGTGTCTATGCTACAGACAGCTTGGATGATGG  
CCCTTCCTTTCTGTGGACCAAATGCCGTGGACCACTTTTTCTGTGATGGTCCCCAGTGTTA  
AACTAGTCACAGTGGATACAACCATGTATGAAATGCAAGCACTTGCCTCCACACTCCTGT  
15 TTATCATGTTTCCCTTTTGTCTCATTTTGGTTTCTACACCCGCATTATCATAACAATTCTG  
AGGATGTCCTCTGCCACTGGCCGCCAGAAGGCATTTTCTACTTGTTCCTCACACCTCATTGT  
GGTGTCCTCTTCTACGGAACAGCCAGTCTGACCTACCTGCGGCCCAAATCAAACAGTCC  
CCTGAGAGCAAGAAGCTAGTGTCAATTGTCTACACTGTCATCACACCTATGCTAAACCCCA  
TCATCTACGGCCTGAGGAACAATGAAGTGAAAGGGGCTGTCAAGAGGACAATCACTCAAA  
AAGTCTTACAGAAGTTAGATGTGTTTTGA (SEQ ID NO: 180)

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**AOLFR97 sequences:**

MTEFHLQSQMPSIRLIFRRLSLGRIKPSQSPRCSTSMVVPFSIAEHWRRMKGANLSQGMFEL  
LGLTDDPQLQRLLFVFLGMYTATLLGNLVMFLLIHVSATLHTPMYSLLSFLDFCYSSSTVV  
PQTLVNFLAKRKVISYFGCMTQFFYAGFATSECYLIAAMAYDRYAAICNPLLYSTIMSPREV  
25 ASLVGSYSAGFLNSLIHTGCIKFCGAHVVTTHFFCDGPPILSLSCVDTSLCEILLFIFAGFNLLS  
CTLILISYFLILNTILKMSSAQGRFAFSTCASHLTAICLFFGTTLFMYLRPRSSYSLTQDRIVA  
VIYTVVIPVLNPLMYSLRNKDVKKALIKVWGRKTME (SEQ ID NO: 181)

30 ATGACAGAGTTTCATCTGCAAAGCCAAATGCCCTCAATAAGACTCATCTTCAGAAGGCTGT  
CCTTAGGCAGAATTAACCCAGTCAGAGCCCCAGGTGTTCAACCTCATTTATGGTGGTGCC  
TTCTTTCTCCATCGCAGAGCACTGGAGAAGGATGAAAGGGGCAAACCTGAGCCAAGGGAT  
GGAGTTTGAAGCTCTTGGGCCTCACCCTGACCCCAAGCTCCAGAGGCTGCTCTTCGTGGTG  
TTCCTGGGCATGTACACAGCCACTCTGCTGGGGAACCTGGTCATGTTTCTCTGATCCATG  
TGAGTGCCACCCTGCACACACCCATGTAATCCCTCTGAAGAGCCTCTCCTTCTTGGATTTC  
35 TGCTACTCCTCCACGGTTGTGCCCCAGACCCTGGTGAACCTTCTTGGCCAAGAGGAAAGTGA  
TCTCTTATTTTGGCTGCATGACTCAGATGTTCTTCTATGCGGGTTTTGCCACCAAGTGA  
TATCTCATCGCTGCCATGGCCTATGACCGCTATGCGGCTATTGTAAACCCCTGCTCTACTC  
AACCATCATGTCTCCTGAGGTCTGTGCCTCGCTGATTGTGGGCTCCTACAGTGCAGGATTC  
CTCAATTCTCTTATCCACACTGGCTGTATCTTTAGTCTGAAATTCTGCGGTGCTCATGTCTG  
40 CACTCACTTCTTCTGTGATGGGCCACCCATCCTGTCTTGTCTGTAGACACCTCACTGT  
GTGAGATCCTGCTCTTCAATTTTGTGTTTCAACCTTTTGAAGCTGCACCTCACCATCTTG  
ATCTCCTACTTCTTAATTCTCAACACCATCCTGAAAATGAGCTCGGCCAGGGCAGGTTTA  
AGGCATTTTCCACCTGTGCATCCACCTCACTGCCATCTGCCTCTTCTTTGGCACAACACTT  
TTTATGTACCTGCGCCCCAGGTCCAGCTACTCCTTGACCCAGGACCGCACAGTTGCTGTCA  
45 TCTACACAGTGGTGATCCAGTGCTGAACCCCTCATGTACTCTTTGAGAAACAAGGATGT  
GAAGAAAGCTTTAATAAAGGTTTGGGGTAGGAAAACAATGGAATGA (SEQ ID NO: 182)

**AOLFR98 sequences:**

MRGFNKTTVVVTQFILVGFSSLGELQLLLFVIFLLLYLTILVANVTIMAVIRFSWTLHTPMYGFLEI  
50 LSFSESCYTFVVIPLLVHLLSDTKTISFMACATQLFFFLGFACTNCLLIAVMGYDRYVAICHPLR  
YTLINKRLGLELISLSGATGFFIALVATNLICDMRFCGPNRVNHYFCDMAPVIKLACTDTHVKE  
LALFSLSILVIMVPFLLILISYGFIVNTILKIPSAEGKAFVTCASHLTVFVHYGCASHYLRPKSK  
SASDKDQLVAVTYTVVTPLLNPLVYSLRNKEVKTALKRVLGMPVATKMS (SEQ ID NO: 183)

55 ATGCGAGGTTTCAACAAAACCACTGTGGTTACACAGTTCATCCTGGTGGGTTTTCTCCAGCC  
TGGGGGAGCTCCAGCTGCTGCTTTTTGTCTATCTTTCTCTCTATACTTGACAATCCTGGTG

5   GCCAATGTGACCATCATGGCCGTTATTGCTTCAGCTGGACTCTCCACACTCCCATGTATG  
 GCTTTCTATTTCATCCTTTTCATTTTCTGAGTCCTGCTACACTTTTGTGTCATCATCCCTCAGCTGC  
 TGGTCCACCTGCTCTCAGACACCAAGACCATCTCCTTCATGGCCTGTGCCACCCAGCTGTT  
 CTTTTTCTTGGCTTTGCTTGCACCAACTGCCTCCTCATTGCTGTGATGGGATATGATCGCT  
 10   ATGTAGCAATTTGTACCCCTCTGAGGTACACACTCATCATAAACAAAAGGCTGGGGTTGGA  
 GTTGATTTCTCTCTCAGGAGCCACAGGTTTCTTTATTGCTTTGGTGGCCACCAACCTCATT  
 GTGACATGCGTTTTTGTGGCCCCAACAGGGTTAACCCTATTTCTGTGACATGGCACCTGT  
 TATCAAGTTAGCCTGCACTGACACCCATGTGAAAGAGCTGGCTTTATTTAGCCTCAGCATC  
 CTGGTAATTATGGTGCCTTTTCTGTTAATTCTCATATCCTATGGCTTCATAGTTAACACCAT  
 15   CCTGAAGATCCCCTCAGCTGAGGGCAAGAAGGCCTTTGTACCTGTGCCTCACATCTCACT  
 GTGGTCTTTGTCCACTATGGCTGTGCCTCTATCATCTATCTGCGGCCCAAGTCCAAGTCTGC  
 CTCAGACAAGGATCAGTTGGTGGCAGTGACCTACACAGTGGTTACTCCCTTACTTAATCCT  
 CTTGTCTACAGTCTGAGGAACAAAGAGGTAAAACTGCATTGAAAAGAGTTCTTGGGAATG  
 CCTGTGGCAACCAAGATGAGCTAA (SEQ ID NO: 184)

15

**AOLFR99 sequences:**

20   MERVNETVVREVIFLGFSSSLARIQQLLFVIFLLLYLFTLGTNAIIISTIVLDRALHIPMYFFLAILSC  
 SEICYTFIIVPKMLVDLLSQKKTISFLGCAIQMFSLFLGCSHSFLLAVMGYDRYIAICNPLRYSV  
 LMGHGVCMLVAAACACGFTVAQITSLVFHLPFYSSNQLHHFFCDIAPVLKLASHHNHFSQIV  
 IFMLCTLVLAIPLLLLVSYVHLSAILQFPSTLGRCKAFSTCVSHLIIVTVHYGCASFYILRPQSNY  
 SSSQDALISVSYTITPLFNPMIYSLRNKEFKSALCKIVRRTISLL (SEQ ID NO: 185)

20

25   ATGGAGCGGGTCAATGAGACTGTGGTGAGAGAGGTCATCTTCCTCGGCTTCTCATCCCTGG  
 CCAGGCTGCAGCAGCTGCTCTTTGTTATCTTCCTGCTCCTCTACCTGTTCACTCTGGGCACC  
 AATGCAATCATCATTTCCACCATTGTCTGGACAGGGCCCTTCATATCCCCTGTACTTCTT  
 CCTTGCCATCCTCTCTTGCTCTGAGATTGCTACACCTTCATCATTGTACCCAAGATGCTGG  
 TTGACCTGCTGTCCAGAAGAAGACCATTCTTTCTCGGCTGTGCCATCCAAATGTTTTCC  
 TTCTCTTCTTGGCTGCTCTCACTCCTTTCTGCTGGCAGTCATGGGTTATGATCGTTACAT  
 30   AGCCATCTGTAACCCACTGCGCTACTCAGTGCTAATGGGACATGGGGTGTGTATGGGACTA  
 GTGGCTGCTGCCTGTGCCTGTGGCTTCACTGTTGCACAGATCATCACATCCTTGGTATTTCA  
 CCTGCCTTTTATTCCCTCCAATCAACTACATCACTTCTTCTGTGACATTGCTCCTGTCTCA  
 AGCTGGCATCTCACCATAACCCTTTAGTCAGATTGTCATCTTCATGCTCTGTACATTGGTC  
 CTGGCTATCCCCTTATTGTTGATCTGGTGTCTATGTTTACATCCTCTCTGCCATACTCA  
 GTTTCCTTCCACACTGGGTAGGTGCAAAGCTTTTTCTACCTGTGTATCTCACCTCATTATTG  
 35   TCACTGTCCACTATGGCTGTGCCTCCTTTATCTACTTAAGGCCTCAGTCCAATACTCCTCA  
 AGCCAGGATGCTCTAATATCAGTATCCTACACTATTATAACTCCATTGTTCAACCCAATGA  
 TTTATAGCTTGAGAAATAAAGAGTTCAAATCAGCTCTTTGTAAAATTGTGAGAAGAACAAT  
 TTCCCTGTTGTAA (SEQ ID NO: 186)

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**AOLFR101 sequences:**

45   MDTGNWSQVAEFILGFPHLQGVQIYLFLLLLLIYLMTVLGNLLIFLVVCLDSRLHTPMYHFVSI  
 LSPSELGYTAATIPKMLANLLSEKKTISFSGCLLQIYFFHSLGATECYLLTAMAYDRYLAICRPL  
 HYPTLMTPTLCABIAIGCWLGGLAGPVVEISLISRLPFCGPNRIQHVFCDPFPVLSLACTDTSINV  
 LVDFVINSCKILATFLLILCSYVQIICTVLRIPSAAGKRKAISTCASHFTVVVIFYGSIISMYVQLK  
 KSYSLDYDQALAVVYSVLTPLNPFYISLRNKEIKEAVRRQLKRIGILA (SEQ ID NO: 187)

45

50   ATGGACACAGGGAAGTGGAGCCAGGTAGCAGAATTCATCATCTTGGGCTTCCCCCATCTCC  
 AGGGTGTCCAGATTTATCTCTTCCTCTTGTGCTTCTCATTTACCTCATGACTGTGTTGGGA  
 AACCTGCTGATATTCCTGGTGGTCTGCCTGGACTCCCGGCTTCACACACCCATGTACCACT  
 TTGTCAGCATTCTCTCCTTCTCAGAGCTTGGCTATACAGCTGCCACCATCCCTAAGATGCTG  
 GCAAACCTTGCTCAGTGAGAAAAAGACCAATTTCTCTCTGGGTGTCTCCTGCAGATCTATT  
 TCTTCACTCCCTTGGAGCGACTGAGTGCTATCTCCTGACAGCTATGGCCTACGATAGGTA  
 TTAGCCATCTGCCGGCCCTCCACTACCCAACCTCATGACCCCAACACTTTGTGCAGAG  
 ATTGCCATTGGCTGTTGGTTGGGAGGCTTGGCTGGGCCAGTAGTTGAAATTTCTTGTGATTT  
 55   CACGCCTCCCATTTCTGTGGCCCCAATCGCATTACAGCACGTCTTTTGTGACTTCCCTCCTGTG  
 CTGAGTTTGGCTTGCATGATACGTCTATAAATGTCCTAGTAGATTTTGTATAAATTCCTG

55



**AOLFR105 sequences:**

MQGLNHTSVSEFILVGFSAPPHLQMLFLLFLLMYLFTLLGNLLIMATVWSESLHMPMYLFLC  
 ALSITEILYTVAIIPRMLADLLSTQRSIAFLACASQMFFSFSFGFTHSFLLTVMGYDRYVAICHPL  
 RYNVLSLRGCTCRVGCWSAGGLVMGMVVTSAIFHLAFCGHKEIHHFFCHVPLLKLACGDD  
 5 VLVVAKGVGLVCITALLGCFLILLSYAFIVAAILKIPSAEGRNKAFTSCASHLTVVVVHYGFAS  
 VIYLPKPGPQSPEGDTLMGITYTVLTPFLSPIIFSLRNKELKVAMKKTCFTKLFPQNC (SEQ ID  
 NO: 193)

ATGCAGGGGCTAAACCACACCTCCGTGTCTGAATTCATCCTCGTTGGCTTCTCTGCCTTCCC  
 10 CCACCTCCAGCTGATGCTCTTCCTGCTGTTCTGCTGATGTACCTGTTACGCTGCTGGGCA  
 ACCTGCTCATCATGGCCACTGTCTGGAGCGAGCGCAGCCTCCACATGCCCATGTACCTCTT  
 CCTGTGTGCCCTCTCCATCACCGAGATCCTCTACACCGTGCCATCATCCCGCGCATGCTG  
 GCCGACCTGCTGTCCACCCAGCGCTCCATCGCCTTCTGCGCTGTGCCAGTCAGATGTTCTT  
 CTCTTCAGCTTCGGGTTTACCCACTCCTTCTGCTCACTGTATGGGCTACGACCGCTACG  
 15 TGGCCATCTGCCACCCCTGCGTTACAACGTGCTCATGAGCCTGCGGGGCTGCACCTGCCG  
 GGTGGGCTGCTCCTGGGCTGGTGGCTTGGTCATGGGGATGGTGGTGACCTCGGCCATTTTC  
 CACCTCGCCTTCTGTGGACACAAGGAGATCCACCATTCTTCTGCCACGTGCCACCTCTGTT  
 GAAGTTGGCCTGTGGAGATGATGTGCTGGTGGTGGCCAAAGGCGTGGGCTTGGTGTGTAT  
 CACGGCCCTGCTGGGCTGTTTTCTCCTCATCCTCCTCTCCTATGCCTTCATCGTGGCCGCCA  
 20 TCTTGAAGATCCCTTCTGCTGAAGGTGCGAACAAGGCCCTTCTCCACCTGTGCCTCTCACCT  
 CACTGTGGTGGTGTGCTGACTATGGCTTTCCTCCGTCAATTAACCTGAAGCCCAAAGGTCCC  
 CAGTCTCCGGAAGGAGACACCTTGATGGGCATCACCTACACGGTCCCTCACACCTTCTCA  
 GCCCCATCATCTTCAGCCTCAGGAACAAGGAGCTGAAGGTGCCATGAAGAAGACTTGCTT  
 CACCAAACCTCTTCCACAGAACTGCTGA (SEQ ID NO: 194)

25

**AOLFR106 sequences:**

METANYTKVTEFVLTLGLSQTPEVQLVLFVIFLSFYLFILPGNILICTISLDPHLTSPMYFLLANLA  
 FLDIWYSSITAPEMLIDFFVERKHSFDGCLAQFLFLHFAGASEMFLLTVMADFLYTAICRPLHYA  
 TIMNQRLCCILVALSWRGGFHSIIQVALIVRLPFCGPNELDSYFCDITQVVRIACANTPPEELVM  
 30 ICSSGLISVVCLIALLSYAFLLALFKKLSGSGENTNRAMSTCYSHITIVLTMFGPSIYTYARPF  
 SFSLDKVVSVFNTLIFPLRNPIIYTLRNKEVKAAMRKLVTKYILCKEK (SEQ ID NO: 195)

ATGGAAACTGCAAATTACACCAAGGTGACAGAATTTGTTCTCACTGGCCTATCCAGACTC  
 CAGAGGTCCAACTAGTCCTATTTGTTATATTTCTATCCTTCTATTTGTTTCATCCTACCAGGA  
 35 AATATCCTTATCATTTGCACCATCAGTCTAGACCCTCATCTGACCTCTCCTATGTATTTCTT  
 GTTGGCTAATCTGGCCTTCCCTTGATATTTGGTACTCTTCCATTACAGCCCCTGAAATGCTCA  
 TAGACTTCTTTGTGGAGAGGAAGATAATTTCTTTTGATGGATGCATTGCACAGCTCTTCTT  
 CTTACACTTTGCTGGGGCTTCGGAGATGTTCTTGCTCACAGTGATGGCCTTTGACCTCTACA  
 CTGCTATCTGCCGACCCCTCCACTATGCTACCATCATGAATCAACGTCTCTGCTGTATCCTG  
 40 GTGGCTCTCTCCTGGAGGGGGGGCTTCATTCTATCATACAGGTGGCTCTCATTGTTT  
 GACTTCCTTTCTGTGGGCCCAATGAGTTAGACAGTTACTTCTGTGACATCACACAGGTTGT  
 CCGGATTGCCTGTGCCAACACCTTCCCAGAGGAGTTAGTGATGATCTGTAGTAGTGGTCTG  
 ATCTCTGTGGTGTGTTTGATTGCTCTGTTAATGTCCTATGCCTTCTTCTGGCCTTGTTCAA  
 GAACTTTTCAGGCTCAGGTGAGAATACCAACAGGGCCATGTCCACCTGCTATTCCCACATT  
 45 ACCATTGTGGTGCTAATGTTTGGGCCATCCATCTACATTTATGCTCGCCATTGACTCGTT  
 TTCCCTAGATAAAGTGGTGTCTGTGTTCAATACTTTAATATTCCTTTACGTAATCCCATTA  
 TTTACACATTGAGAAACAAGGAAGTAAAGGCAGCCATGAGGAAGTTGGTCACCAAATATA  
 TTTTGTGTAAAGAGAAGTGA (SEQ ID NO: 196)

**AOLFR107 sequences:**

MELWNFTLGSFILVGILNDSGSPELLCATITILYLLALISNGLLLAITMEARLHMPMYLLGQ  
 LSLMDLLFTSVVTPKALADFLRRENTISFGGALQMFLALTMGGAEDLLAFMAYDRYVAICH  
 PLTYMTLMSSRACWLMVATSWILASLSALIYTVYTMHYPCRAQEIRHLLCEIPHLLKVACAD  
 TSRYELMVYVMGVTFILPSLAAILASYTQILLTVLHMPSNEGRKKALVTCSSHLTVVGMFYGA  
 55 ATFMVYVLPSSFHSTRQDNISVFYITVTPALNPLIYSLRNKEVMRALRRVLGKYMLPAHSTL  
 (SEQ ID NO: 197)

ATGGAGCTCTGGAACCTTCACCTTGGGAAGTGGCTTCATTTTGGTGGGGATTCTGAATGACA  
 GTGGGTCTCCTGAACTGCTCTGTGCTACAATTACAATCCTATACTTGTGGCCCTGATCAG  
 CAATGGCCTACTGCTCCTGGCTATCACCATGGAAGCCCGGCTCCACATGCCCATGTACCTC  
 5 CTGCTTGGGCAGCTCTCTCATGGACCTCCTGTTTACATCTGTTGTCACTCCCAAGGCCCT  
 TGGCGACTTTCTGCGCAGAGAAAAACACATCTCCTTTGGAGGCTGTGCCCTTCAGATGTTT  
 CTGGCACTGACAAATGGGTGGTGTGAGGACCTCCTACTGGCCTTCATGGCCTATGACAGGT  
 ATGTGGCCATTTGTCATCCTCTGACATACATGACCCTCATGAGCTCAAGAGCCTGCTGGCT  
 CATGGTGGCCACGTCCTGGATCCTGGCATCCCTAAGTGCCCTAATATATACCGTGTATACC  
 10 ATGCACTATCCCTTCTGCAGGGCCAGGAGATCAGGCATCTTCTCTGTGAGATCCCACT  
 TGCTGAAGGTGGCCTGTGCTGATACCTCCAGATATGAGCTCATGGTATATGTGATGGGTGT  
 GACCTTCCTGATTCCCTCTCTTGCTGCTATACTGGCCTCCTATACACAAATTCTACTCACTG  
 TGCTCCATATGCCATCAAATGAGGGGAGGAAGAAAGCCCTTGTACCTGCTCTTCCACCT  
 GACTGTGGTTGGGATGTTCTATGGAGCTGCCACATTCATGTATGTCTTGGCCAGTTCTTCC  
 15 ACAGCACCAGACAAGACAACATCATCTCTGTTTTCTACACAATTGTCACTCCAGCCCTGAA  
 TCCACTCATCTACAGCCTGAGGAATAAGGAGGTCATGCGGGCCTTGAGGAGGGTCTGGG  
 AAAATACATGCTGCCAGCACACTCCACGCTCTAG (SEQ ID NO: 198)

**AOLFR108 sequences:**

20 MCSFFLCQTGKQAKISMGEENQTFVSKFIFLGLSQDLQTQILLFILFLIYLLTVLGNQLIILIFLD  
 SRLHTPMYFFLRNLSFADLCFSTSIQVVLVHFLVVRKTISFYGCMTQIIFLLVGCNECALLAV  
 MSYDRYVAVCKPLYYSTIMTQVRVCLWLSFRSWASGALVSLVDTSTFHLPHYWGQNIINHIFCE  
 PPALLKLASIDTYSTEMAIFSMGVVILLAPVSLILGSYWNISTVIQMOSGEGRLKAFSTCGSHLI  
 VVVLFGSGIFTYMRPNSTTKELDKMISVFYTAFTPMLNPIIYSLRNKDVKGALRKLVRKRC  
 25 FSHRQ (SEQ ID NO: 199)

ATGTGTTCTTTTTTCTTGTGCCAAACAGGTAAACAGGCAAAAATATCAATGGGAGAAGAAA  
 ACCAAACCTTTGTGTCCAAGTTTATCTTCTGGGTCTTTCACAGGACTTGCAGACCCAGAT  
 CCTGCTATTTATCCTTTTCTCATCTTTATCTGCTGACCGTGCTTGGAAACCAGCTCATCA  
 30 TCATTCTCATCTTCTGGATTCTCGCCTTCACACTCCCATGTATTTTTTTCTTAGAAATCTCT  
 CCTTTCAGATCTCTGTTTCTCTACTAGCATTGTCCCTCAAGTGTTGGTTCACTTCTTGGTA  
 AAGAGGAAAACCATTTCTTTTTATGGGTGTATGACACAGATAATTGTCTTTCTTCTGGTTG  
 GGTGTACAGAGTGTGCGCTGCTGGCAGTGATGTCCTATGACCGGTATGTGGCTGTCTGCAA  
 GCCCTGTACTACTCTACCATCATGACACAACGGGTGTGTCTCTGGCTGTCTTCAAGTCCCT  
 35 GGGCCAGTGGGGCACTAGTGTCTTTAGTAGATACCAGCTTTACTTTCCATCTTCCCTACTG  
 GGGACAGAATATAATCAATCACTACTTTTGTGAACCTCCTGCCCTCCTGAAGCTGGCTTCC  
 ATAGACACTTACAGCACAGAAATGGCCATCTTTTCAATGGGCGTGGTAATCCTCCTGGCCC  
 CTGTCTCCCTGATTCTTGGTTCTTATTGGAATATTATCTCCACTGTTATCCAGATGCAGTCT  
 GGGGAAGGGAGACTCAAGGCTTTTCCACCTGTGGCTCCCATCTTATTGTTGTTGCTCTT  
 40 CTATGGGTCAGGAATATTCACCTACATGCGACCAAACCTCAAGACTACAAAAGAACTGGA  
 TAAAATGATATCTGTGTTCTATACAGCGGTGACTCCAATGTTGAACCCCATATTTATAGC  
 TTGAGGAACAAAGATGTCAAAGGGGCTCTCAGGAACTAGTTGGGAGAAAGTGCTTCTCT  
 CATAGGCAGTGA (SEQ ID NO: 200)

**AOLFR109 sequences:**

45 MLRNGSIVTEFILVGFQSSSTSTRALLFALFLALYSLTMMAMNGLIIFITSWTDPKLNSPMYFFLG  
 HSLLDVCFITTTIPQMLIHLVVRDHIVSFVCCMTQMYFVFCVGVABECILLAFMAYDRYVAICY  
 PLNYVPISQKVCVRLVGTAWFFGLINGFLEYISFREPPFRDNHIESFFCEAPIVIGLSCGDPQFSL  
 WAIFADAIVVILSPMVLTVTSYVHILATILSKASSSGRGKTFSTCASHLTVVIFLYTSAMFSYMN  
 50 PHSTHGPDKDKPFSLLYTITPMCNPIIYSFRNKEIKEAMVRALGRTRLAQPQSV (SEQ ID NO:  
 201)

ATGCTAAGGAATGGCAGCATAGTGACGGAATTTATCCTCGTGGGCTTTCAGCAGAGCTCCA  
 CTTCACACGAGCATTGCTCTTTGCCCTCTTCTTGGCCCTCTACAGCCTCACCATGGCCATG  
 55 AATGGCCTCATCATCTTTATCACCTCCTGGACAGACCCCAAGCTCAACAGCCCCATGTACT  
 TCTTCTCGGCCATCTGTCTCTCCTGGATGTCTGCTTCATCACTACTACCATCCCACAGATG

TTGATCCACCTCGTGGTCAGGGACCACATTGTCTCCTTTGTATGTTGCATGACCCAGATGT  
 ACTTTGTCTTCTGTGTTGGTGTGGCCGAGTGCATCCTCTTGGCTTTCATGGCCATGACCGT  
 TATGTTGCTATCTGCTACCCACITAACTATGTCCCGATCATAAGCCAGAAGGTCTGTGTCA  
 GGCTTGTGGGAACTGCCTGGTTCTTTGGGCTGATCAATGGCATCTTTCTCGAGTATATTTT  
 5 ATTCCGAGAGCCCTTCCGCAGAGACAACCACATAGAAAAGCTTCTTCTGTGAGGCCCCCATA  
 GTGATTGGCCTCTCTTGTGGGGACCCTCAGTTTAGTCTGTGGGCAATCTTTGCCGATGCCA  
 TCGTGGTAATTCTCAGCCCATGGTGTCACTGTCACTTCTATGTGCACATCCTGGCCACC  
 ATCCTCAGCAAAGCCTCCTCCTCAGGTCGGGGGAAGACTTTCTCTACTTGTGCCTCTCACC  
 TGACTGTGGTCATCTTTCTCTACACTTCAGCTATGTTCTCTTACATGAACCCCCACAGCACA  
 10 CATGGGCCTGACAAAGACAAACCTTTCTCCCTCCTGTACACCATCATTACCCCCATGTGCA  
 ACCCATCATTTATAGTTTCCGCAACAAGGAAATTAAGGAGGCCATGGTGAGGGCACTTG  
 GAAGAACCAGGCTGGCCAGCCACAGTCTGTCTAG (SEQ ID NO: 202)

**AOLFR110 sequences:**

15 MKIANNTVVTEFILLGLTQSQDIQLLVFVLILIFYLILPGNFLIIFTIRSDPGLTAPLYLFLGNLAF  
 DASYSFIVAPRMLVDLSEKKVISYRGCTQLFFLHFLGGEGLLLVMAFDRIAICRPLHCST  
 VMNPRACYAMMLALWLGGFVHSIQVVLILRLPFCGPNQLDNFFCDVRQVIKLA CTDMFVVEL  
 LMVFN SGLMTLLCFLGLLASA YAVLCHVRRASEGKNKAMSTCTTRVIBLLMFGPAIFTYMC  
 20 RALPADKMVSLFHTVIFPLMNPMTYTLRNQEVKTS MKRLLSRHVVCQVDFIURN (SEQ ID NO:  
 203)

ATGAAGATAGCAAACAACACAGTAGTGACAGAATTTATCCTCCTTGGTCTGACTCAGTCTC  
 AAGATATTCAGCTCTTGGTCTTTGTGCTGATCTTAATTTTCTACCTTATCATCCTCCCTGGA  
 AATTTTCTCATTATTTTACCATAAGGTCAGACCCTGGGCTCACAGCCCCCTCTATTTATT  
 25 TCTGGGCAACTTGGCCTTCCCTGGATGCATCCTACTCCTTCATTGTGGCTCCCAGGATGTGG  
 TGGACTTCTCTCTGAGAAAAAGGTAATCTCCTACAGAGGCTGCATCACTCAGCTCTTTTT  
 CTTGCACTTCTTGGAGGAGGGGAGGGATTACTCCTTGTGTGATGGCCTTTGACCGCTAC  
 ATCGCCATCTGCCGGCCTCTGCACTGTTCAACTGTCATGAACCCTAGAGCCTGCTATGCAA  
 TGATGTTGGCTCTGTGGCTTGGGGGTTTGTCCACTCCATTATCCAGGTGGTCTCATCCTC  
 30 CGCTTGCCTTTTTGTGGCCCAAACCAGCTGGACAACTTCTTCTGTGATGTCCGACAGGTCA  
 TCAAGCTGGCTTGCACCGACATGTTTGTGGTGGAGCTTCTAATGGTCTTCAACAGTGGCCT  
 GATGACACTCCTGTGCTTTCTGGGGCTTCTGGCTTCTCTATGCAGTCATCCTCTGCCATGTT  
 GTAGGGCAGCTTCTGAAGGGAAGAACAAGGCCATGTCCACGTGCACCACTCGTGTCTATTA  
 TTATACTTCTTATGTTTGGACCTGCTATCTTCATCTACATGTGCCCTTTAGGGCCTTACCA  
 35 GCTGACAAGATGGTTTCTCTCTTTTACACAGTGATCTTTCCATTGATGAATCCTATGATTTA  
 TACCTTTCGCAACCAGGAAGTGAAAACCTCCATGAAGAGGTTATTGAGTCGACATGTAGTC  
 TGTCAAGTGGATTTTATAATAAGAACTGA (SEQ ID NO: 204)

**AOLFR111 sequences:**

40 MCYIYLIFKEWTLIFYFSLLLFLQITPAIMANLTIVTEFILMGFSTNKNMCLHSILFLLIYLCALM  
 GNVLIIMITTLDHHLHTPVYFFLKNLSFLDLCLISVTAPKSIANS LIHNNSISFLGCVSQVFLLS  
 ASABELLLTVMSFDRTAICHPLHYDVIMDRSTCVQRATVSWLYGGGLI VMHTAGTFSLSYCG  
 SNMVHQFFCDIPQLLAISCENLIREIALILINVLD FCCFIVIIITYVHVFS TVKKIPSTEGQSKAY  
 45 SICLPHLLVVLFLSTGFIA YLKPASESPSILDAVISVFYTM LPPTFNP IYSLRNKA I KVALGMLIKG  
 KLTKK (SEQ ID NO: 205)

ATGTGTTATATATATTTAATATTTAAAGAGTGGACATTGATATTTTACTTCAGTCTTCTCCT  
 TTTCTGCAATTACTCCTGCAATAATGGCAAATCTCACAATCGTGACTGAATTTATCCTTA  
 TGGGGTTTTCTACCAATAAAAATATGTGCATTTTGCATTGATTCTCTTCTGTGATTTAT  
 50 TTGTGTGCCCTGATGGGGAATGTCTCATTATCATGATCACAACITTTGGACCATCATCTCC  
 ACACCCCCGTGATTTTCTTCTGAAGAATCTATCTTCTTGGATCTCTGCCTTATTTCAGTC  
 ACGGCTCCCAAATCTATCGCCAATTCTTTGATACACAACAACCTCCATTTCATTCTTGGCTG  
 TGTTTCCAGGTCTTTTTGTGCTTTCTTCAGCATCTGCAGAGCTGCTCCTCCTCACGGTGA  
 TGTCTTTGACCGCTATACTGCTATATGTCAACCTCTGCACTATGATGTCATCATGGACAGG  
 55 AGCACCTGTGTCAAAGAGCCACTGTGTCTTGGCTGTATGGGGGTCTGATTGCTGTGATGC  
 ACACAGCTGGCACCTTCTCCTTATCCTACTGTGGGTCCAACATGGTCCATCAGTCTCTCTGT

GACATTCCCCAGTTATTAGCTATTTCTTGCTCAGAAAATTTAATAAGAGAAAATTGCACTCA  
 TCCTTATTAATGTAGTTTTGGATTTCTGCTGTTTTATTGTCATCATCATTACCTATGTCCAC  
 GTCTTCTCTACAGTCAAGAAGATCCCTTCCACAGAAGGCCAGTCAAAAGCCTACTCTATTT  
 GCCTTCCACACTTGCTGGTTGTGTTATTTCTTTCCACTGGATTCAATTGCTTATCTGAAGCCA  
 5 GCTTCAGAGTCTCCTTCTATTTTGGATGCTGTAATTTCTGTGTTCTACACTATGCTGCCCC  
 AACCTTTAATCCCATTATATACAGTTTGAGAAACAAGGCCATAAAGGTGGCTCTGGGGATG  
 TTGATAAAGGGAAAGCTCACCAAAAAGTAA (SEQ ID NO: 206)

**AOLFR113 sequences:**

10 MKFWHGFSSHLNPMFSSFLLYLSLPWINTTIQAWLNLCSLALPVWAMSGAGFLSCCYWHTCSP  
 SVVTCSSSQSSDWMQLCTHLCTTSLVFPSWSCGQLPLSLRCLIFSRRKPFLQDASFRPTSS  
 TPWGACECYLLTAMAYDRYLAICRPLHYPIIMTTTLCAKMAAACWTCGFLCPISEVILASQLPF  
 CAYNEIQHIFCDPPLSLACKDTSANILVDFAINAFILITFFIMISYARIIGAVLKIKTASGRKK  
 AFSTCASHLAVVLIFGSIIFMYVRLKKSYSLTLDRTLAIVYSVLTPMVNPIHYSLRNKEIHKAIKR  
 15 TIFQKGDKASLAHL (SEQ ID NO: 207)

ATGTGTCAACAAATCTTACGGGATTGCATTCTTCTCATACATCATTTGTGCATTAACAGGA  
 AAAAAGTCTCACTTGTGATGCTGGGTCCAGCTTATAACCACACAATGGAAACCCCTGCCCTC  
 CTTCCTCCTTGTGGGTATCCCAGGACTGCAATCTTCACATCTTTGGCTGGCTATCTCACTGA  
 20 GTGCCATGTACATCATAGCCCTGTTAGGAAACACCATCATCGTGACTGCAATCTGGATGGA  
 TTCCACTCGGCATGAGCCCATGTATTGCTTTCTGTGTGTTCTGGCTGCTGTGGACATTGTTA  
 TGGCCTCCTCGGTGGTACCCAAGATGGTGAGCATCTTCTGCTCAGGAGACAGCTCAATCAG  
 CTTTAGTGCTTGTTCCTCAGATGTTTTTGTCCACTTAGCCACAGCTGTGGAGACGGGG  
 CTGCTGCTGACCATGGCTTTTGACCGCTATGTAGCCATCTGCAAGCCTCTACACTACAAGA  
 25 GAATTCTCACGCCTCAAGTGATGCTGGGAATGAGTATGGCCATCACCATCAGAGCTATCAT  
 AGCCATAACTCCACTGAGTTGGATGGTGAGTCATCTACCTTTCTGTGGCTCCAATGTGGTT  
 GTCCACTCCTACTGTGAGCACATAGCTTTGGCCAGGTTAGCATGTGCTGACCCCGTGCCCA  
 GCAGTCTCTACAGTCTGATTGGTTCCCTCTCTTATGGTGGGCTCTGATGTGGCCTTCATTGCT  
 GCCTCCTATATCTTAATTCTCAAGGCAGTATTTGGTCTCTCCTCAAAGACTGCTCAGTTGAA  
 30 AGCATTAAGCACATGTGGCTCCCATGTGGGGGTTATGGCTTTGTACTATCTACCTGGGATG  
 GCATCCATCTATGCGGCCTGGTTGGGGCAGGATGTAGTGCCCTTGCACACCCAAGTCCTGC  
 TAGCTGACCTGTACGTGATCATCCGACCACTTAAATCCCATCATCTATGGCATGAGGAC  
 CAAACAACGCGGGAGAGAATATGGAGTTATCTGATGCATGTCCTCTTTGACCATTCCAAC  
 CTGGGTTTCATGA (SEQ ID NO: 208)

35

**AOLFR114 sequences:**

MERINHNTSSVSEFILLGLSSRPEDQKTLFVLFLIVYLVTTTGNLLILAIRFNPHLQTPMYFFLSFLS  
 LTDICFTTSVVPKMLMNFLEKKTISYAGCLTQMYFLYALGNSDSCLLAVMAFDRYVAVCDPF  
 HYVTMTSHHHCVLLVAFSCSPHLHSLHLLNRLTFCDNSNVIHHFLCDLSPVLKLSCSSIFVN  
 40 EIVQMTEAPIVLVTRFLCIAFSYIRILTTVLKIPSTSGKRKAFTSCGFYLTIVTLFYGSIFCVYLQP  
 PSTYAVKDHVATIVYTVLSSMLNPFYSLRNKDLKQGLRKLMSKRS (SEQ ID NO: 209)

ATGGAAAGAATCAACCACACCAGCAGTGTCTCCGAGTTTATCCTCCTGGGACTCTCCTCCC  
 GGCCTGAGGACCAAAAGACACTCTTTGTTCTCTTCTCATCGTGACCTGGTCACCATAAC  
 45 AGGGAACCTGCTCATCATCCTGGCCATTGCTTCAACCCCATCTTCAGACCCCTATGTATT  
 TCTTCTTGAGTTTTCTGTCTCTCACTGATATTTGCTTTACAACAAGCGTTGTCCCAAGATG  
 CTGATGAACTTCTGTGAGAAAAGAAGACCATCTCCTATGCTGGGTGTCTGACACAGATGT  
 ATTTTCTCTATGCCTTGGGCAACAGTGACAGCTGCCTTCTGGCAGTCATGGCCTTTGACCG  
 CTATGTGGCCGCTGTGTGACCCTTTCCACTATGTCAACCACCATGAGCCACCACCACTGTGTCC  
 50 TGCTGGTGGCCTTCTCCTGCTCATTTCTCCTCACTCCACTCACTCCTGCACACACTTCTGCTG  
 AATCGTCTCACCTTCTGTGACTCCAATGTTATCCACCACCTTCTCTGTGACCTCAGCCCTGT  
 GCTGAAATTGTCTGCTCTTCCATATTTGTCAATGAAATTGTGCAGATGACAGAAGCACCT  
 ATTTTGGTGACTCGTTTTCTCTGCTGATTGCTTTCTCTTATATACGAATCCTCAACAGT  
 TCTCAAGATTCCCTCTACTTCTGGGAAACGCAAGCCTTCTCCACCTGTGGTTTTTACCTCA  
 55 CCGTGGTGACGCTCTTTTATGGAAGCATCTTCTGTGCTATTTACAGCCCCCATCCACCTAC  
 GCTGTCAAGGACCACGTGGCAACAATTGTTACACAGTTTTGTCTATCCATGCTCAATCCTT

TTATCTACAGCCTGAGAAACAAAGACCTGAAACAGGGCCTGAGGAAGCTTATGAGCAAGA  
GATCCTAG (SEQ ID NO: 210)

**AOLFR115 sequences:**

5 MEGFYLRSSHBLQGMGKPGRVNQTTVSDFLLLGLSEWPPEEQPLLFGIFLGMVLTVMVGNLLII  
LAISSDPHLHTPMYFFLANLSLTDACFTSASIPKMLANIHTQSQIISYSGCLAQLYFLLMFGGLD  
NCLLAVMAYDRYVAICQPLHYSTSMSPQLCALMLGVCWVLTNCPALMHITLLLRVAFCAQK  
AIPHFYCDPSALLKLACSDTHVNELMIITMGLLFLTVPPLLIVFSYVRIFWAVFVISSPGGRWKA  
10 FSTCGSHLTVVLLFYGSLMGVYLLPPSTYSTERESRAAVLYMVIHPTLNPFIYSLNRNDRMKEALG  
KLFVSGKTFFL (SEQ ID NO: 211)

ATGGAAGGTTTTATCTGCGCAGATCACACGAACTACAAGGGATGGGAAAACCAGGCAGA  
GTGAACCAAACCACTGTTTCAGACTTCCTCCTTCTAGGACTCTCTGAGTGGCCAGAGGAGC  
AGCCTCTTCTGTTTGGCATCTTCCTTGGCATGTACCTGGTCACCATGGTGGGGAACCTGCTC  
15 ATTATCCTGGCCATCAGCTCTGACCCACACCTCCATACTCCCATGTACTTCTTTCTGGCCAA  
CCTGTCAATTAAGTATGCTGCTGTTTCACTTCTGCCTCCATCCCCAAAATGCTGGCCAAACATT  
ATACCCAGAGTCAGATCATCTCGTATTCTGGGTGCTTGGCACAGCTATATTTCTCCTTATG  
TTTGGTGGCCTTGACAACCTGCCTGCTGGCTGTGATGGCATATGACCGCTATGTGGCCATCT  
GCCAACCCTCCATTACAGCACATCTATGAGTCCCCAGCTCTGTGCACTAATGCTGGGTGT  
20 GTGCTGGGTGCTAACCAACTGTCCTGCCCTGATGCACACACTGTTGCTGACCCGCGTGGCT  
TTCGTGCCCAGAAAGCCATCCCTCATTTCTATTGTGATCCTAGTGCTCTCCTGAAGCTTGC  
CTGCTCAGATAACCATGTAAACGAGCTGATGATCATCACCATGGGCTTGCTGTTCTCACT  
GTTCCCTCCTGCTGATCGTCTTCTCCTATGTCCGCATTTTCTGGGCTGTGTTTGTCTCTC  
ATCTCCTGGAGGGAGATGGAAGGCCTTCTCTACCTGTGGTCTCATCTCACGGTGGTCTG  
25 CTCTCTATGGGTCTCTTATGGGTGTGTATTACTTCTCCATCAACTACTCTACAGAGAG  
GGAAAGTAGGGCTGCTGTTCTCTATATGGTGATTATCCACGCTAAACCCATTCAATTTAT  
AGCTTGAGGAACAGAGACATGAAGGAGGCTTTGGGTAAACTTTTTGTGAGTGGAACAA  
TTCTTTTATGA (SEQ ID NO: 212)

**AOLFR116 sequences:**

30 MDEANHSVSEFVFLGLSDSRKIQLLLFLFFSVFYVSSLMGNLLIVLTVTSDPRLOSPMYFLLAN  
LSINLVFCSSTAPKMIYDLFRKHKTISFGGCVVQIFFIHAVGGTEMVLLIAMAFDRYVAICKPLH  
YLTIMNPQRCLFLVISWIIHHSVIQLAFVVDLLFCGPNELDSFFCDLPRFIKLACIETYTLGFMV  
TANSGFISLASFLILISYIFILVTQKKSSGGIFKAFSMLSAHVIVVVLVFGPLIFFYIFPPTSHLD  
35 KFLAIFDAVITPVLNPVIYTFRNKEMMVAMRRRCSSQFVNYSKIF (SEQ ID NO: 213)

ATGGATGAAGCCAATCACTCTGTGGTCTCTGAGTTTGTGTTCTCCTGGGACTCTCTGACTCGC  
GGAAGATCCAGCTCCTCCTCTTCTCTTTTCTCAGTGTCTATGTATCAAGCCTGATGGGA  
AATCTCCTCATTGTGCTAACTGTGACCTCTGACCCCTCGTTTACAGTCCCCCATGTACTTCCT  
40 GCTGGCCAACCTTTCCATCATCAATTTGGTATTTTGTTCCTCCACAGCTCCCAAGATGATTT  
ATGACCTTTTCAGGAAGCACAAGACCATCTCTTTGGGGGCTGTGTAGTTCAGATCTTCTT  
TATCCATGCAGTTGGGGGAACCTGAGATGGTGTCTCATAGCCATGGCTTTTGACCGATAT  
GTGGCCATATGTAAGCCTCTCCACTACCTGACCATCATGAACCCACAAAGGTGCATTTTGT  
TTTTAGTCATTTCTGGATTATAGGTATTATCACTCAGTGATTGAGTTGGCTTTTGTGTA  
45 GACCTGCTGTTCTGTGGCCCTAATGAATTAGATAGTTTCTTTTGTGATCTTCTCGATTAT  
CAAACCTGGCTTGCATAGAGACCTACACATTGGGATTGATGGTACTGCCAATAGTGGATTT  
ATTTCTCTGGCTTCTTTTAAATCTCATAATCTCTTACATCTTATTTTGGTGACTGTTTCTCAG  
AAAAATCTTCAGGTGGTATATTCAAGGCTTTCTCTATGCTGTGAGCTCATGTCAATTGTGG  
TGGTTTGGTCTTTGGGCCATTAATCTTTTCTATATTTTCCATTTCCACATCACATCTTG  
50 ATAAATTCCTTGCCATCTTTGATGCAGTTATCACTCCCGTTTTGAATCCAGTCATCTATACT  
TTTAGAAATAAGAGATGATGGTGGCAATGAGAAGACGATGCTCTCAGTTTGTGAATTAC  
AGTAAATCTTTTAA (SEQ ID NO: 214)

**AOLFR117 sequences:**

55 MNNTIVFVIKIQIEKSDLKYRAISLQEISKISLLFWVLLLVISRLLAMTLGNSTEVTEFYLLGFGA  
QHEFWCILFIVFLLIYVTSIMGNSGILLINTDSRFQTLTYFFLQHLAFVDICYTSAITPKMLQSFT



BEKNLILFQGCVIQFLVYATFATSDCYLLAMMAVDPYVAICKPLHYTVIMSRTVCIRLVAGSYI  
MGSINASVQTGFTCSLSFCKSNSINHHFFCDVPPILALSCSNVDINIMLLVVFVGSNLIFTGLVVIFS  
YYIMATILKMSSSAGRKKSFSSTCASHLTAVTIFYGTLSYMYLQSHSNNSQENMKVAFIFYGTVI  
PMLNPLIYSLRNKEVKEALKVIGKKLF (SEQ ID NO: 215).

5

ATGAATAACACTATTGTATTTGTCATAAAAAATACAAATAGAAAAAAGTGACTTGAAATATA  
GAGCCATTTTCATTGCAAGAAATCTCAAAGATTTCCCTTCTTTCTGGGTCCTTCTCTTGGTC  
ATTTCTAGACTTTTACTAGCCATGACACTAGGAAACAGCACTGAAGTCACTGAATTCTATC  
TTCTGGGATTTGGTGCCAGCATGAGTTTGGTGTATCCTCTTCATTGTATTCCTTCTCATC  
10 TATGTGACCTCCATAATGGGTAATAGTGGAATAATCTTACTCATCAACACAGATTCCAGAT  
TTCAAACACTCACGTACTTTTTTCTACAACATTTGGCTTTTGTGATATCTGTTACACTTCT  
GCTATCACTCCCAAGATGCTCCAAAGCTTCACAGAAGAAAAGAATTTGATATTATTTTCAGG  
GCTGTGTGATACAATTCTTAGTTTATGCAACATTTGCAACCAAGTGACTGTTATCTCCTGGCT  
ATGATGGCAGTGGATCCTTATGTTGCCATCTGTAAGCCCCCTTCACTATACTGTAATCATGT  
15 CCCGAACAGTCTGCATCCGTTTGGTAGCTGGTTCATACATCATGGGCTCAATAAATGCCTC  
TGTACAAACAGGTTTTACATGTTCACTGTCTTCTGCAAGTCCAATAGCATCAATCACTTTT  
TCTGTGATGTTCCCCCTATTCTTGCTCTTTTCATGCTCCAATGTTGACATCAACATCACTGTA  
CTTGTGTCTTGTGGGATCTAAGTTGATATTCACTGGGTTGGTCTGCTATCTTTTCTACAT  
CTACATCATGGCCACCATCCTGAAAATGTCTTCTAGTGCAGGAAGGAAAAAATCCTTCTCA  
20 ACATGTGCTTCCCACCTGACCGCAGTCACCATTTTCTATGGGACACTCTCTTACATGTATTT  
GCAGTCTCATTCTAATAATTCCCAGGAAAAATATGAAAGTGGCCTTTATATTTTATGGCACA  
GTTATTCCCATGTTAAATCCTTTAATCTATAGCTTGAGAAATAAGGAAGTAAAAGAAGCTT  
TAAAAGTGATAGGGAAAAAGTTATTTTAA (SEQ ID NO: 216)

25 **AOLFR118 sequences:**

MNHMSASLKISNSSKFQVSEFILLGFPGIHSWQHWSLPLALLYLSALAANTLILIIWQNPSLQQ  
PMYIFLGILCMVDMGLATTIIPKILAIWFDAKVISLPECFAQIYAIHFFVGMESGILLCMAFDY  
VAICHPLRYPISVTSLLKATLFMVLRNGLFVTPVPVLAQRDYCSKNEIHCCLSNLGVTSLA  
CDDRRPNSICQLVLAWLGMGSDLILSYILILYSVLRNLNSAEAAAKALSTCSSHLTLILFFYTIV  
30 VVISVTHLTEMKATLIPVLLNVLHNIIPSLNPTVYALQTKELRAAFQKVLFAITKEIRS (SEQ ID  
NO: 217)

ATGAATCATATGTCTGCATCTCTCAAAATCTCCAATAGCTCCAAATTCAGGTCTCTGAGTT  
CATCCTGCTGGGATTCCCGGGCATTACAGCTGGCAACACTGGCTATCTCTGCCCTGGCA  
35 CTACTGTATCTCTCAGCACTTGCTGCAAAACACCTCATCCTCATCATCTGGCAGAACCC  
TTCTTTACAGCAGCCCATGTATATTTTCTTGGCATCCTCTGTATGGTAGACATGGGTCTGG  
CCACTACTATCATCCCTAAGATCCTGGCCATCTTCTGGTTTGATGCCAAGGTTATTAGCCTC  
CCTGAGTGCTTTGCTCAGATTTATGCCATTCACTTCTTTGTGGGCATGGAGTCTGGTATCCT  
ACTCTGCATGGCTTTTGATAGATATGTGGCTATTTGTCACCCTCTTCGCTATCCATCAATTG  
40 TCACCAGTTCCTTAATCTTAAAAGCTACCCTGTTTCATGGTGTGAGAAATGGCTTATTTGTC  
ACTCCAGTGCCTGTGCTTGAGCAGCAGCGTGATTATTGCTCCAAGAATGAAATTGAACACT  
GCCTGTGCTCTAACCTTGGGGTCACAAGCCTGGCTTGTGATGACAGGAGGCCAAACAGCAT  
TTGCCAGTTGGTTCTGGCATGGCTTGGAAATGGGGAGTGATCTAAGTCTTATTATACTGTCA  
TATATTTTGATTCTGTACTCTGTACTTAGACTGAAGTCAAGCTGCAGCCAAGGCC  
45 TGAGCACTTGTAGTTCACATCTCACCCTCATCCTTTTCTTTTACACTATTGTTGTAGTGATT  
TCAGTGACTCATCTGACAGAGATGAAGGCTACTTTGATTCCAGTTCCTACTTAATGTGTTGC  
ACAACATCATCCCCCTTCCCTCAACCCTACAGTTTATGCACTTCAGACCAAGAACTTAG  
GGCAGCCTTCCAAAAGGTGCTGTTTGCCCTTACAAAAGAAATAAGATCTTAG (SEQ ID NO:  
218)

50

**AOLFR119 sequences:**

MPLFNSLCWFPTIHTVTPPSFILNGIPGLERVHVWISLPLCTMYIIFLVGNLGLVYLIYYEESLHHP  
MYFFFGHALSLIDLTTCTTLPNALCIFWFSLEINFNACLAQMFFVHGFTGVESGVLMLMALD  
RYIAICYPLRYATTLNPIIAKAELATFLRGVLLMIPFPFLVKRLPFCQSNISHTYCDHMSVVKL  
55 SCASIKVNVYGLMVALLIGVFDICCSLSYTLILKAAISLSSSDARQKAFSTCTAHISAMITYVPA

FFTTFAHRFGGHTIPPSLHIIVANLYLLLPTLNPIVYGVKTKQIRKSVIKFFQGDKGAG (SEQ ID NO: 219)

5 ATGCCTCTATTTAATTCATTATGCTGGTTTCCAACAATTCATGTGACTCCTCCATCTTTTAT  
TCTTAATGGAATACCTGGTCTGGAAAGAGTACATGTATGGATCTCCCTCCCACTCTGCACA  
ATGTACATCATCTTCCTTGTGGGGAATCTTGGTCTTGTGTACCTCATTTATTATGAGGAGTC  
CTTACATCATCCGATGTATTTTTTTTTTGGCCATGCTCTCTCCCTCATTGACCTCCTTACCTG  
CACCACCACTCTACCCAATGCACTCTGCATCTTCTGGTTCAGTCTCAAAGAAATTAACCTCA  
10 ATGCTTGCTTGGCCAGATGTTCTTTGTTTCATGGGTTTACAGGTGTGGAGTCTGGGGTGCT  
CATGCTCATGGCTCTAGACCGCTATATAGCCATTTGCTACCCTTTGCGTTATGCTACCACAC  
TCACCAACCCTATCATTGCCAAGGCTGAGCTTGCCACCTTCCTGAGGGGTGATTGCTGAT  
GATTCCTTTCCCATTTCTTGGTTAAGCGTTTGCCTTTCTGCCAAAGCAATATTATCTCCCAT  
CGTACTGCGACCACATGTCTGTAGTAAAGCTATCTTGTGCCAGCATCAAGGTCAATGTAAT  
15 CTATGGTCTAATGGTTGCTCTCCTGATTGGAGTGTGACATTTGTTGTATATCTTTGTCTT  
ACACTTTGATCCTCAAGGCAGCGATCAGCCTCTCTTCATCAGATGCTCGGCAGAAGGCTTT  
CAGCACCTGCACTGCCCATATATCTGCCATCATCATCACCTATGTTCCAGCATTCTTCACTT  
TCTTTGCCACCGTTTTTGGGGGACACACAATCCCCCTTCTCTTCACATCATTGTGGCTAAT  
CTTTATCTTCTTCTTCCCCCACTCTAAACCCTATTGTTTATGGAGTAAAGACAAAACAGAT  
ACGCAAGAGTGTCTATAAAGTTCTTCCAGGGTGATAAGGGTGCAGGTTGA (SEQ ID NO: 220)

**AOLFR120 sequences:**

25 MQPYTKNWTQVTEFVMMGFAGIHEAHLFFILFLTMYLFTLVENLAAILVVGLDHRLRRPMYF  
FLTHLSLEIWTYSVTVPKMLAGFIGVDGKNISYAGCLSQLFIFTLGATECFLLAAMAYDRY  
VAICMPLHYGAFVSWGTCIRLAAACWLVGFLTPILPIYLLSQLTFCGPNVIDHFSCDASPLLALS  
CSDVTWKETVDFLVSLAVLLASSMVIAVSYGNIVWTLHIRSAAERWKAFTCAHLTVVSLF  
YGTLFFMYVQTKVTSSINFNKVVSFYSVVTMLNPLIYSLRNKEVKGALGRVFSLNFWKGQ  
(SEQ ID NO: 221)

30 ATGCAACCATATACCAAAAACCTGGACCCAGGTAACCTGAATTTGTCATGATGGGCTTTGCTG  
GCATCCATGAAGCACACCTCCTCTTCTTCATACTCTTCCTCACCATGTACCTGTTACCTTG  
GTGGAGAATTTGGCCATCATTTTAGTGGTGGGTTTGGACCACCGACTACGGAGACCCATGT  
ATTTCTTCTGACACACTTGTCTGCCTTGAAATCTGGTACACTTCTGTTACAGTGCCCAAG  
ATGCTGGCTGGTTTTATTGGGGTGGATGGTGGCAAGAATATCTCTTATGCTGGTTGCCTAT  
35 CCCAGCTCTTCATCTTCACTTTCTTGGGGCAACTGAGTGTTCCTACTGGCTGCCATGGCC  
TATGATCGTTATGTGGCCATTTGTATGCCTCTCCACTATGGGGCTTTTGTGTCTGGGGCAC  
CTGCATCCGTCTGGCAGCTGCCTGTTGGCTGGTAGGTTTCCTCACACCCATCTTGCCAATCT  
ACCTCTTGTCTCAGCTAACATTTTGTGGCCCAAATGTCATTGACCATTTCCTCTGTGATGCC  
TCACCCCTTGCTAGCCTTGTCTGTGCTCAGATGTCACCTGGAAGGAGACTGTGGATTTCTGG  
TGCTCTGGCTGTGCTACTGGCCTCCTCTATGGTCATTGCTGTGTCTATGGCAACATCGTC  
40 TGGACACTGCTGCACATCCGCTCAGCTGCTGAGCGCTGGAAGGCCTTCTCTACCTGTGCAG  
CTCACCTGACTGTGGTGAGCCTCTTCTATGGCACTCTTTTCTTTATGTATGTCCAGACCAAG  
GTGACCTCCTCCATCAACTTCAACAAGGTGGTATCTGTCTTCTACTCTGTTGTACGCCCAT  
GCTCAATCCTCTCATCTACAGTCTTAGGAACAAGGAAGTGAAGGGAGCTCTGGGTGCGAGTC  
TTTCTCTCAACTTTTGAAGGGACAGTGA (SEQ ID NO: 222)

45

**AOLFR121 sequences:**

50 MKRKNFTEVSEFIFLGFSSFGKHQITLFVVFLTVYILTLVANIIVTHCIDHHLHTPMYFFLSMLA  
SSETVYTLVIVPRMLLSLIFHNQPISLAGCATQMFFVILATNNCFLLTAMGYDRYVAICRPLRY  
TVIMSKGLCAQLVCGSFGIGLTMAVLHVTAMFNLFPFCGTVVDHFFCDIYPVMKLSCIDTTINEII  
NYGVSSVFVPIGLIFISYVLVISSILQIASAEGRKKTATCVSHLTVVIVHCGCASIAYLKPKSES  
SIEKDLVLSVTYTIITPLLPVVYSLRNKEVKDALCRVVGRNIS (SEQ ID NO: 223)

55 ATGAAGAGAAAGAACTTCACAGAAGTGTGAGAATTCATTTTCTTGGGATTTTCTAGCTTTG  
GAAAGCATCAGATAACCCTCTTTGTGGTTTTCTTAACCTGTCTACATTTTAACTCTGGTTGCT  
AACATCATCATTGTGACTATCATCTGCATTGACCATCATCTCCACACTCCCATGTATTCTT  
CCTAAGCATGCTGGCTAGTTTACAGAGACGGTGTACACACTGGTCATTGTGCCACGAATGCTT

TTGAGCCTCATTITTTTCATAACCAACCTATCTCCTTGGCAGGCTGTGCTACACAAATGTTCTT  
 TTTTGTTATCTTGGCCACTAATAATTGCTTCTGCTTACTGCAATGGGGTATGACCGCTATG  
 TGGCCATCTGCAGACCCCTGAGATACACTGTCATCATGAGCAAGGGACTATGTGCCAGCT  
 GGTGTGTGGGTCTTTGGCATTGGTCTGACTATGGCAGTTCTCCATGTGACAGCCATGTTT  
 5 AATTTGCCGTTCTGTGGCACAGTGGTAGACCACCTTCTTTTGTGACATTTACCCAGTCATGA  
 AACTTTCTTGCATTGATACCACTATCAATGAGATAATAAATTATGGTGTAAGTTCAATTTGT  
 GATTTTGTGCCCATAGGCCTGATATTTATCTCCTATGTCCTTGTGTCATCTCTTCCATCCTTC  
 AAATTGCCTCAGCTGAGGGCCGGAAGAAGACCTTTGCCACCTGTGTCTCCCACCTCACTGT  
 GGTATTTGTCCACTGTGGCTGTGCCTCCATTGCCACCTCAAGCCGAAGTCAGAAAAGTTCA  
 10 ATAGAAAAAGACCTTGTCTCTCAGTGACGTACACCATCATCACTCCCTTGTGTAACCCTG  
 TTGTTTACAGTCTGAGAAACAAGGAGGTAAAGGATGCCCTATGCAGAGTTGTGGGCAGAA  
 ATATTTCTTAA (SEQ ID NO: 224)

**AOLFR122 sequences:**

15 MEWENQTLVEFFLKGHSVHPRLLELFFVLIFIMYVVILLGNGTLILISILDPHLHTPMYFFLGNL  
 SFLDICYTTSIPSTLVSLSERKTISFSGCAVQMFLGLAMGTTECVLLGMMAFDRYVAICNPLR  
 YPIIMSKNAYVPMAGVSWFAGIVNSAVQTTFFVQLPFCRKNVINHFSCEILAVMKLACADISGN  
 EFLMLVATILFTLPLLLIVISYSLIISILKHSSEGRSKAFSTCSAHLTVVIFYGTLFMYMKPKS  
 KETLNSDDL DATDKIISMFYGVMTMPMMNPLIYSLRNKDVKEAVKHLNRRFFSK (SEQ ID NO:  
 20 225)

ATGGAATGGGAAAACCAAACCATTTCTGGTGGAATTTTTTCTGAAGGGACATTCTGTTACC  
 CAAGGCTTGAGTTACTCTTTTTTGTGCTAATCTTCATAATGTATGTGGTCATCTTCTGGGG  
 AATGGTACTCTCATTTTAATCAGCATCTTGGACCCCTCACCTTCACACCCCTATGTACTTCTT  
 25 TCTGGGGAACCTCTCCTTCTTGGACATCTGCTACACCACCACCTCTATTCCCTCCACACTAG  
 TGAGCTTCTTTTCAGAAAGAAAGACCATTTCCTTTTCTGGCTGTGCAGTGCAGATGTTCTT  
 GGCTTGGCCATGGGGACAACAGAGTGTGTGCTTCTGGGCATGATGGCCTTTGACCGCTATG  
 TGGCTATCTGCAACCCTCTGAGATATCCCATCATCATGAGCAAGAATGCCTATGTACCCAT  
 GGCTGTTGGGTCTGGTTTGCAGGGATTGTCAACTCTGCAGTACAACTACATTTGTAGTA  
 30 CAATTGCCCTTTCTGCAGGAAGAATGTCATCAATCATTTCTCATGTGAAATTCTAGCTGTCAT  
 GAAGTTGGCCTGTGCTGACATCTCAGGCAATGAGTTCTCATGCTTGTGGCCACAATATTG  
 TTCACATTGATGCCACTGCTCTTGATAGTTATCTCTTACTCATTAATCATTTCCAGCATCCT  
 CAAGATTCACTCCTCTGAGGGGAGAAGCAAGCTTTCTCTACCTGCTCAGCCCATCTGACT  
 GTGGTCATAATATTCTATGGGACCATCCTCTTCATGTATATGAAGCCCAAGTCTAAAGAGA  
 35 CACTTAATTCAGATGACTTGGATGCTACCGACAAAATTATATCCATGTTCTATGGGGTGAT  
 GACTCCCATGATGAATCCTTTAATCTACAGTCTTAGAAACAAGGATGTGAAAGAGGCAGT  
 AAAACACCTACCGAACAGAAGGTTCTTTAGCAAGTGA (SEQ ID NO: 226)

**AOLFR123 sequences:**

40 MYRFTDFDVSNISYLNHVLFYTTQQAGDLEHMETRNYSAMTEFFLVGLSQYPELQLFLFLCL  
 IMYMILLGNSLLIITILDSRLHTPMYFFLGNL SFLDICYTSSSIPMLIIFMSERKSISFIGALQM  
 VVSLGLGSTECVLLAVMAYDHYVAICNPLRYSIIMNGVLVYQMAAWSWIIGCLTSLLQTVLT  
 MMLPFCGNVIDHITCEILALLKLVCS DITINVLMITVTNIVSLVILLLLIFISYVFILSSILRINCAE  
 GRKKAFTSCSAHSIVVILFYGSALFMYMKPKSKNTNTSDEIIGLSYGVVSPMLNPIIYSLRNKEV  
 45 KEAVKKVLSRHLHLLKM (SEQ ID NO: 227)

ATGTACAGATTTACAGATTTTGATGTATCAAACATTTCAATTTACCTGAATCATGTCCTTTT  
 CTATACTACCCAGCAGGCAGGTGACCTAGAACACATGGAGACAAGAAATTACTCTGCCAT  
 GACTGAATTTCTTCTGGTGGGGCTTTCCCAATATCCAGAGCTCCAGCTTTTCTGTTCTCCTGC  
 50 TCTGCCTCATCATGTACATGATAATCCTCCTGGGAAATAGCCTCCTCATTATCATCACCATC  
 TTGGATTCTCGCCTCCATACTCCCATGTATTTCTTTCTTGGAAACCTCTCATTCTTGGACAT  
 CTGTTACACATCCTCATCCATTCTCCTCAATGCTTATTATATTTATGTCTGAGAGAAAATCCA  
 TCTCCTTCAATTGGCTGTGCTCTGCAGATGGTGTGTGCCCTTGGCTTGGGCTCCACTGAGTGT  
 GTCCTCCTGGCTGTGATGGCCTATGACCACTATGTGGCCATCTGCAACCCACTGAGGTACT  
 55 CCATCATCATGAACGGAGTGCTGTATGTGCAAATGGCTGCATGGTCTGGATCATAGGCTG  
 TCTGACCTCCCTATTGCAAACAGTTCTGACAATGATGTTGCCTTTCTGTGGGAATAATGTC

ATTGATCATATTACCTGTGAAATTTTGGCCCTTCTAAAACCTGTTTGTTCAGATATCACCAT  
 CAATGTGCTTATCATGACAGTGACAAATATTGTTTCACTGGTGATTCTTCTACTGTTAATTT  
 TCATCTCCTATGTGTTTATTCTCTCTTCCATCCTGAGAATTAATTGTGCTGAGGGAAGAAAG  
 AAAGCCTTCTCTACCTGTTTCTGAGCGCACTCGATTGTGGTCATCTTATTCTACGGTTCAGCCCT  
 5 TTTTATGTACATGAAACCCAAGTCAAAGAACACTAATACATCTGATGAGATTATTGGGCTG  
 TCTTATGGAGTGGTAAGCCCAATGTTAAATCCCATCATCTATAGCCTCAGGAATAAAGAGG  
 TCAAAGAGGCTGTAAAGAAAGTCCTGAGCAGACATCTGCATTTATTGAAAATGTGA (SEQ  
 ID NO: 228)

10 **AOLFR124 sequences:**

MNHSVVTEFIILGLTKPELQHIIFLFLIVYLVAFLGNMLIIIAKIYNNTLHTPMYVFLTLAVV  
 DIICTHIIPKMLGTMLTSENTISYAGCMSQLFLFTWSLGAEMVLFITMAYDRYVAICFPLHYST  
 VMNHHMVCVALLSMVMAIAVTNSWVHTALIMRLTFCGPNTIDHFFCEIPPLLALSCSPVRINEV  
 MVYVADITLAIGDFILTCISYGFIIIVAILRIRTVGKRKAFTSCSSHLTVVTLYYSPVIYTYIRPASS  
 15 YTFERDKVVAALYTLVPTLNPVVSFQNRMQAGIRKVFAFLKH (SEQ ID NO: 229)

ATGAATCACAGCGTTGTAAGTGAAGTTCATTATTCTGGGCCTCACCAAAAAGCCTGAACTCC  
 AGGGAATTATCTTCTCTTTTTTCTCATTGTCTATCTTGTGGCTTTTCTCGGCAACATGCTC  
 ATCATCATTGCCAAAATCTATAACAACACCTTGCATACGCCCATGTATGTTTTCTTCTGAC  
 20 ACTGGCTGTTGTGGACATCATCTGCACAACAAGCATCATACCGAAGATGCTGGGGACCAT  
 GCTAACATCAGAAAATACCATTTTCATATGCAGGCTGCATGTCCCAGCTCTTCTTGTTCACA  
 TGGTCTCTGGGAGCTGAGATGGTCTCTTACCACCATGGCCTATGACCGCTATGTGGCCA  
 TTTGTTTCCCTCTTCACTACAGTACTGTTATGAACCACCATATGTGTGTAGCCTTGCTCAGC  
 ATGGTCATGGCTATTGCAGTCACCAATTCCTGGGTGCACACAGCTCTTATCATGAGGTTGA  
 25 TTCTGTGTGGCCAAACACCATTGACCACCTTCTTCTGTGAGATACCCCATTTGTGGCTTTG  
 TCCTGTAGCCCTGTAAGAATCAATGAGGTGATGGTGTATGTTGCTGATATTACCCTGGCCA  
 TAGGGGACTTTATTCTTACCTGCATCTCCTATGGTTTTATCATTGTTGCTATTCTCCGTATC  
 CGCACAGTAGAAGGCAAGAGGAAGGCCTTCTCAACATGCTCATCTCATCTCACAGTGGTG  
 ACCCTTTACTATTCTCCTGTAATCTACACCTATATCCGCCCTGCTTCCAGCTATACATTTGA  
 30 AAGAGACAAGGTGGTAGCTGCACTCTATACTCTTGTGACTCCACATTAAACCCGATGGTG  
 TACAGCTTCCAGAATAGGGAGATGCAGGCAGGAATTAGGAAGGTGTTTGCATTTCTGAAA  
 CACTAG (SEQ ID NO: 230)

**AOLFR125 sequences:**

35 MTNQTQMMEFLLVRFTENWVLLRLHALLFSLIYLTAVLMNLVILLMILDHRLHMAMYFFLRH  
 LSFLDLCLISATVPKSLNSVASTDSISFLGCVLQLFLVLLAGSEIGILTAMSYDRYAAICCPHLC  
 BAVMSRGLCVQLMALSWLNRGALGLLYTAGTFSLNFYGSDELHQFFCDVPALLKLTCSEKHA  
 ISVSVAIGVCYAFSCLVCIVVSYYIFSAVLRISQRQRQSKAFSNCVPHLIVVTVFLVTGAVAYL  
 KPGSDAPSILDLLVSFYSVAPPTLNPVIYCLKNKDIKSALSKVLWNVRSSGVMKDD (SEQ ID  
 40 NO: 231)

ATGACCAATCAGACACAGATGATGGAATTTCTGCTTGTGAGATTTACTGAGAATTGGGTGC  
 TCCTGAGGCTGCATGCTTTGCTCTTCTCACTGATCTACCTCACGGCTGTGCTGATGAATTTA  
 GTCATCATTCTCCTCATGATTCTGGACCATCGTCTCCACATGGCAATGTACTTTTTCTCCCG  
 45 ACATTTGTCTTCTTAGACCTGTGTCTCATTTCTGCCACAGTCCCCAAATCCATCCTCAACT  
 CTGTGCGCTCCACTGACTCCATCTCCTTCTGGGGTGTGTGTGTCAGCTCTTCTTGGTGGTA  
 CTGCTGGCTGGATCAGAGATTGGCATCCTTACTGCCATGTCTATGACCGCTATGCTGCCA  
 TCTGCTGCCCCCTACACTGTGAGGCTGTCATGAGCAGAGGGCTCTGTGTCCAGTTGATGGC  
 TCTGTCTGGCTCAACAGAGGGGCTTGGGACTCTTGTACACAGCTGGAACATTCTCTCTG  
 50 AATTTTTATGGCTCTGATGAGCTACATCAGTCTTCTGCGATGTCCCTGCCCTACTAAAGCT  
 CACTGTCTTAAAGAACATGCCATCATTAGTGTGAGTGTGGCCATTGGGGTCTGTTATGCA  
 TTTTCATGTTTAGTTTGCATTGTAGTTTCTTCTGTGTACATTTTCTCTGCTGTGTTAAGGAT  
 ATCACAGAGACAGAGACAATCCAAAGCCTTTTCCAACCTGTGTGCCTCACCTCATTGTTGTC  
 ACTGTGTTTCTTGTAAACAGGTGCTGTTGCTTATTTAAAGCCAGGGTCTGATGCACCTTCTAT  
 55 TCTAGACTTGCTGGTGTCTGTGTTCTATTCTGTGCGACCTCCAACCTTGAACCTGTTATCT

ACTGTCTGAAGAACAAGGACATTAAATCCGCTCTGAGTAAAGTCCTGTGGAATGTTAGAA  
GCAGTGGGGTAATGAAAGATGACTAA (SEQ ID NO: 232)

**AOLFR126 sequences:**

5 MFLYLCFIFQRTCSEEMEBENATLLTEFVLTGFLHQPDCKIPLFLAFLVIYLITMGNLGLIVLIW  
KDPHLHIPMYLFLGSLAFVDASLSSTVTPKMLINFLAKSKMISLSECMVQFFSLVTTVTTECFLL  
ATMAYDRYVAICKALLYPVIMTNELCIQLLVLSFIGGLLHALIHEAFSFRITFCNSNIQHIFYCDII  
PLLKISCTDSSINFLMVFI FAGSVQVFTIGTILISYTIILFTILEKKSIKIRKAVSTCGAHLLSVSLY  
YGPLTFKYLGSASPQADDQDMMESLFYTVIVPLLNPMIYSLRNKQVIASFTKMFKSNV (SEQ ID  
10 NO: 233)

ATGTTCCCTTTACCTTTGCTTCATTTTTTCAGAGGACATGCAGTGAGGAGATGGAAGAGGAAA  
ATGCAACATTGCTGACAGAGTTTGTCTCACAGGATTTTTACATCAACCTGACTGTAAAAT  
ACCGCTCTTCCTGGCATTCTTGGTAATATATCTCATCACCATCATGGGAATCTTGGTCTAA  
15 TTGTTCTCATCTGGAAAGACCCTCACCTTCATATCCCAATGTACTTATTCCTTGGGAGTTTA  
GCCTTTGTGGATGCTTCGTTATCATCCACAGTGACTCCGAAGATGCTGATCAACTTCTTAG  
CTAAGAGTAAGATGATATCTCTCTCTGAATGCATGGTACAATTTTTTCCCTTGTAACCACT  
GTAACCACAGAATGTTTTCTCTTGGCAACAATGGCATATGATCGCTATGTAGCCATTTGCA  
AAGCTTTACTTTATCCAGTCATTATGACCAATGAACTATGCATTACAGCTATTAGTCTTGTC  
20 TTTATAGGTGGCCTTCTTCATGCTTTAATCCATGAAGCTTTTTTCATTTCAGATTAACTTCTG  
TAATTCCAACATAATAACAACCTTTACTGTGACATTATCCCATTTGTTAAAGATTTCTGTGTA  
CTGATTCCTCTATTAACCTTTCTAATGGTTTTATTTTCGCAGGTTCTGTTCAAGTTTTACCA  
TTGGAACATACTTATATCTTATACAATTAATCCTCTTTACAATCTTAGAAAAGAAGTCTATC  
AAAGGGATACGAAAAGCTGTCTCCACCTGTGGGGCTCATCTCTTATCTGTATCTTTATACT  
25 ATGGCCCCCTCACCTTCAAATATCTGGGCTCTGCATCTCCGCAAGCAGATGACCAAGATAT  
GATGGAGTCTCTATTTTACACTGTCATAGTTCTTTATTAATCCCATGATCTACAGCCTGA  
GAAACAAGCAAGTAATAGCTTCATTCACAAAATGTTCAAAAGCAATGTTTAG (SEQ ID  
NO: 234)

**AOLFR127 sequences:**

30 MSNEDMEQDNTLLTEFVLTLTYQPEWKMPFLVFLVIYLITIVWNLGLIALIWNDPQLHIPM  
YFFLGLSALFVDAWISSTVTPKMLVNFLAKNRMISLSECMIQFFSFAFGGTTECFLLATMAYDRY  
VAICKPLLYPVIMNNSLCIRLLAFSFLGGFLHALIHEVLIIFRLTFCNSNIHHIFYCDIIPLFMISCTD  
PSINFLMVFILSGSIQVFTIVTVLNSYTFALFTILKKKSVRGVRKAFSTCGAHLLSVSLYYGPLIF  
35 MYLRPASQADDQDMIDSVFYTTIIPLLNPIIYSLRNKQVIDSFTKMKVRNV (SEQ ID NO: 235)

ATGTCGAATGAGGACATGGAACAGGATAATACAACATTGCTGACAGAGTTTGTCTCACA  
GGACTTACATATCAGCCAGAGTGGAAAATGCCCTGTTCTTGGTGTTCTTGGTGATCTATC  
TCATCACTATTGTGTGGAACCTTGGTCTGATTGCTCTTATCTGGAATGACCCACAACCTCAC  
40 ATCCCCATGTACTTTTTCTTGGGAGTTTAGCCTTTGTTGATGCTTGGATATCTTCCACAGT  
AACTCCCAAAATGTTGGTTAATTTCTTGGCCAAAAACAGGATGATATCTCTGTCTGAATGC  
ATGATTCAATTTTTCTTTCATTGTCATTGGGAACTACAGAATGTTTTCTTGGCAACAAT  
GGCATATGATCGCTATGTAGCCATATGCAAACTTTACTATATCCAGTGATTATGAACAAT  
TCACTATGCATACGGCTGTTAGCCTTCTCATTTTTAGGTGGCTTCCCTCCATGCCTTAATTCA  
45 TGAAGTCCTTATATTCAGATTAACTTCTGCAATTCTAACATAATACATCATTTTTACTGTG  
ATATTATACCACTGTTTATGATTTCTGTACTGACCCTTCTATTAATTTCTAATGGTTTTTA  
TTTTGTCTGGCTCAATTCAGGTATTCACCATTTGTGACAGTTCTTAATTCTTACACATTTGCT  
CTTTTCACAATCCTAAAAAAGAGTCTGTTAGAGGCGTAAGGAAAGCCTTTTCCACCTGTG  
GAGCCCATCTCTTATCTGTCTCTTTATATTATGGCCCACTTATCTTCATGTATTTGCGCCCT  
50 GCATCTCCACAAGCAGATGACCAAGATATGATAGACTCTGTCTTTATACAATCATAATTC  
CTTTGCTAAATCCCATTATCTACAGTCTGAGAAATAACAAGTAATAGATTCAATTCACAAA  
AATGGTAAAAAGAAATGTTTAG (SEQ ID NO: 236)

**AOLFR128 sequences:**

55 METQNLTVVTEFILLGLTQSQDAQLLVFVLVLIIFYLIILPGNFIIFTIKSDPGLTAPLYFFLGNLA  
LLDASYSFIVVPRMLVDFLSEKKVISYRSCITQLFFLHFLGAGEMFLLVVMFAFDRYIAICRPLHY

STIMNPRACYALSLVLWLGGFIHSIVQVALILHLPFCGPNQLDNFFCDVPQVIKLACTNTFVVVEL  
LMVSNSSGLLSLLCFLGLLASYAVILCRIREHSSEKSKAISTCTTHIIIFLMFGPAIFIYTCPFQAF  
ADKVVSLFHTVIFPLMNPVIYTLRNQEVKASMRKLLSQHMF (SEQ ID NO: 237)

- 5 ATGGAAACACAGAACCTCACAGTGGTGACAGAATTCATTCTTCTTGGTCTGACCCAGTCTC  
AAGATGCTCAACTTCTGGTCTTTGTGCTAGTCTTAATTTTCTACCTTATCATCCTCCCTGGA  
AATTTCTCATCATTTTACCATAAAGTCAGACCCTGGGCTCACAGCCCCCTCTATTTCTT  
TCTGGGCAACTTGGCCTTACTGGATGCATCCTACTCCTTCATTGTGGTTCACAGGATGTTG  
GTGGACTTCTCTCTGAGAAGAAGGTAATCTCCTATAGAAGCTGCATCACTCAGCTCTTTT  
10 TCTTGCAATTTTCTTGGAGCGGGAGAGATGTTCTCCTCCTCGTTGTGATGGCCTTTGACCGCTAC  
ATCGCCATCTGCCGGCCTTTACACTATTCAACCATCATGAACCCTAGAGCCTGCTATGCAT  
TATCGTTGGTTCTGTGGCTTGGGGGCTTTATCCATTCCATTGTACAAGTAGCCCTTATCCTG  
CACTTGCCTTTCTGTGGCCCA<sup>A</sup>ACCAGCTCGATAACTTCTTCTGTGATGTTCCACAGGTCAT  
CAAGCTGGCCTGCACCAATACCTTTGTGGTGGAGCTTCTGATGGTCTCCAACAGTGGCCTG  
15 CTCAGCCTCCTGTGCTTCTGGGCCTTCTGGCCTCCTATGCAGTCATCCTCTGTGCTATAAG  
GGAGCACTCCTCTGAAGGAAAGAGCAAGGCTATTTCCACATGCACCACCCATATTATCATT  
ATATTTCTCATGTTTGGACCTGCTATTTTCATCTACACTTGGCCCTTCCAGGCTTTCCAGC  
TGACAAGGTAGTTTCTCTTTTCCATACTGTCATCTTTCCTTTGATGAACCCTGTTATTTATA  
CGCTTCGCAACAGGAGGTGAAAGCTTCCATGAGGAAGTTGTTAAGTCAACATATGTTTTG  
20 CTGA (SEQ ID NO: 238)

**AOLFR129 sequences:**

- MALYFSLILHGMSDLFFLSTGHPRASCRMEAMKLLNQSQVSEFILLGLTSSQDVEFLFLAFLSVI  
YVVTVLGNLLIIVTVFNTPNLNTPMYFLLGNLSFVDMTLASFATPKVILNLLKKQKVISFAGCFT  
25 QIFLLHLLGGVEMVLLVSMAFDRYVAICKPLHYMTIMNKKVCVLLVVTSWLLGLLHSGFQIPF  
AVNLPFCGPNVDSIFCDLPLVTKLACIDIYFVQVVIVANSGLSLSCFILLISYSLILITIKNHSP  
GQSKARSTLTAHITVILFFGPCIFIYWPFGNHSVDKFLAVFYTITPILNPIIYTLRNKEMKISM  
KLWRAVNSREDT (SEQ ID NO: 239)

- 30 ATGGCTCTTTATTTTCACTCATACTCCATGGTATGAGTGATCTTTTCTTCTCTCTACAGG  
TCATCCAAGAGCGAGCTGTAGGATGGAGGCCATGAAACTATTAATCAATCTCAAGTGTC  
AGAATTCATTTTGTGGGACTGACCAGCTCCCAGGATGTAGAGTTTCTTCTCTTGGCCCTCT  
TCTCGGTTATCTATGTGGTCACAGTTTTGGGTAACCTTCTTATTATAGTCACAGTGTTAAC  
ACCCCTAACCTGAATACTCCCATGTATTTCTCCTTGGTAATCTCTCTTTGTAGATATGAC  
35 CCTTGCTTCTTTGCCACCCCTAAGGTGATTCTGAACCTGTAAAAAAGCAGAAGGTAATT  
TCTTTTGTGGGTGCTTCACTCAGATATTTCTCCTTCACTTACTGGGTGGGTTGAAATGGT  
ACTGTTGGTCTCCATGGCTTTTGACAGATATGTGGCCATTTGTAAGCCCCTACACTACATG  
ACCATCATGAACAAGAAGGTATGTGTTTTGCTTGTAGTGACCTCATGGCTCTTGGGTCTCC  
TTCACTCAGGGTTTCAGATACCATTGCTGTGAACCTTGGCCTTTTGTGGTCCCAATGTGGTA  
40 GACAGCATTTTTTGTGACCTCCCTTTGGTTACTAAGCTTGCCTGTATAGACATATATTTGT  
ACAGGTAGTCATTGTTGCCAACAGTGGCATAATCTCCCTGAGCTGTTTCATTATTTTGCTTA  
TCTCCTACAGTCTGATCCTCATAACCATTAAAGAACCACTCTCCTACTGGGCAATCTAAAGC  
CCGTTCCACTTTGACTGCTCACATCACAGTGGTGATTCTCTTCTTTGGCCCATGCATCTTA  
TCTACATTTGGCCCTTCGGCAACCACTCTGTAGATAAGTTCCTTGCTGTGTTTTATACCATC  
45 ATCACTCCTATCTTGAATCCAATTATCTATACTCTGAGAAACAAAGAAATGAAGATATCCA  
TGAAAAAACTCTGGAGAGCTTTTGTGAATTCTAGAGAAGATACTTAG (SEQ ID NO: 240)

**AOLFR131 sequences:**

- MASTSNVTELI FTGLFQDPAVQSVCFVFLPVYLATVVGNGLIVLTVSISKSLDSPMYFFLSCLS  
15 LVEISYSSTIAPKFIDLLAKIKTISLEGCLTQIFFHFHFGVAEILLIVVMAYDCYVAICKPLHYMNI  
ISRQLCHLLVAGSWLGGFCHSHIQLVIIQLPFCGPNVIDHYFCDLQPLFLACTDTFMEGVIVLA  
NSGLFSVFSFLILVSSYIVILVNLNRHSAEGRHKALSTCASHITVILFFGPAIFLYMRPSSSTFTED  
KLVAVFYTVITPMLNPIIYTLRNAEVKIAIRRLWSKKENPGRE (SEQ ID NO: 241)

- 55 ATGGCCAGTACAAGTAATGTGACTGAGTTGATTTTCACTGGCCTTTTCCAGGATCCAGCTG  
TGCAGAGTGATGCTTTGTGGTGTCTCCCCGTGTACCTTGCCACGGTGGTGGGCAATGG

CCTCATCGTTCTGACGGTCAGTATCAGCAAGAGTCTGGATTCTCCCATGTACTTCTTCCTTA  
 GCTGCGTGTCTTGGTGGAGATCAGTTATTCTCCACTATCGCCCCATAAATTCATCATAGAC  
 TTAATTGCCAAGATTA AAAACCATCTCTCTGGAAGGCTGTCTGACTCAGATATTCTTCTTCCA  
 CTTCTTTGGGGTTGCTGAGATCCTTTTGATTGTGGTGATGGCCTATGATTGCTACGTGGCC  
 5 ATTTGCAAGCCTCTTCATTATATGAACATTATCAGTCGTCAACTGTGTACCTTCTGGTGGC  
 TGGTTCTGGCTGGGGGGCTTTTGTCACTCCATAATTAGATTCTCGTTATCATCCAATTGC  
 CCTTCTGTGGTCCCAATGTGATTGACCACTATTTCTGTGACCTCCAGCCTTTATTCAAGCTT  
 GCCTGCACTGACACCTTCATGGAGGGGGTTATTGTGTGGCCAACAGTGGATTATTCTCTG  
 TCTTCTCCTTCTCATCTTGGTGTCTCTTATATTGTCACTTCTGGTCAACTTGAGGAACCAT  
 10 TCTGCAGAGGGGAGGCACAAAGCCCTCTCCACCTGTGCTTCTCACATCACAGTGGTCATCT  
 TGTTTTTTGGACCTGCTATCTTCTCTACATGCGACCTTCTTCCACTTTCAGTGAAGATAAA  
 CTTGTGGCTGTATTCTACACGGTTCATACCCCCATGCTGAACCCCATCATTTACACACTCAG  
 GAATGCAGAGGTGAAAATCGCCATAAGAAGATTGTGGAGCAAAAAGGAGAATCCAGGGA  
 GGGAGTGA (SEQ ID NO: 242)

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**AOLFR132 sequences:**

MVATNNVTEIIFVGFSQNWSEQRVISVMFLMYTAVVLGNGLIVVTLASKVLTSPMYFFLSYL  
 SFVEICYCSVMAPKLIFDSFIKRKVISLKGCLTQMFSLHFFGGTEAFLLMVMA YDRYVAICKPL  
 HYMAIMNQRMCGLLVRIA WGGGLLSVVGQTLIFQLPFCGPNIMDHYFCDVHPVLELACADT  
 20 FFISLLITNGGSISVVSFFVLMA SYLILHFLRSHNLEGQHKALSTCASHVTVDLFFIPCSLVYIR  
 PCVTLPADKIVAVFYTVVTPLLNPVIYSFRNAEVKNAMRRFIGGKVI (SEQ ID NO: 243)

ATGGTTGCTACAAACAATGTGACTGAAATAATTTTCGTGGGATTTTCCAGAAATTGGAGTG  
 AGCAGAGGGTCAATTTCTGTGATGTTTCTCCTCATGTACACAGCTGTTGTGCTGGGCAATGG  
 25 CCTCATTGTGGTGACCATCCTGGCCAGCAAAGTGCTCACCTCCCCCATGTATTTCTTTCTCA  
 GCTACTTATCCTTTGTGGAGATCTGCTACTGTTCTGTCATGGCCCCCAAGCTTATCTTTGAC  
 TCCTTTATCAAGAGGAAAGTCATTTCTCTCAAGGGCTGCCTCACACAGATGTTTCCCTCC  
 ATTTCTTTGGTGGCACTGAGGCCCTTCTCCTGATGGTGATGGCCTATGACCGCTATGTGGC  
 CATCTGCAAGCCCTTGCACTACATGGCCATCATGAACCAGCGAATGTGTGGTCTCCTCGTG  
 30 AGGATAGCATGGGGCGGGGGCCTGCTGCATTCTGTTGGGCAAACCTTCTGATTTTCCAGC  
 TCCCGTTCTGTGGCCCCAACATCATGGACCACTACTTCTGTGATGTCCACCCAGTGCTGGA  
 GCTGGCCTGCGCAGACACCTTCTTCATTAGCCTGCTGATCATCAACCAATGGCGGCTCCATC  
 TCCGTAGTCAGTTTCTTCGTGCTGATGGCTTCTACCTGATCATCCTGCACTTCTTGAGAAG  
 CCACAACCTGGAGGGGCGAGCACAAGGCCCTCTCCACCTGTGCCTCTCATGTCACAGTTGTC  
 35 GACCTGTTCTTCATACCTTGCTCCTTGGTCTATATTAGGCCCTGTGTACCCCTCCCTGCAGA  
 CAAGATAGTTGCTGTATTTTATACAGTGGTCAACCTCTCTTAAACCCTGTGATTTACTCCT  
 TCAGGAATGCTGAAGTGAAAAATGCCATGAGGAGATTTATTGGGGGAAAAGTAATTTGA  
 (SEQ ID NO: 244)

40

**AOLFR133 sequences:**

MTEFIFLVLSPNQEVQRVCFVIFLFLYTAIVLGNFLIVLTVMTSRLGSPMYFFLSYLSFMEICYS  
 SATAPKLISDLLAERKVISWWGCMALFFLHFFGGTEIFLLTVMAYDHYVAICKPLSYTTIMN  
 WQVCTVLVGLAVWVGFMHSFAQILLIFHLLFCGPNVINHYFCDLVPLKLACSDTFLIGLLIVAN  
 45 GGTLSVISFGVLLASYMVILLHLRTWSSEGWCKALSTCGSHFAVVILFFGPCVFNSLRPSTTLPI  
 DKMVA VFYTVTTAILNPVIYSLRNAEMRKAMKRLWIRTLRLNEK (SEQ ID NO: 245)

ATGACTGAATTCATTTTCTGGTACTTTCTCCCAACCAGGAGGTGCAGAGGGTTTGCTTTG  
 TGATATTTCTGTTCTTGACACAGCAATTGTGCTGGGGAATTTCTCATTGTGCTCACTGTC  
 50 ATGACCAGCAGAAGCCTTGGTTCCCCCATGTACTTCTCCTCAGCTACCTCTCCTTCATGGA  
 GATCTGCTACTCCTCCGCTACAGCCCCAAACTCATCTCAGATCTGCTGGCTGAAAGGAAA  
 GTCATATCTTGGTGGGGCTGCATGGCACAGCTTTTCTTCTTGCACTTCTTTGGTGGCACTGA  
 GATTCTCCTGCTCACTGTGATGGCCTATGACCACTATGTGGCCATCTGCAAGCCCCCAGC  
 TACACCACCATCATGAACCTGGCAGGTGTGTACTGTCTTGTAGGAATAGCATGGGTGGGA  
 GGCTTCATGCATTCTTTGCACAAATCCTTCTCATCTTCCACCTGCTCTTCTGTGGCCCCAA  
 55 TGTGATCAATCACTATTTCTGTGACCTAGTTCCCCTTCTCAAACTTGCTGCTGACACCT  
 TCTCATTTGGTCTGCTGATTGTTGCCAATGGAGGCACCCTGTCTGTGATCAGTTTTGGGGT

CCTCTTAGCATCCTATATGGTCATCTTGCTCCATCTGAGAACCTGGAGCTCTGAAGGGTGG  
 TGCAAAGCCCTCTCCACCTGTGGGTCCCATTTCGCTGTGGTTATCTTGTTCTTTGGGCCCTG  
 CGTCTTCAACTCTCTGAGGCCCTTCTACCACTCTGCCCATAGACAAGATGGTGGCTGTGTTCT  
 ACACAGTGATAACCGCGATCCTGAACCCTGTCATCTACTCTCTGAGAAATGCTGAAATGAG  
 5 GAAGGCCATGAAGAGGCTGTGGATTAGGACATTGAGACTAAATGAGAAATAG (SEQ ID  
 NO: 246)

**AOLFR134 sequences:**

MTTILEVDNHTVTTRFILLGFPTRPAPQLLFFSIFLATYLLTLENLLIILAIHSDGQLHKPMYFFL  
 10 SHLSFLEMWYVTVISPKMLVDFLSHDKSISFNGCMTQLYFFVTFVCTEYILLAIMAFDRYVAIC  
 NPLRYPVIMTNQLCGTLAGGCWFCGLMTAMIKMVFIQLHYCGMPQINHYFCDISPLLNVSCE  
 DASQAEMVDFFLALMVIAIPLCVVVASYAAILATILRIPSAQGRQKAFSTCASHLTVVILFYMS  
 LFTYARPKLMYA YNSNKVSVLYTVIVPLLNPIIYCLRNHEVKAALRKTHICRGSQPQNGAFS  
 S (SEQ ID NO: 247)

15 ATGACCACCATAATTCTGGAAGTAGATAATCATACAGTGACAACACGTTTCATTCTTCTGG  
 GTTTTCCAACACGACCAGCCTTCCAGCTTCTCTTTTTCTCCATTTTCTGGCAACCTATCTG  
 CTGACACTGCTGGAGAATCTTCTTATCATCTTAGCTATCCACAGTGATGGGCAGCTGCATA  
 AGCCCATGTACTTCTTCTGAGCCACCTCTCCTTCTGGAGATGTGGTATGTCACAGTCATC  
 20 AGCCCCAAGATGCTTGTGACTTCTCAGTCATGACAAGAGTATTTCCITCAATGGCTGCA  
 TGACTCAACTTTACTTTTTTGTGACCTTTGTCTGCACTGAGTACATCCTTCTTGCTATCATG  
 GCCTTTGACCGCTATGTAGCCATTTGTAATCCACTACGCTACCCAGTCATCATGACCAACC  
 AGCTCTGTGGCACACTGGCTGGAGGATGCTGGTCTGTGGACTCATGACTGCCATGATTAA  
 GATGGTTTTTATAGCACAACTTCACTACTGTGGCATGCCTCAGATCAATCACTACTTTTTGTG  
 25 ATATCTCTCCACTCCTTAACGTCTCCTGTGAGGATGCCTCACAGGCTGAGATGGTGGACTT  
 CTTCTTGCCCTCATGGTCATTGCTATTCTCTTTGTGTGTGGTGGCATCCTACGCTGCTA  
 TCCTTGCCACCATCCTCAGGATCCCTTCTGCTCAGGGCCGCCAAAAGGCATTCTCCACCTG  
 TGCCTCCACCTGACCGTCGTAATTCTCTTCTATTCCATGACACTTTTCACCTATGCCCGTC  
 CCAAACCTCATGTATGCCTACAATTCCAACAAAGTGGTATCTGTTCTCTACACTGTCATTGTT  
 30 CCACTCCTCAACCCCATCATTTACTGTCTGAGGAACCATGAAGTAAAGGCAGCCCTCAGAA  
 AGACCATACATTGCAGAGGAAGTGGGCCCCAGGGAAATGGGGCTTTTCAGTAGTTAA (SEQ  
 ID NO: 248)

**AOLFR135 sequences:**

35 MIFPSHDSQAFSTVDMVEVGNCTILTEFILLGFSADSQWQPILFGVFLMLYLITLSGNMTLVILRT  
 DSHLHTPMYFFIGNLSFLDFWYTSVYTPKILASCVSEDKRISLAGCGAQLFFSCVVAYTECYLL  
 AAMAYDRHAAICNPLLYSGTMTALCTGLVAGSYIGGFLNAIAHTANTFRLHFCGKNIDHFFC  
 DAPPLVKMSCTNTRVYEKVLGTVGFTVLSLAILISYVNILLAILRIHSASGRHKAFTCASHL  
 40 ISVMLFYGSLFMYSRPSSTYSLERDKVAALFYTVINPLNPLIYSLRNKDIKEAFRKATQTIQPO  
 T (SEQ ID NO: 249)

ATGATTTTCCCTTCTCATGATAGTCAGGCTTTCACCTCCGTGGACATGGAAGTGGGAAATT  
 GCACCATCCTGACTGAATTCATCTTGTGTTGGGTTTCTCAGCAGATTCCCAGTGGCAGCCGAT  
 TCTATTTGGAGTGTTTCTGATGCTCTATTTGATAACCTTGTGAGGAAACATGACCTTGGTTA  
 45 TCTTAATCCGAACCTGATTCCCACTTGCATACACCTATGTACTTTTTTCATTGGCAATCTGTCT  
 TTTTGGATTCTGGTATACCTCTGTGTATACCCCCAAAATCCTGGCCAGTTGTGTCTCAGA  
 AGATAAGCGCATTTCTTGGCTGGATGTGGGGCTCAGCTGTTTTTTCTGTGTTGTAGCCT  
 ACACTGAATGCTATCTCCTGGCAGCCATGGCATATGACCGCCATGCAGCAATTTGTAACCC  
 ATTGCTTTATTCAAGTACCATGTCCACCGCCCTCTGTACTGGGCTTGTGCTGGCTCCTACA  
 50 TAGGAGGATTTTTGAATGCCATAGCCCATAGCCCAATACATTCCGCCTGCATTTTTGTGG  
 TAAAAATATCATTGACCACTTTTCTGTGATGCACCAACATTGGTAAAAATGTCTGTACA  
 AACACCAGGGTCTACGAAAAAGTCTGCTTGGTGTGGTGGGCTTCACAGTACTCTCCAGCA  
 TTCTTGCTATCCTGATTTCTATGTCAACATCCTCCTGGCTATCCTGAGAATCCACTCAGCT  
 TCAGGAAGACACAAGGCATTCTCCACCTGTGCTTCCACCTCATCTCAGTCATGCTCTTCTA  
 55 TGGATCATTGTTGTTTATGTATTCAAGGCCTAGTTCCACCTACTCCCTAGAGAGGGACAAA  
 GTAGCTGCTCTGTTCTACACCGTGATCAACCCACTGCTCAACCCTCTCATCTATAGCCTGAG



AAACAAAGATATCAAAGAGGCCTTCAGGAAAGCAACACAGACTATACAACCACAAACATG  
A (SEQ ID NO: 250)

**AOLFR136 sequences:**

5 MTMENYSMAAQFVLDGLTQQABELQLPLFLLFLGIYVVTVVGNLGMILLIAVSPLLHTPMYYFL  
SSLSFVDFCYSSVITPKMLVNFLGKKNLILYSECMVQLFFFVVFVVAEGYLLTAMAYDRYVAIC  
SPLLYNAMSSWVCSLLVLAFFLGLSALHTSMMKLSFCKSHIINHFCVDLPLLNLSCSNT  
HLNELLFLIAGFNTLVPTLAVAVSYAFILYSLHIRSSEGRSKAFGTCSHLMMAVVIFFGSITFMY  
FKPPSSNSLDQEKVSSVFYTTVIPMLNPLIYSLRNKDVKKALRKVLVGK (SEQ ID NO: 251)

10 ATGACCATGGAAAATTATTCTATGGCAGCTCAGTTTGTCTTAGATGGTTTAAACACAGCAAG  
CAGAGCTCCAGCTGCCCCCTCTCCTCCTGTTCTCCTGGGAATCTATGTGGTCACAGTAGTGGG  
CAACCTGGGCATGATTCTCCTGATTGCAGTCAGCCCTCTACTTCACACCCCCATGTAATATT  
TCCTCAGCAGCTTGCTCCTTCGTCGATTCTGCTATTCTCCTCTGTCATTACTCCCAAAATGCTG  
15 GTGAACCTTCTAGGAAAGAAGAATAACAATCCTTTACTCTGAGTGCATGGTCCAGCTCTTTT  
TCTTTGTGGTCTTTGTGGTGGCTGAGGGTTACCTCCTGACTGCCATGGCATATGATCGCTA  
TGTTGCCATCTGTAGCCCACTGCTTTATAATGCGATCATGTCCTCATGGGTCTGCTCACTGC  
TAGTGCTGGCTGCCTTCTTCTTGGGCTTTCTCTCTGCCTTGACTCATACAAGTGCCATGATG  
AAACTGTCCTTTTGCAAATCCACATTATCAACCATTACTTCTGTGATGTTCTTCCCCTCCT  
20 CAATCTCTCCTGCTCCAACACACACCTCAATGAGCTTCTACTTTTTATCATTGCGGGGTTA  
ACACCTTGGTGCCACCCCTAGCTGTTGCTGTCTCCTATGCCTTCATCCTCTACAGCATCCTT  
CACATCCGCTCCTCAGAGGGCCGGTCCAAAGCTTTTGGAACATGCAGCTCTCATCTCATGG  
CTGTGGTGATCTTCTTGGGTCCATTACCTTCATGTATTTCAGGCCCTTCAAGTAACCTCC  
CTGGACCAGGAGAAGGTGTCCTCTGTGTTCTACACCACGGTGATCCCCATGCTGAACCCTT  
25 TAATATACAGTCTGAGGAATAAGGATGTGAAGAAAGCATTAAAGGAAGGTCTTAGTAGGAA  
AATGA (SEQ ID NO: 252)

**AOLFR137 sequences:**

30 MSPENQSSVSEFLLGLPIRPEQQAFFALFLGMYLTTVLGNLLIMLLIQLDSHLHTPMYFFLSH  
LALTDISFSSVTPKMLNMNMQTHLAVFYKGCISQTYFFIFFADLDSFLITSMAYDRYVAICHPL  
HYATIMTQSQCVM LVAGSWVIACACALLHTLLLAQLSFCADHIIPHYFCDLGALLKLSCSDTSL  
NQLAIFTAALTAIMLPFLCILVSYGHIGVTLQIPSTKGICKALSTCGSHLSVVTIYRTIIGLYFLP  
PSSNTNDKNIIASVIYTA VTPMLNPFYISLRNKDIKGALRKLLSRGAVAHACNLSTLGG (SEQ  
ID NO: 253)

35 ATGAGCCCTGAGAACCAGAGCAGCGTGTCCGAGTTCCTCCTCCTGGGCCTCCCCATCCGGC  
CAGAGCAGCAGGCCGTGTTCTTCGCCCTGTTCTCCTGGGCATGTACCTGACCACGGTGCTGGG  
GAACCTGCTCATCATGCTGCTCATCCAGCTAGACTCTCACCTTCACACCCCCATGTAATCTT  
TCCTTAGCCACTTGGCCCTCACTGACATCTCCTTTTCATCTGTCACTGTCCCTAAGATGCTG  
40 ATGAACATGCAGACTCAGCACCTAGCCGTCTTTTACAAGGGATGCATTTACAGACATATT  
TTTTCATATTTTTTGCTGACTTAGACAGTTTCTTATCACTTCAATGGCATATGACAGGTAT  
GTGGCCATCTGTATCCTCTACATTATGCCACCATGACTCAGAGCCAGTGTGTCTATGC  
TGGTGGCTGGGTCCTGGGTCTATCGCTTGTGCGTGTGCTCTTTTGATACCCCTCCTCCTGGCC  
CAGCTTTCTTCTGTGCTGACCACATCATCCCTCACTACTTCTGTGACCTTGGTGCCCTGCT  
45 CAAGTTGTCCTGCTCAGACACCTCCCTCAATCAGTTAGCAATCTTTACAGCAGCATTGACA  
GCCATTATGCTTCCATTCTGTGCTATCCTGGTTCTTATGGTCACATTGGGGTCAACATCCT  
CCAGATTCCCTCTACCAAGGGCATATGCAAAGCCTTGTCCACTTGTGGATCCACCTCTCA  
GTGGTGACTATCTATTATCGGACAATTATTGGTCTCTATTTTCTTCCCCCATCCAGCAACAC  
CAATGACAAGAACATAATTGCTTCAGTGATATACACAGCAGTCACTCCCATGTTGAACCCA  
50 TTCATTTACAGTCTGAGAAATAAAGACATTAAAGGGAGCCCTAAGAAAACCTTTGAGTAGG  
TCAGGCGCAGTGGCTCATGCCTGTAATCTCAGCACTTTGGGAGGCTGA (SEQ ID NO: 254)

**AOLFR138 sequences:**

55 MLNFTDVTEFILLGLTSRREWQVLFFIVFLVYIITVVGNIGMMLLIKVSPQLNSPMYFFLSHLS  
FVDVWFSSNVTPKMLENLFSDDKKTISYADCLAQCFFFIALVHVEIFILAAIAFDRTYVIGNPLLY  
GSKMSRGVCIRLITFPYTYGFLTSLTATLWYGLYFCGKIEINHFCADPPLIKMACAGTFVKEY

TMLILAGINFTYSLTVIIISYLFILAILMRSAEGRQKAFSTCGSHPTAVIIFYGTLIFMYLRRPTE  
ESVEQGMVAVFYTTVIPMLNPMIYSLRNKDVKKAMMKVISRSC (SEQ ID NO: 255)

5 ATGCTCAATTTACCGATGTGACAGAGTTCATTCTTTTGGGGCTAACGAGCCGTCGGGAAT  
GGCAAGTTCTCTTCTTCATCGTTTTTCTTGTGGTCTACATTATCACCGTGGTGGGCAATATC  
GGCATGATGTTGTTAATCAAGGTCAGTCCTCAGCTTAACAGCCCCATGTACTTTTTCTCTCA  
GTCACTTGTCAATTTGTTGATGTGTGGTTTTCTTCCAATGTCACCCCTAAAATGTTGGaAAAT  
CTGTTATCAGATAAAAAACAATTTCTTATGCTGGCTGTTAGCACAGTGTTCCTTCTTCAT  
10 TTGAAATCCTTTGCTTTATGGCAGCAAAATGTCAAGGGATGTCTGTATTGACTGATTAC  
TTTCCCTTACATTTATGGTTTTCTGACGAGTCTGACAGCAACATTATGGACTTATGGCTTGT  
ACTTCTGTGGAAAAATTGAGATCAACCATTCTACTGTGCAGATCCACCTCTCATCAAAAT  
GGCCTGTGCCGGGACCTTTGTAAAAGAATATACAATGCTCATACTGCCGGCATCAACTTC  
ACATATCCCTGACTGTAATTATCATCTCTTACTTATTCATCCTCATTGCCATTCTGCGAAT  
15 GCGCTCAGCAGAAGGAAGGCAGAAGGCCTTTTCCACATGTGGGTCCCCTGACAGCTGT  
CATCATATTCTATGGTACTCTGATCTTCATGTATCTCAGACGTCCACAGAGGAGTCTGTG  
GAGCAGGGGAAGATGGTGGCTGTGTTCTATACCACAGTGATCCCCATGTTGAATCCCATGA  
TCTACAGTCTGAGGAACAAGGATGTGAAAAAGGCCATGATGAAAGTGATCAGCAGATCAT  
GTAA (SEQ ID NO: 256)

20

**AOLFR139 sequences:**

MGFPGIHSWQHWLSLPLALLYLLALSANILLIINKEAALHQPMYYFLGILAMADIGLATTIMP  
KILAILWFNAKTISLLECFMQMYAIHCFVAMESSTFVCMADRYVAICRPLRYPSTITESFVFKAN  
GFMALRNSLCLISVPLLAQRHYCSQNQIEHCLCSNLGVTSLSCDDRRINSINQVLLAWTLMGS  
25 DLGLILSYALILYSVLKLNSPAASKALSTCTSHLILFFYTVIIVISITRSTGMRVPLIPVLLNL  
HNVIPPALNPMVYALKNKELRQGLYKVLRLGVKGT (SEQ ID NO: 257)

ATGGGATTCCCTGGCATTACAGTTGGCAGCACTGGCTCTCCCTGCCCTGGCTCTGCTCT  
ACCTCTTAGCTCTCAGTGCCAACATCCTTATCCTGATCATCATCAACAAAGAGGCAGCACT  
30 GCACCAGCCTATGTACTATTTCTGGGCATCTTGGCTATGGCAGACATAGGCCTGGCTACC  
ACCATCATGCCTAAGATTTTGGCCATCTTATGGTTCAATGCTAAGACCATCAGTCTCCTGG  
AGTGCTTTGCTCAGATGTATGCCATACATTGCTTTGTGGCCATGGAATCAAGTACCTTTGT  
CTGCATGGCTATTGATAGATATGTAGCCATTGTGCGACCGCTACGATATCCATCAATCATC  
ACTGAATCTTTTGTTCAAAGCAAATGGGTTTCATGGCACTGAGAAACAGCCTGTGTCTCA  
35 TCTCAGTGCCCTCTGTTGGCTGCCAGAGGCATTACTGCTCCCAGAATCAAATGAGCACTG  
TCTTTGTTCTAACCTTGGAGTCACTAGCCTATCTTGTGATGATCGAAGAATCAATAGCATG  
AACCAGGTCCTTTTGGCTTGGACACTCATGGGAAGTGACCTGGGTTTGATTATTTTATCAT  
ATGCTCTAATACTTTACTCTGTCTGAAGCTGAACTCTCCAGAAGCTGCATCCAAGGCCTT  
AAGTACCTGCACCTCCACCTCATCTTAATCCTTTTCTTCTACACAGTCATCATTGTGATTT  
40 CCATTACTCGTAGTACAGGAATGAGAGTTCCCCTTATTCCAGTTCTACTTAATGTGCTACA  
CAATGTCATTCCCCCTGCCCTGAACCCCATGGTATATGCACTCAAGAACAAGGAAGTCAAG  
CAAGGCTTATACAAGGTACTTAGACTGGGAGTGAAGGGCACCTGA (SEQ ID NO: 258)

**AOLFR140 sequences:**

45 MLTLNKTDLPASFILNGVPGLDTQLWISFPFCSMYVVMVGNCGLLYLIHYEDALHKPMYY  
FLAMLSFTDLVMCSSTIPKALCIFWFHLKDIGFDECLVQMFFIHTFTGMESGVLMLMALDRYV  
AICYPLRYSTILTNPVIAKVGTATFLRGVLLIIPFTFLTKRLPYCRGNILPHTYCDHMSVAKLSCG  
NVKVNAIYGLMVALLIGGFDILCITISYTMILRAVVSLSADARQKAFNTCTAHICAIVFSYTPAF  
50 FSFFSHRFGHEIIPPSCHIVANIYLLLPPTMNPVYGVKTKQIRDCVIRILSGSKDTKSYSM (SEQ  
ID NO: 259)

ATGCTAACACTGAATAAAACAGACCTAATACCAGCTTCATTTATTCTGAATGGAGTCCAG  
GACTGGAAGACACAACTCTGGATTTCCTTCCCATTCTGCTCTATGTATGTTGTGGCTAT  
GGTAGGGAATTGTGGACTCCTCTACCTACCTATGAGGATGCCCTGCACAAACCCATG  
55 TACTACTTCTGGCCATGCTTTCTTCTTACTGACCTTGTTATGTGCTCTAGTACAATCCCTAA  
AGCCCTCTGCATCTTCTGGTTTCATCTCAAGGACATTGGATTTGATGAATGCCTTGTCCAG

ATGTTCTTCATCCACACCTTCACAGGGATGGAGTCTGGGGTGCTTATGCTTATGGCCCTGG  
 ATCGCTATGTGGCCATCTGCTACCCCTTACGCTATTCAACTATCCTACCAATCCTGTAATT  
 GCAAAGGTTGGGACTGCCACCTTCCTGAGAGGGGTATTACTCATTATTCCCTTTACTTTCCT  
 CACCAAGCGCCTGCCCTACTGCAGAGGCAATATACTTCCCCATACCTACTGTGACCACATG  
 5 TCTGTAGCCAAATTGTCCTGTGGTAATGTCAAGGTCAATGCCATCTATGGTCTGATGGTTG  
 CCCTCCTGATTGGGGGCTTTGACATACTGTGTATCACCATCTCCTATACCATGATTCTCCGG  
 GCAGTGGTCAGCCTCTCCTCAGCAGATGCTCGGCAGAAGGCCCTTAATACCTGCACTGCCC  
 ACATTTGTGCCATTGTTTTCTCCTATACTCCAGCTTTCTTCTCCTTCTTTTCCACCGCTTTG  
 10 GGGAACACATAATCCCCCTTCTTGCCACATCATTGTAGCCAATATTTATCTGCTCCTACCA  
 CCCACTATGAACCCTATTGTCTATGGGGTGAAAACCAAACAGATACGAGACTGTGTCTATAA  
 GGATCCTTTTCAGGTTCTAAGGATACCAAATCCTACAGCATGTGA (SEQ ID NO: 260)

#### AOLFR141 sequences:

MSSTLGHNMESPNHTDVPDSVFLLGIPGLEQFHLWLSLPVCGLGTATVGNITILVVVATEPVL  
 15 HKPVYLFCLMLSTIDLAASVSTVPKLLAIFWCGAGHISASACLAQMFFIHAFCMMESTVLLAM  
 AFDTRYVAICHPLRYATILDTIIAHIGVAAVVRGSLMLPCPFLIGRLNFCQSHVILHTYCEHMA  
 VVKLACGDTRPNRVYGLTAALLVIGVDLFCIGLSYALSAQAVLRLSSHEARSKALGTCGSHVC  
 VILISYTPALFSFFTHRFHHVPVHHILLANVYLLLPALNPVYGVKTKQIRKRVVRVFQSGQ  
 GMGIKASE (SEQ ID NO: 261)

20 ATGTCCAGCACTCTTGCCACAACATGGAATCTCCTAATCACACTGATGTTGACCCTTCTG  
 TCTTCTTCTCCTGGGCATCCCAGGTCTGGAACAATTTCAATTTGTGGCTCTCACTCCCTGTG  
 TGTGGCTTAGGCACAGCCACAATTGTGGGCAATATAACTATTCTGGTTGTTGTGCCACTG  
 AACAGTCTTGACACAAGCCTGTGTACCTTTTTCTGTGCATGCTCTCAACCATCGACTTGGCT  
 25 GCCTCTGTCTCCACAGTTCCTAAGCTACTGGCTATCTTCTGGTGTGGAGCCGGACATATAT  
 CTGCCTCTGCCTGCCTGGCACAGATGTTCTTCATTCATGCCTTCTGCATGATGGAGTCCACT  
 GTGCTACTGGCCATGGCCTTTGATCGCTACGTGGCCATCTGCCACCCACTCCGCTATGCCA  
 CAATCCTCACTGACACCATCATTGCCACATAGGGGTGGCAGCTGTAGTGCGAGGCTCCCT  
 GCTCATGCTCCCATGTCCCTTCCTTATTGGGCGTTTGAACCTTCTGCCAAAGCCATGTGATCC  
 30 TACACACGTA CTGTGAGCACATGGCTGTGGTGAAGCTGGCCTGTGGAGACACCAGGCCTA  
 ACCGTGTGTATGGGCTGACAGCTGCACTGTTGGTCAATGGGGTTGACTTGTTTTGCATTGG  
 TCTCTCCTATGCCCTAAGTGCACAAGCTGTCTTCGCCTCTCATCCCATGAAGCTCGGTCCA  
 AGGCCCTAGGGACCTGTGGTTCCCATGTCTGTGTCATCCTCATCTCTTATACACAGCCCTC  
 TTCTCCTTTTTTACACACCGCTTTGGCCATCACGTTCCAGTCCATATTACATTCTTTTGGC  
 35 CAATGTTTATCTGCTTTTGCCACCTGCTCTTAATCTGTGGTATATGGAGTTAAGACCAAAC  
 AGATCCGTAAAAGAGTTGTCAAGGTGTTTCAAAGTGGGCAGGGAATGGGCATCAAGGCAT  
 CTGAGTGA (SEQ ID NO: 262)

#### AOLFR143 sequences:

40 MLGLNGTPFPATLQLTGPIQTGLTWVALIFCILYMISIVGNLSILTLVFWEPALHQPMMYYFL  
 SMLALNDLGVSFSTLPTVISTFCFNYNHVAFNACLVMFFIHTFSFMESGILLAMSLDRFVAICY  
 PLRYVTVLTHNRILAMGLGILTKSFTTLFPFFVVKRLPFCKGNVLHHSYCLHPDLMKVACGDI  
 HVNNIYGLLVIFTYGMDSFTILLSYALILRAMLVISQEQRLKALNTCMSHICAVLAFYVPIIAVS  
 MIHRFWKSAPPVHVMMMSNVYLFVPPMLNPIIYSVKTKAIRKILKFFHKSQA (SEQ ID NO:  
 45 263)

ATGCTGGGTCTCAATGGCACCCCTTCCAGCCAGCAACACTCCAGCTGACAGGCATTCTCTG  
 GGATACAAACAGGCCTCACCTGGGTGCCCCTGATTTTCTGCATCCTCTACATGATCTCCATT  
 GTAGGTAACCTCAGCAATCTCACTCTGGTGTGTTTGGGAGCCTGCTCTGCATCAGCCCATGT  
 50 ACTACTTCTCTCTATGCTCGCTCTCAATGATCTGGGAGTGTCTTTTCTACACTTCCCACT  
 GTGATTTCTACTTTCTGCTTCAACTACAACCATGTTGCGTTTAATGCTTGCCTGGTCCAGAT  
 GTTCTTTCATCCACACTTTCTCCTTCATGGAGTCAGGCATACTGCTGGCCATGAGCTTGGATC  
 GCTTTGTGGCTATTTGTTATCCATTACGCTATGTCACTGTGCTCACTCACAACCGTATATTG  
 GCTATGGGTCTGGGCATCCTTACCAAGAGTTTCAACCACTCTCTTCCCTTTCCCTTTTGTGGT  
 55 GAAACGACTGCCCTTCTGCAAAGGCAATGTTTTGCATCACTCCTACTGTCTCCATCCAGAT  
 CTCATGAAAGTAGCATGTGGAGACATCCATGTTAACAACATTTATGGGCTCTTGGTGATCA

TTTTTACCTATGGTATGGACTCAACTTTTCATCCTGCTTTCCTACGCATTGATCCTGAGAGCC  
 ATGCTGGTCATCATATCCCAGGAACAGCGGCTCAAGGCACTCAACACCTGCATGTCACACA  
 TCTGTGCAGTGCTGGCCTTTTATGTGCCCATAAATTGCTGTCTCCATGATTCACCGCTTCTGG  
 AAAAGTGCTCCACCTGTTGTTTCATGTCATGATGTCCAATGTCTACCTGTTTGTACCACCCAT  
 5 GCTCAACCCTATCATCTACAGTGTGAAAACCAAGGAGATCCGCAAAGGGATTCTCAAGTTC  
 TTCCATAAATCCCAGGCCTGA (SEQ ID NO: 264)

**AOLFR144 sequences:**

MGLFNVTHPAFFLLTGIPGLESSHWSLGPLCVMYAVALGGNTVILQAVRVERPSLHEPMYYFL  
 10 SMLSFSDDVAISMATLPTVLRTFCLNARNITFDACLIQMFLIHFFSMMESGILLAMSFDRYVAICD  
 PLRYATVLTTEVIAAMGLGAAARSFTLFLPLFLIKRLPICRSNVLSHSYCLHPDMMRLACADISI  
 NSIYGLFVLVSTFGMDLFFIFLSYVILRLSVMATASREERLKALNTCVSHILAVLAFYVPMIGVS  
 TVHRFGKHVPCYIHLVMSNVYLFVPPVLNPLIYSAKTKEIRRAIFRMFHHIKI (SEQ ID NO: 265)

15 ATGGGGTTGTTCAATGTCACTCACCTGCATTCTTCCTCCTGACTGGTATCCCTGGTCTGGA  
 GAGCTCTCACTCCTGGCTGTCAGGGCCCTCTGCGTGATGTATGCTGTGGCCCTTGGGGGA  
 AATACAGTGATCCTGCAGGCTGTGCGAGTGGAGCCCAGCCTCCATGAGCCCATGTACTACT  
 TCCTGTCCATGTTGTCTTCAGTGATGTGGCCATATCCATGGCCACACTGCCCCACTGTACTC  
 CGAACCTTCTGCCTCAATGCCCCGAACATCACTTTTGTATGCCTGTCTAATTCAGATGTTTCT  
 20 TATTCACCTTCTTCTCCATGATGGAATCAGGTATTCTGCTGGCCATGAGTTTTGACCGCTATG  
 TGGCCATTTGTGACCCCTTGCGCTATGCAACTGTGCTCACCCTGAAGTCATTGCTGCAAT  
 GGGTTTAGGTGCAGCTGCTCGAAGCTTCATCACCTTTTCCCTCTTCCCTTCTTATTAAGA  
 GGCTGCCTATCTGCAGATCCAATGTTCTTCTCACTCCTACTGCCTGCACCCAGACATGATG  
 AGGCTTGCCTGTGCTGATATCAGTATCAACAGCATCTATGGACTCTTTGTTCTTGTATCCAC  
 25 CTTTGGCATGGACCTGTTTTTATCTTCTCTCCTATGTGCTCATTCTGCGTTCTGTCATGG  
 CCACTGCTTCCCGTGAGGAACGCCTCAAAGCTCTCAACACATGTGTGTACATATCCTGGC  
 TGTACTTGCATTTTATGTGCCAATGATTGGGGTCTCCACAGTGCACCGCTTTGGGAAGCAT  
 GTCCCATGCTACATACATGTCCTCATGTCAAATGTGTACCTATTTGTGCCTCCTGTGCTCAA  
 CCCTCTCATTTATAGCGCCAAGACAAAGGAAATCCGCCGAGCCATTTCCGCATGTTTCAC  
 30 CACATCAAAATATGA (SEQ ID NO: 266)

**AOLFR145 sequences:**

MSVQYSLSPQFMLLSNITQFSPIFYLTSPFGLGKHWIFIPFFFMVMVAISGNCFILIIKTNPRLH  
 35 TPMYYLLSLLALDGLCVSTLPTTMGIFWFNSQSIYFGACQIQMFCIHSFSFMESVLLMMSFD  
 RFVAICHPLRYSVIITGQQVVRAGLIVIFRGPVATIPVLLLKAFPYCGSVVLSSHFLHQEVIQLA  
 CTDITFNNLYGLMVVFTVMDLVLIASLYGLILHTVAGLASQEEQRRAFQCTAHLCAVLVVF  
 FVPMMLSLVHRFGKHAPPAIHLMLANVYLFVPPMLNPIIYSIKTKEIHRAIKLLGLKKASK  
 (SEQ ID NO: 267)

40 ATGTCAGTCCAATATTCGCTCAGTCCTCAATTCATGCTGCTATCCAACATTACTCAGTTTAG  
 CCCCATATTCTATCTCACCAGCTTTCCTGGATTGGAAGGCATCAAACACTGGATTTTCATCC  
 CCTTTTCTTTATGTACATGGTTGCCATCTCAGGCAATTGTTTCATTCTGATCATTATTAAG  
 ACCAACCCTCGTCTGCACACACCCATGTACTATCTACTATCCTTGCTGGCCCTCACTGACCT  
 45 GGGGCTGTGTGTGTCCACGTTGCCACCACTATGGGGATCTTCTGGTTTAACTCCCAGAGT  
 ATCTACTTTGGAGCGTGTCAAATCCAGATGTTCTGCATCCACTCTTTTCTCCTCATGGAGTC  
 CTCAGTGCTCCTCATGATGTCTTTGACCGCTTTGTGGCCATCTGCCACCCTCTGAGGTATT  
 CGGTCATTATCACTGGCCAGCAAGTGGTCAGAGCAGGCCTAATTGTCATCTTCCGGGGACC  
 TGTGGCCACTATCCCTATGTCTCCTCCTGAAGGCTTTTCCCTACTGTGGATCTGTGGTCC  
 TCTCCCACTCATTTTGCCTGCACCAGGAAGTGATACAGCTGGCCTGCACAGATACACCTT  
 50 CAATAATCTGTATGGACTGATGGTGGTAGTTTTCACTGTGATGCTGGACCTGGTGCTCATC  
 GCACTGTCTATGGACTCATCCTGCACACAGTAGCAGGCCTGGCCTCCCAAGAGGAGCAGC  
 GCGGTGCCCTTTCAGACATGCACCGCTCATCTCTGTGCTGTGCTAGTATCTTTGTGCCCATG  
 ATGGGGCTGTCCCTGGTGCACCGTTTTTGGGAAGCATGCCCCACCTGCTATTTCATCTTCTTAT  
 GGCCAATGTCTACCTTTTTGTGCCTCCCATGCTTAACCCAATCATATACAGCATTAAAGACC  
 55 AAGGAGATCCACCGTGCCATTATCAAACCTCCTAGGTCTTAAAAAGGCCAGTAAATGA (SEQ  
 ID NO: 268)

**AOLFR146 sequences:**

- MSQVNTNTTQEGIFYLTDIPGFEASHIWISIPVCCLYTISIMGNTTILTVIRTEPSVHQRMVFLSLM  
 LALTDLGLTLTTLPTVMQLLWFNVRRISSEACFAQFFFLHGFSFMESSVLLAMSVDCYVAICCP  
 5 LHYASILTNEVIGRTGLAIICCCVLAVLPSLFLKRLPFCHSHLLSRSYCLHQDMIRLVACADIRLN  
 SWYGFALALLIIVDPLLVISYTLILKNILGTATWAERLRALNNCLSHLAVLVLYIPMVGVSMT  
 HRFKAKHASPLVHVIMANIYLLAPPVMNPITYSVKNKQIQWGMNLNLSLKNMHSR (SEQ ID NO:  
 269)
- 10 ATGTCCCAGGTGACTAACACCACACAAGAAGGCATCTACTTCATCCTCACGGACATCCCTG  
 GATTTGAGGCCTCCCACATCTGGATCTCCATCCCCGCTGCTGTCTCTACACCATCTCCATC  
 ATGGGCAATACCACCATCCTCACTGTCTATCGCACAGAGCCATCTGTCCACCAGCGCATGT  
 ATCTGTTTCTCTCCATGCTGGCCCTGACGGACCTGGGTCTCACCCCTCACCCCTACCCACA  
 GTCATGCAGCTTCTCTGGTTCAACGTTTCGTAGAATCAGCTCTGAGGCCTGTTTTGCTCAGTT  
 15 TTTCTTCCCTTCATGGATTCTCCTTTATGGAGTCTTCTGTCTCCTGGCTATGTCCGTTGACT  
 GCTATGTGGCCATCTGCTGTCCCCTCCATTATGCCTCCATCCTCACCAATGAAGTCATTGGT  
 AGAACTGGGTAGCCATCATTGCTGCTGTGTCTGGCGGTTCTTCCCTCCCTTTTCTTACT  
 CAAGCGACTGCCTTTCTGCCACTCCCACCTTCTCTCTCGCTCCTATTGCCTCCACCAGGATA  
 TGATCCGCCTGGTCTGTGCTGACATCAGGCTCAACAGCTGGTATGGATTGCTCTTGCCTT  
 20 GCTCATTATTATCGTGGATCCTCTGCTCATTGTGATCTCCTATACACTTATTCTGAAAAATA  
 TCTTGGGCACAGCCACCTGGGCTGAGCGACTCCGTGCCCTCAATAACTGCCTGTCCACAT  
 TCTAGCTGTCTGGTCTCTACATTCCCATGGTTGGTGTATCTATGACTCATCGCTTTGCCA  
 AGCATGCCCTCTCCACTGGTCCATGTTATCATGGCCAATATCTACCTGCTGGCACCCCGGT  
 GATGAACCCCATCATTTACAGTGTAAGAACAAGCAGATCCAATGGGGAATGTTAAATTTT  
 25 CTTTCCCTCAAAAATATGCATTCAAGATGA (SEQ ID NO: 270)

**AOLFR147 sequences:**

- MPSASAMIIFNLSSYNPGPFILVGIPGLEQFHVWIGIPFCHYIVAVVGNCLLYLIVVEHSLHEPMF  
 FFLSMLAMTDLILSTAGVPKALSIFWLGAIREITFGCLTQMFFLHYNFVLDLAILMAMAFDHVY  
 30 AICSPLRYTTILTPKTIKSAMGISFRSFCILPDVFLLTCLPFCRTRIIPHTYCEHIGVAQLACADISI  
 NFWYGFVPIMTVISDVILIAVSYAHILCAVFGPLSQDACQKALGTCGSHVCVILMFYTPAFFSI  
 LAHRFGHNVSRTFHIMFANLYVIPPALNPMVYGVKTKQIRDKVILLFSKGTG (SEQ ID NO:  
 271)
- 35 ATGCCATCTGCCTCTGCCATGATCATTTTCAACCTGAGCAGTTACAATCCAGGACCCCTTCAT  
 TCTGGTAGGGATCCCAGGCCTGGAGCAATTCCATGTGTGGATTGGAATTCCCTTCTGTATC  
 ATCTACATTGTAGCTGTTGTGGGAAACTGCATCCTTCTCTACCTCATTGTGGTGGAGCATA  
 GTCTTCATGAACCCATGTTCTTCTTCTCTCCATGCTGGCCATGACTGACCTCATCTTGTCC  
 ACAGCTGGTGTGCCTAAAGCACTCAGTATCTTTTGGCTAGGGGCTCGCGAAATCACATTCC  
 40 CAGGATGCCTTACACAAATGTTCTTCTTCACTATAACTTTGTCTGATTTCAGCCATTCTG  
 ATGGCCATGGCATTGATCACTATGTAGCTATCTGTTCTCCCTTGAGATATAACCACCATCTT  
 GACTCCCAAGACCATCATCAAGAGTGCTATGGGCATCTCCTTTCGAAGCTTCTGCATCATC  
 CTGCCAGATGTATTCTTGTGCTGACATGCCTGCCCTTCTGCAGGACACGCATCATACCCACA  
 CATACTGTGAGCATATAGGTGTTGCCAGCTCGCCTGTGCTGATATCTCCATCAACTTCTG  
 45 GTATGGCTTTTGTGTTCCCATCATGACGGTCATCTCAGATGTGATTCTCATTGCTGTTTCT  
 ACGCACACATCCTCTGTGCTGTCTTTGGCCTTCCCTCCCAAGATGCCTGCCAGAAAGCCCT  
 CGGCACTTGTGGTTCTCATGTCTGTGTCATCCTCATGTTTTATACACCTGCCTTTTCTCCA  
 TCCTCGCCCATCGCTTTGGACACAATGTCTCTCGCACCTTCCACATCATGTTTGCCAATCTC  
 TACATTGTTATCCCACCTGCACTCAACCCATGGTTTACGGAGTGAAAGACCAAGCAGATCA  
 50 GAGATAAGGTTATACTTTTGTCTTCTAAGGGTACAGGATGA (SEQ ID NO: 272)

**AOLFR148 sequences:**

- MPTVNHSGTSHTVFHLLGIPGLQDQHMWISIPFFISYVTALLGNSLLIFILTKRSLHEPMYFLC  
 MLAGADIVLSTCTIPQALAIWFVFRAGDISLDRCTQLFFIHSTFISEGILLVMAFDHYIAICYPLR  
 55 YTTLTNALIKKICVTVSLRSYGTIFPIIFLLKRLTFCQNNIIPHTFCEHIGLAKYACNDIRINIWYG

FSILMSTVVLDVVLIFISYMLILHAVFHMPSPDACHKALNTFGSHVCHILFYGSGIFTILTQRFGR  
HIPPCIHIPLANVCILAPPM LNPIHYGIKTKQIQEQVVQFLFIKQKITLV (SEQ ID NO: 273)

5 ATGCCTACTGTAAACCACAGTGGCACTAGCCACACAGTCTTCCACTTGCTGGGCATCCCTG  
GCCTACAGGACCAGCACATGTGGATTTCTATCCCATTCTTCATTTCCTATGTCACCGCCCTT  
CTTGGAACAGCCTGCTCATCTTCATTATCCTCACAAAGCGCAGCCTCCATGAACCCATGT  
ACCTCTTCCTCTGCATGCTGGCTGGAGCAGACATTGTCTCTCCACGTGCACCATTCCTCAG  
GCCTTAGCTATCTTCTGGTTCCGTGCTGGGGACATCTCCCTGGATCGTTGCATCACTCAGCT  
10 CTTCTTCATCCATTCCACCTTCATCTCTGAGTCAGGGATCTTGCTGGTGATGGCCTTTGACC  
ACTATATTGCCATATGCTACCCACTGAGGTACACCACCATTCCTACAAATGCTCTGATCAA  
GAAAATTTGTGTGACTGTCTCTCTGAGAAGTTATGGTACAATTTTCCCTATCATATTTCTTT  
TAAAAAGATTGACTTTCTGCCAGAATAATATTATTCACACACCTTTTGTGAACACATTGG  
CCTAGCCAAATATGCATGTAATGACATTTCGAATAAACATTTGGTATGGGTTTTCCATTCTA  
15 ATGTCGACGGTGGTCTTAGATGTTGTAATAATTTTATTTCTATATGCTGATTCTCCATGC  
TGCTCTCCACATGCCTTCTCCAGATGCTTGCCACAAAGCTCTCAACACATTTGGCTCCCATG  
TCTGCATCATCATCCTCTTTTATGGGTCTGGCATCTTCACAATCCTTACCCAGAGGTTTGA  
CGCCACATTCCACCTTGTATCCACATCCCCTGGCTAATGTCTGCATTCTGGCTCCACCTAT  
GCTGAATCCCATTATTTATGGGATCAAAACCAAGCAAATCCAGGAACAGGTGGTTCAGTTT  
20 TTGTTTATAAAACAGAAAATAACTTTGGTTTAA (SEQ ID NO: 274)

**AOLFR149 sequences:**

MSNASLLTAFILMGLPHAPALDAPLFGVFLVVYVLTVLGNLLILLVIRVDSHLHTTMYYFLTNL  
SFIDMWESTVTVPKLLMTLVFPSGRAISFHSMAQLYFFHFLGGTECFLYRVMSCDRYLAISSP  
25 LRYTSMMTGRSCTLLATSTWLSGSLHSAVQAILTFHLPYCGPNWQHYLCDAPPILKLACADTS  
AIETVIFVTGVIVASGCFVLIVLSYVSIVCSILRRTSEGKHRAFTCAASHCIVLCCFFGPGLFTYLR  
PGSRKAVDGVVAVFYTVLTPLLNPVYTLRNKEVKKALLKLKDKVAHSQSK (SEQ ID NO:  
275)

30 ATGTCCAACGCCAGCCTACTGACAGCGTTCATCCTCATGGGCCTTCCCCATGCCCCAGCGC  
TGGACGCCCCCTCTTTGGAGTCTTCTGGTGGTTTACGTGCTCACTGTGCTGGGGAACCT  
CCTCATCCTGCTGGTGATCAGGGTGGATTCTCACCTCCACACCACCATGTACTACTTCTCA  
CCAACCTGTCGTTTCATTGACATGTGGTTCTCCACTGTCACGGTGCCCAAATTGCTGATGAC  
TTTGGTGTTCCTCAAGTGGCAGGGCTATCTCCTTCCACAGCTGCATGGCTCAGCTCTATTTC  
35 TTCCTTCTAGGGGGCACCAGTGTTCCTCTACAGGGTCATGTCTGTGATCGCTACCT  
GGCCATCAGTTACCCGCTCAGGTACACCAGCATGATGACTGGGCGCTCGTGTACTCTTCTG  
GCCACGCACTTGGCTCAGTGGCTCTCTGCACTCTGCTGTCCAGGCCATATTGACTTTCC  
ATTTGCCCTACTGTGGACCCCACTGGATCCAGCACTATTTGTGTGATGCACCGCCATCCT  
GAAACTGGCCTGTGCAGACACCTCAGCCATAGAGACTGTCATTTTTGTGACTGTTGGAATA  
GTGGCCTCGGGCTGCTTTGTCCTGATAGTGCTGTCCTATGTGTCCATCGTCTGTTCCATCCT  
40 GCGGATCCGCACCTCAGAGGGGAAGCACAGAGCCTTTCAGACCTGTGCCTCCCACTGTATC  
GTGGTCTTTGCTTCTTTGGCCCTGGTCTTTTCACTTACCTGAGGCCAGGCTCCAGGAAAGC  
TGTGGATGGAGTTGTGGCCGTTTTCTACACTGTGCTGACGCCCTTCTCAACCCTGTTGTGT  
ACACCCTGAGGAACAAGGAGGTGAAGAAAGCTCTGTTGAAGCTGAAAGACAAAGTAGCAC  
ATTCTCAGAGCAAATAG (SEQ ID NO: 276)

45

**AOLFR150 sequences:**

MELGNVTRVKEFIFLGLTQSQDQSLVFLFLCLVYMTLLGNLLIMVTVTCESRLHTPMYFLLR  
NLAILDICFSSTTAPKVLLDLLSKKKTISYTSMTQIFLHLLGGADIFSLSVMAFDCYMAISKPL  
HYVTIMSRGQCTALISASWMGGFVHSIVQISLLLPLFCGPNVLDTFYCDVPQVLKLTCTDTFA  
50 LEFLMISNNGLVTTLWFIFLLVSYTVILMTLRSQAGGRRKAISTCTSPHHCGRPFCALHLCLC  
PALHCPPHRKGHLCCHLHCHLPSAEPFDLHSEEPGNEVSHEKTEEKTRAF (SEQ ID NO: 277)

55 ATGGAGTTGGGAAATGTCACCAGAGTAAAGAATTTATATTTCTGGGACTTACTCAATCCC  
AAGACCAGAGTTGGTCTTGTTTCTTTTTTATGTCTTGTTACATGACGACTCTGCTGGGA  
AACCTCCTCATCATGGTCACCGTGACCTGTGAGTCTCGCCTTCACACCCCATGTACTTCT  
GCTCCGCAATCTAGCCATCCTTGACATCTGCTTCTCCTCCACAACTGCTCCTAAAGTCTTGC

TGGACCTTCTGTCAAAGAAAAAGACCATATCCTATACAAGCTGCATGACACAGATATTTCT  
 CTCCACCTCCTTGGTGGGGCAGACATTTTCTCTCTCTGTGATGGCGTTTGACTGCTACA  
 TGGCCATCTCCAAGCCCCTGCACTATGTGACCATCATGAGTAGAGGGCAATGCACTGCCCT  
 CATCTCTGCCCTCTGGATGGGGGGCTTTGTCCACTCCATCGTGCAGATCTCCCTGTTGCTGC  
 5 CTCTCCCTTTCTGTGGACCCAATGTTCTTGACACTTTCTACTGCGATGTCCCCCAGGTCTC  
 AAACCTCACTTGCACTGACACTTTTGCTCTTGAGTTCTTGATGATTTCCAACAATGGCCTGGT  
 CACTACCTGTGGTTTATCTTCCTGCTTGTGTCTACACAGTCATCCTAATGACGCTGAGGT  
 CTCAGGCAGGAGGGGGCAGGAGGAAAGCCATCTCCACTTGACCTCCCCACATCACTGTG  
 GTGACCCTGCATTTTGTGCCCTGCATCTATGTCTATGCCCGGCCCTTCACTGCCCTCCCCAC  
 10 AGAAAAGGCCATCTCTGTACCTTCACTGTCTATCTCCCTCTGCTGAACCTTTGATCTACA  
 CTCTGAGGAACCAGGAAATGAAGTCAGCCATGAGAAGACTGAAGAGAAGACTCGTGCCTT  
 CTGA (SEQ ID NO: 278)

**AOLFR151 sequences:**

15 MFSPNHTIVTEFILLGLTDDPVLEKILFGVFLAIYLITLAGNLCMILLIRTNSHLQTPMYFFLGHL  
 FVDICYSSNVTNPNMLHNFLEBQKTIISYAGCFTQCLLFIALVITEFYILASMLDRYVAICSPHYS  
 SRMSKNICVCLVTIPYMYGFLSGFSQSLTFHLSFCGSLEINHFYCADPPLIMLACSDTRVKKMA  
 MFVVAGFNLSSSLFIILLSYLFIFAAIFRIRSAEGRHKAFTSCASHLTIVTLFYGTLCFMYVRPPSE  
 KSVEESKITAVFYTLSPMLNPLIYSLRNTDVLAMQQMIRGKSFHKIAV (SEQ ID NO: 279)

20 ATGTTCTCCCCAAACCACACCATAGTGACAGAATTCATTCTCTTGGGACTGACAGACGACC  
 CAGTGCTAGAGAAGATCCTGTTTGGGGTATTCCTTGCGATCTACCTAATCACACTGGCAGG  
 CAACCTGTGCATGATCCTGCTGATCAGGACCAATTCCCACCTGCAAACACCCATGTATTTT  
 TTCCTTGGCCACCTCTCCTTTGTAGACATTTGCTATTCTTCCAATGTTACTCCAAATATGCT  
 25 GCACAATTTCTCTCAGAACAGAAGACCATCTCCTACGCTGGATGCTTCACACAGTGTCTT  
 CTCTTCATCGCCCTGGTGATCACTGAGTTTTACATCCTTGCTTCAATGGCATTGGATCGCTA  
 TGTAGCCATTTGCAGCCCTTTGCATTACAGTTCCAGGATGTCCAAGAACATCTGTGTCTGT  
 CTGGTCACTATCCCTTACATGTATGGGTTTCTTAGTGGGTCTCTCAGTCACTGCTAACCTT  
 TCACTTATCCTTCTGTGGCTCCCTTGAAATCAATCATTTCTACTGCGCTGATCCTCCTCTTA  
 30 TCATGTCTGGCCTGCTCTGACACCCGTGTCAAAAAGATGGCAATGTTTGTAGTTGCAGGCTT  
 TAATCTCTCAAGCTCTCTCTTCATCTTCTGCTCTATCTTTTCATTTTTCAGCGATCTT  
 CAGGATCCGTCTGCTGAAGGCAGGCACAAAGCCTTTTCTACGTGTGCTTCCCACCTGACA  
 ATAGTCACTTTGTTTTATGGAACCTCTTCTGCATGTACGTAAGGCCTCCATCAGAGAAAGT  
 CTGTAGAGGAGTCCAAAATAACTGCAGTCTTTTATACTTTTTTGAGCCCAATGCTGAACCC  
 35 ATTGATCTATAGCCTACGGAACACAGATGTAATCCTTGCCATGCAACAAATGATTAGGGGA  
 AATCCTTTCATAAAATTGCAGTTTAG (SEQ ID NO: 280)

**AOLFR152 sequences:**

MDQINHTNVKEFFFLTRSRLEFFLFVVFVAVYVATVLGNALIVVTITCESRLHTPMYFLLRN  
 40 KSVLDIVFSSITVPKFLVDLLSDRKTISYNDQMAQIFFHFAGGADIFFLSVMAYDRYLAIKPL  
 HYVTMMRKEVWVALVVASWVSGGLHSIIQVILMLPFPFCGPNTLDAFYCYVLQVVKLACTDT  
 FALFLFMISNNGLVTLWFLLLGSYTVILVMLRSHSGEGRNKALSTCTSHMLVVTLHFVPCV  
 YIYCRPFMTLPMDTTISINNTVITPMLNPIIYSLRNQEMKSAMQRLQRRLLGPSESERKWG (SEQ ID  
 NO: 281)

45 ATGGACCAGATCAACCACACTAATGTGAAGGAGTTTTTCTTCCTGGAACCTTACACGTTCCC  
 GAGAGCTGGAGTTTTTCTTGTGTTGTGGTCTTCTTTGCTGTGTATGTAGCAACAGTCCCTGGG  
 AAATGCACTCATTGTGGTCACTATTACCTGTGAGTCCCGCCTACACACTCCTATGTACTTTC  
 TCCTGCGGAACAAATCAGTCTGACATCGTTTTTTCATCTATCACCGTCCCCAAGTTCCTG  
 50 GTGGATCTTTTATCAGACAGGAAAACCATCTCCTACAATGACTGCATGGCACAGATCTTTT  
 TCTTCCACTTTGCTGGTGGGGCAGATATTTTTCTCTCTGTGATGGCCTATGACAGATAC  
 CTTGCAATCGCCAAGCCCCTGCACTATGTGACCATGATGAGGAAAGAGGTGTGGGTGGCC  
 TTGGTGGTGGCTTCTTGGGTGAGTGGTGGTTTGCATTCAATCATCCAGGTAATTCTGATGC  
 TTCCATTCCCCTTCTGTGGCCCCAACACACTGGATGCCTTCTACTGTTATGTGCTCCAGGTG  
 55 GTAAAACCTGGCCTGCACTGACACCTTTGCTTTGGAGCTTTTCATGATCTCTAACAACGGAC  
 TGGTGACCCTGCTCTGGTTCCTCCTGCTCCTGGGCTCCTACACTGTCATTCTGGTGATGCTG

AGATCCCACTCTGGGGAGGGGCGGAACAAGGCCCTCTCCACGTGCACGTCCCACATGCTG  
GTGGTGACTCTTCACTTCGTGCCTTGTGTTTACATCTACTGCCGGCCCTTCATGACGCTGCC  
CATGGACACAACCATATCCATTAATAACACGGTCATTACCCCCATGCTGAACCCCATCATC  
TATTCCTGAGAAATCAAGAGATGAAGTCAGCCATGCAGAGGCTGCAGAGGAGACTTGGG  
5 CCTTCCGAGAGCAGAAAATGGGGGTGA (SEQ ID NO: 282)

**AOLFR153 sequences:**

MSKTSLVTAFILTLGLPHAPGLDAPLFGIFLVVYVLTVLGNLILLVIRVDSHLHTPMYYFLTNLS  
FIDMWFSTVTVPKMLMTLVSPSGRAISFHSCVAQLYFFHFLGSTECFLYTVMSYDRYLAISYPL  
10 RYTSMMSGSRCALLATSTWLSGSLHSAVQTILTFHLPYCGPNQIQHYLCDAPPILKLACADTSA  
NEMVIFVDIGLVASGCFLLIVLSYVSIVCSILRIHTSEGRHRAFQTCASHCTVVLCEFFVXCVFIYLR  
PGSRD VVDGVVAIFYTVLTPLLNPVVYTLRNKEVKKAVLKLRDKVAHSQGE (SEQ ID NO:  
283)

15 ATGTCCAAGACCAGCCTCGTGACAGCGTTTCATCCTCACGGGCCCTTCCCCATGCCCCAGGGC  
TGGACGCCCCACTCTTTGGAATCTTCTGGTGGTTTACGTGCTCACTGTGCTGGGGAACCT  
CCTCATCCTGCTGGTGATCAGGGTGGATTCTCACCTCCACACCCCCATGTACTACTTCCTCA  
CCAACCTGTCCTTCATTGACATGTGGTTCTCCACTGTACGGTGCCCCAAATGCTGATGAC  
CTTGGTGTCCCCAAGCGGCAGGGCTATCTCCTTCCACAGCTGCGTGGCTCAGCTCTATTTTT  
20 TCCACTTCCTGGGGAGCACCGAGTGTTTCTCTACACAGTCATGTCCTATGATCGCTACTTG  
GCCATCAGTTACCCGCTCAGGTACACCAGCATGATGAGTGGGAGCAGATGTGCCCTCCTGG  
CCACCAGCACTTGGCTCAGTGGCTCTCTGCACTCTGCTGTCCAGACCATATTGACTTTCCAT  
TTGCCCTACTGTGGACCCAACCAGATCCAGCACTATTTGTGTGATGCACCGCCCATCCTGA  
AAGTGGCCTGTGCAGACACCTCAGCCAACGAGATGGTCATCTTTGTGGACATTGGGCTAGT  
25 GGCTCGGGCTGCTTTCTCCTGATAGTGCTGTCTTATGTGTCCATCGTCTGTTCCATCCTGC  
GGATCCACACCTCAGAGGGGAGGCACAGAGCCTTTCAGACCTGTGCCTCCCACTGCATCGT  
GGTCTTTTGCTTTTTTTGTNNCCTGTGTTTTCACTTACCTGAGACCAGGCTCCAGGGACGTCG  
TGGATGGAGTTGTGGCCATTTTCTACACTGTGCTGACACCCCTTCTCAACCTGTTGTGTAC  
ACCCTGAGAAACAAGGAGGTGAAGAAAGCTGTGTTGAAACTGAGAGACAAAGTAGCACAT  
30 TCTCAGGGAGAATAA (SEQ ID NO: 284)

**AOLFR156 sequences:**

MCWAMPSPTGSSTRNMESRNQSTVTEFIFTGFPQLQDGSLLYFFPLLFYTFIIDNLLIFS AVRL  
DTHLGNPMYNFISFISFLEIWYTTATIPKMLSNLISEKKAISMTGCILQMYFFHSLENSEGILLTT  
35 MAIDRYVAICNPLRYQMIMTPRLCAHLSAGSCLFGLILLPEIVMISTLPFCGPNQIQHIFCDLVP  
VLSLACTDTSMLIEDVIHAVTIIITFLIALSYVRIVTVILRIPSEGRQKAXSTCAGHLMVFLIFFG  
SVSLMYLRFSNTYPPVLDTAIALMFTVLAPFFNPFIYSLRNKDMNNAIKKLFCLQKVLNKP GG  
(SEQ ID NO: 285)

40 ATGTGCTGGGCTATGCCCTCTCCATTTACAGGTAGCTCTACTAGAAATATGGAGAGCAGAA  
ACCAATCAACAGTGACTGAATTTATCTTCACTGGATTCCCTCAGCTTCAGGATGGTAGTCT  
CCTGTACTTCTTTCTTTACTTTTTCATCTATACTTTTATTATCATTGATAACTTATTAATCTT  
CTCTGCTGTAAGGCTGGACACCCATCTGGGCAACCCCATGTATAATTTTATCAGTATATTTT  
CCTTTCTGGAGATCTGGTACACCACAGCCACCATTCCCAAGATGCTCTCCAACCTCATCAG  
45 TGAAAAGAAGGCCATCTCAATGACTGGCTGCATCTTGCAGATGTATTTCTTCCACTCACTT  
GAAAACCTCAGAGGGGATCTTGCTGACCACCATGGCCATTGACAGATACGTTGCCATCTGCA  
ACCCTCTTCGCTATCAAAATGATCATGACCCCCCGGCTCTGTGCTCACCTCTCTGCAGGTTCC  
TGCTCTTCGGTTTCTTATCTTGCTTCCCGAGATTGTGATGATTTCCACACTGCCTTTCTG  
TGGGCCCCAACCAATCCATCAGATCTTCTGTGACTTGGTCCCTGTGCTAAGCCTGGCCTGT  
50 ACAGACACGTCCATGATTCTGATTGAGGATGTGATTCACTGTGCTGTGACCATCATCATTACCT  
TCTAATCATTGCCCTGTCTTATGTAAGAATTGTCACTGTGATATTGAGGATTCCCTCTTCT  
GAAGGGAGGC AAAAGGCTNTTCTACCTGTGCAGGCCACCTCATGGTCTTCTGATATTCT  
TTGGCAGTGTATCACTCATGTACTTGCCTTTCAGCAACACTTATCCACCAGTTTGGACAC  
AGCCATTGCACTGATGTTTACTGTACTTGTCTCATTCTTCAATCCCATCATITATAGCCTGA  
55 GAAACAAGGACATGAACAATGCAATTA AAAAAACTGTTCTGTCTTCAAAAAGTGTTGAACA  
AGCCTGGAGGTTAA (SEQ ID NO: 286)



**AOLFR157 sequences:**

MAMDNVTAVFQFLIGISNYPQWRDTFFTLVLIYLSLTLGNGFMIFLIHFDPNLHTPIYFFLSNL  
 SFLDLCYGTASMPQALVHCFSTHPYLSYPRCLAQTSVSLALATAECLLLAAMAYDRVVAISNP  
 5 LRYSVVMNGPVCVCLVATSWGTSLVLTAMLILSLRLHFCGANVINHFACEILSLIKLTCSDTSL  
 NEFMILITSIFTLLLPFGFVLLSYRIAMAIIRIRSLQGRKAFITTCGSHLTVVITIFYGSAISMYMKT  
 QSKSSPDQDKFISVFYGALTPMLNPLIYSLRKKDVKRAIRKVMLKRT (SEQ ID NO: 287)

ATGGCCATGGACAATGTCACAGCAGTGTTCAGTTTCTCCTTATTGGCATTCTAACTATCC  
 10 TCAATGGAGAGACACGTTTTTCACATTAGTGCTGATAATTTACCTCAGCACATTGTTGGGG  
 AATGGATTATGATCTTTCTTATTCACTTTGACCCCAACCTCCACACTCCAATCTACTTCTT  
 CCTTAGTAACCTGTCTTTCTTAGACCTTTGTTATGGAACAGCTTCCATGCCCCAGGCTTTGG  
 TGCATTGTTTCTCTACCCATCCCTACCTCTCTTATCCCCGATGTTTGGCTCAAACGAGTGTC  
 TCCTTGGCTTTGGCCACAGCAGAGTGCTCCTACTGGCTGCCATGGCCTATGACCGTGTGG  
 15 TTGCTATCAGCAATCCCCTGCGTTATTAGTGCTTATGAATGGCCCAGTGTGTGTCTGCTT  
 GGTTGCTACCTCATGGGGGACATCACTTGTGCTCACTGCCATGCTCATCCTATCCCTGAGG  
 CTTCACTTCTGTGGGGCTAATGTCATCAACCATTTTGCTGTGAGATTCTCTCCCTCATTAA  
 GCTGACCTGTTCTGATACCAGCCTCAATGAATTTATGATCCTCATCACCAGTATCTTACCCC  
 TGCTGCTACCATTTGGGTTTGTCTCCTCTCCTACATACGAATTGCTATGGCTATCATAAGG  
 20 ATTCGCTCACTCCAGGGCAGGCTCAAGGCTTTACCACATGTGGCTCTCACCTGACCGTGG  
 TGACAATCTTCTATGGGTGACCCATCTCCATGTATATGAAAACCTCAGTCCAAGTCTCCCC  
 TGACCAGGACAAGTTTATCTCAGTGTTTTATGGAGCTTTGACACCCATGTTGAACCCCTG  
 ATATATAGCCTGAGAAAAAAGATGTTAAACGGGCAATAAGGAAAGTTATGTTGAAAAGG  
 ACATGA (SEQ ID NO: 288)

25

**AOLFR158 sequences:**

MKAGNFSDPPEFFLLGLSGDPELQPIFLFSLMYLATMLGNLLILAVNSDSLHTPMYFLLSI  
 LSLVDICFTSTTMPKMLVNIQAQAQSINYTGCLTQICFVLVFGLENGILVMMAYDRFVAICHP  
 LRYNVIMNPKLCGLLLLLSFIVSVLDALLHTLMVLQLTFCIDLEIPHFCELAHILKLACSDVLIN  
 30 NILVYLVTSLGLVPLSGIIFSYTRIVSSVMKIPSAGGKYKAFSICGSHLIVVSLFYGTGFGVYLSS  
 GATHSSRKGAIASVMYTVVTPMLNPLIYSLRNKMDMLKALRKLISRIPSFH (SEQ ID NO: 289)

ATGAAAGCAGGAAACTTCTCAGACACTCCAGAATTCTTTCTCTTGGGATTGTGAGGGGATC  
 CGGAGCTGCAGCCCATCCTCTTCATGCTGTTCTGTCCATGTACCTGGCCACAATGCTGGG  
 35 GAACCTGCTCATCATCCTGGCCGTCAACTCTGACTCCCACCTCCACACCCCCATGTACTTCC  
 TCCTCTCTATCCTGTCTTGGTGCACATCTGTTTACCTCCACCACGATGCCCAAGATGCTG  
 GTGAACATCCAGGCACAGGCTCAATCCATCAATTACACAGGCTGCCTCACCCAAATCTGCT  
 TTGTCCTGGTTTTTGTGGATTGGAAAATGGAATTCTGGTCATGATGGCCTATGATCGATT  
 TGTGGCCATCTGTCACCCACTGAGGTACAATGTCATCATGAACCCCAAACTCTGTGGGCTG  
 40 CTGCTTCTGCTGTCTTCATCGTTAGTGTCTGGATGCTCTGCTGCACACGTTGATGGTGCT  
 ACAGCTGACCTTCTGCATAGACCTGGAAATTCCCCACTTTTCTGTGAAGTAGCTCATATTC  
 TCAAGCTCGCCTGTTCTGATGTCCTCATCAATAACATCCTGGTGTATTTGGTGACCAGCCT  
 GTTAGGTGTTGTTCTCTCTGCGGATCATTTTCTCTTACACACGAATTGTCTCCTCTGTCA  
 TGAATAATTCCATCAGCTGGTGGAAAGTATAAAGCTTTTCCATCTGCGGGTCACATTTAAT  
 45 CGTTGTTTCTTGTATGGAACAGGGTTTGGGGTGTACCTTAGTTCTGGGGCTACCCACT  
 CCTCCAGGAAGGGTGCAATAGCATCAGTGATGTATACCGTGGTCACCCCATGCTGAACCC  
 ACTCATTTACAGCCTGAGAAACAAGGACATGTTGAAGGCTTTGAGGAAACTAATATCTAG  
 GATACCATCTTCCATTGA (SEQ ID NO: 290)

**AOLFR159 sequences:**

MGPRNQTA VSEFLMKVTEDEPELKLIPFSLFSLMYLVLTILGNLLILAVISDSLHTPMYFLLFN  
 LSFTDICLTTTTVPKILVNIQAQNSITYTGCLTQICLVLVFAGLESCFLAVMAYDRYVAICHP  
 RYTVLMNVHFWGLLLSMFMSTMDALVQSLMVLQLSFCKNVEIPLFFCEVVQVIKLACSDTL  
 INNILYFASSVFGAIPLSGIIFSYQIVTSVLRMP SARGKYKAFSTCGCHLSVFSLFYGTAFGVYIS  
 55 SAVAESSRITAVASVMYTVVPMNPFYSLRNKEMKKALRKLIGRLFPF (SEQ ID NO: 291)

ATGGGACCCAGAAACCAAACAGCTGTTTCAGAATTTCTTCTCATGAAAGTGACAGAGGAC  
 CCAGAACTGAAGTTAATCCCTTTTCAGCCTGTTCCCTGTCCATGTACCTGGTCACCATCCTGG  
 GGAACCTGCTCATTTCTCCTGGCTGTCATCTCTGACTCCACCTCCACACCCCCATGTACTTC  
 CTTCTCTTTAATCTCTCCTTTACTGACATCTGTTTAAACCACAACCACAGTCCCAAAGATCCT  
 5 AGTGAACATCCAAGCTCAGAATCAGAGTATCACTTACACAGGCTGCCTCACCAGATCTGT  
 CTTGCTCTGGTTTTTGGCTGGCTTGGAAAGTTGCTTTCTTGCAGTCATGGCCTACGACCGCTA  
 TGTGGCCATTTGCCACCCACTGAGGTACACAGTCCTCATGAATGTCCATTTCTGGGGCTTG  
 CTGATTCTTCTCTCCATGTTTCATGAGCACTATGGATGCCCTGGTTCAGAGTCTGATGGTATT  
 GCAGCTGTCTTCTGCAAAAACGTTGAAATCCCTTTGTTCTTCTGTGAAGTCGTTTCAGGTC  
 10 ATCAAGCTCGCCTGTTCTGACACCTCATCAACAACATCCTCATATATTTTGAAGTAGTGT  
 ATTTGGTGCAATTCCTCTCTCTGGAATAATTTTCTCTTATTCTCAAATAGTCACCTCTGTTT  
 TGAGAATGCCATCAGCAAGAGGAAAGTATAAAGCGTTTTCCACCTGTGGCTGTCACCTCTC  
 TGTTTTTTCCTTGTTCTATGGGACAGCTTTTGGGGTGTACATTAGTTCTGCTGTTGCTGAGT  
 CTTCCCGAATTACTGCTGTGGCTTCAGTGATGTACACTGTGGTCCCTCAAATGATGAACCC  
 15 CTTTCATCTACAGCCTGAGAAATAAGGAGATGAAGAAAGCTTTGAGGAAACTTATTGGTAG  
 GCTGTTTCCTTTTAG (SEQ ID NO: 292)

**AOLFR160 sequences:**

MPMQLLLTDFIIFSIRFIINSMEARNQTAISKFLLLGLIEDPELQPVLFSLFLSMYLVITLGNLLILL  
 20 AVISDHLHTPMYFFLSNLSFLDICLSTTIPKMLVNIQAQNRSTYSGCLTQICFVLFAGLENC  
 LLAAMAYDRYVAICHPLRYTVIMNPLCGLLILLSLTSVNVNALLSLMVLRLSFCTDLEIPLFF  
 CELAQVIQLTCSDTLNNILYFAACIFGGVPLSGHLSYQTITSCVLRMPSASGKHKAIVSTCGSHL  
 SIVLLFYGAGLGVYISSVVTDSPRKTAVASVMYSVFPQMVNPFYSLRNKDMKGTLRKFIGRIP  
 SLLWCAICFGFRFLE (SEQ ID NO: 293)

25 ATGCCGATGCAGCTGCTGCTTACAGATTTTATTATCTTTTCCATCAGATTCATCATCAACAG  
 CATGGAAGCGAGAAACCAAACAGCTATTTCAAAATTCCTTCTCCTGGGACTGATAGAGGAT  
 CCGGAAGTGCAGCCCGTCTTTTTCAGCCTGTTCCCTGTCCATGTACTTGGTCACCATCCTGGG  
 GAACCTGCTCATCCTCTTGGCTGTCATCTCTGACTCTCACCTCCACACCCCCATGTACTTCT  
 30 TCCTCTCCAATCTCTCCTTTTTGGACATTTGTTTAAAGCACAACCACGATCCCAAAGATGCTG  
 GTGAACATCCAAGCTCAGAATCGGAGCATCACGTACTCAGGCTGCCTCACCAGATCTGCT  
 TTGCTTGTTTTTTGGCTGGCTTGGAAATTTGTCTCCTTGACAGCAATGGCCTATGACCGCTAT  
 GTGGCCATTTGTCACCCCCTTAGATACACAGTCATCATGAACCCCGCCTCTGTGGCCTGC  
 TGATTCTTCTCTCTCTGTTGACTAGTGTGTGAATGCCCTTCTTCTCAGCCTGATGGTGTG  
 35 AGGCTGTCTTCTGCACAGACCTGGAAATCCCGCTCTTCTTCTGTGAAGTGGCTCAGGTCA  
 TCCAAGTCACTGTTTGCAGACACCTCATCAATAACATCCTGATATATTTTGCAGCTTGCATA  
 TTTGGTGGTGTCTCTGTCTGGAATCATTTTGTCTTACACTCAGATCACCTCCTGTGTTTT  
 GAGAATGCCATCAGCAAGTGGAAAGCACAAGCAGTTTCCACCTGTGGGTCTCACCTCTCC  
 ATTGTTCTCTTGTCTATGGGGCAGGTTTGGGGGTGTACATTAGTTCTGTGGTTACTGACTC  
 40 ACCTAGGAAGACTGCAGTGGCTTCAGTGATGTATTCTGTGTTCCCTCAAATGGTGAACCC  
 TTTATCTATAGTCTGAGGAATAAGGACATGAAAGGAACCTTGAGGAAGTTTCATAGGGAGG  
 ATACCTTCTCTTCTGTGGTGTGCCATTTGCTTTGGATTTCAGGTTTCTAGAGTAA (SEQ ID  
 NO: 294)

**AOLFR161 sequences:**

45 MBPRNQTSAQFILLGLSEKPEQETLLFSLFFCMYLVMMVGNLLILLAISIDSHLHTPMYFFLANL  
 SLVDFCLATNTIPKMLVSLQTGSKAISYPCLIQMYFFHFFGIVDSVIIAMMAYDRFVAICHPLH  
 YAKIMSLRLCRLLVGALWAFSCFISLTHILLMARLVFCGSHEVPHYFCDLTPILRLSCTDTSVNR  
 IFILIVAGMVIATPFVCILASYARILVAIMKVPSAGGRKAFSTCSSHLSVVALFYGTIGVYLCF  
 50 SSVLTTVKEKASAVMYTAVTPMLNPFYSLRNRLDKGALRKLVRNKITSSS (SEQ ID NO: 295)

ATGGAACCAAGAAACCAAACAGTGCATCTCAATTCATCCTCCTGGGACTCTCAGAAAAGC  
 CAGAGCAGGAGACGCTTCTCTTTTCCCTGTTCTTCTGCATGTACCTGGTCATGGTCGTGGG  
 GAACCTGCTCATCATCCTGGCCATCAGCATAGACTCCACCTCCACACCCCCATGTACTTCT  
 55 TCCTGGCCAACCTGTCCCTGGTTGATTTCTGTCTGGCCACCAACACCATCCCTAAGATGCT  
 GGTGAGCCTTCAAACCGGGAGCAAGGCCATCTCTTATCCCTGCTGCCTGATCCAGATGTAC

TTCTTCCATTTCTTTGGCATCGTGGACAGCGTCATAATCGCCATGATGGCTTATGACCGGTT  
 CGTGGCCATCTGCCACCCATTGCACTACGCCAAGATCATGAGCCTACGCCTCTGTGCGCTG  
 CTGGTCGGCGCCCTCTGGGCGTTTTCTGCTTCATCTCACTCACTCACATCCTCCTGATGGC  
 CCGTCTCGTTTTCTGCGGCAGCCATGAGGTGCCTCACTACTTCTGCGACCTCACTCCCATCC  
 5 TCCGACTTTTCGTGCACGGACACCTCTGTGAATAGGATCTTCATCCTCATTGTGGCAGGGAT  
 GGTGATAGCCACGCCCTTTGTCTGCATCCTGGCCTCCTATGCTCGCATCCTTGTGGCCATCA  
 TGAAGGTCCCTCTGCAGGCGGCAGGAAGAAAGCCTTCTCCACCTGCAGCTCCACCTGTC  
 TGTGGTTGCTCTCTTCTATGGGACCACCATTTGGCGTCTATCTGTGTCCCTCCTCGGTCCTCA  
 CCACTGTGAAGGAGAAAGCTTCTGCGGTGATGTACACAGCAGTCACCCCATGCTGAATCC  
 10 CTTTCATCTACAGCTTGAGGAACAGAGACCTGAAAGGGGCTCTCAGGAAGCTGGTCAACAG  
 AAAGATCACCTCATCTTCCTGA (SEQ ID NO: 296)

#### AOLFR162 sequences:

MMRLMKEVRGRNQTEVTEFLLGLSDNPDLQGVLFALFLLIYMANMVGNLGMIVLIKIDLCLH  
 15 TPMYFFLSSLSFVDASYSSSVTPKMLVNLMAENKAISFHGCAAQFYFFGSFLGTECFLLAMMA  
 YDRAAIWNPLLYPVLVSGRICFLLIATSFLAGCGNAIHTGMTFRLSFCGSNRINHFYCDTPPL  
 LKLSGSDTHFNIVIMAFSSFIVISCVMIVLISYLCIFIAVLKMPSEGRHKAFSTCASYLMAVTIF  
 FGTILFMYLRPTSSYSMBQDKVVSFYTIVIPVLNPLIYSLKNKDVKKALKKILWKHIL (SEQ ID  
 NO: 297)

20 ATGATGAGACTTATGAAAGAGGTTTCGAGGCAGAAATCAAACAGAAGTAACAGAATTTCTC  
 CTCTTAGGACTTTCCGACAATCCAGATCTACAAGGAGTCCTCTTTGCATTGTTTCTGTTGAT  
 CTATATGGCAAACATGGTGGGCAATTGGGGATGATTGTATTGATTAGATTGATCTCTGT  
 CTCCACACCCCATGTATTTCTTTCTCAGTAGCCTCTCTTTTGTAGATGCCTCTTACTCTTCT  
 25 TCCGTCACTCCCAAGATGCTGGTGAACCTCATGGCTGAGAATAAGGCCATTTCTTTTCATG  
 GATGTGCTGCCCAGTTCTACTTCTTTGGCTCCTTCTGGGGACTGAGTGCTTCTGTTGGCC  
 ATGATGGCATATGACCGCTATGCAGCCATTGGAACCCCTGCTCTACCCAGTTCTCGTGT  
 CTGGGAGAATTTGCTTTTGTCTAATAGCTACCTCCTTCTTAGCAGGTTGTGGAAATGCAGC  
 CATAACATACAGGGATGACTTTTAGGTTGTCTTTTGTGGTTCTAATAGGATCAACCATTTCT  
 30 ACTGTGACACCCCGCCACTGCTCAAACCTCTCTTGCTCTGATACCCACTTCAATGGCATTTGTG  
 ATCATGGCATTCTCAAGTTTATTGTCTCATCAGCTGTGTTATGATTGTCTCTACCTTCTACCT  
 GTGTATCTCATTTGCGGTCTTGAAGATGCCTTCGTTAGAGGGCAGGCACAAAGCCTTCTCC  
 ACCTGTGCCTCTTACCTCATGGCTGTCACCATATTCTTTGGAACAATCCTCTTCATGTACTT  
 GCGCCCTACATCTAGCTACTCAATGGAGCAAGACAAGGTTGTCTCTGTCTTTTATACAGTA  
 35 ATAATCCCTGTGCTAAATCCCCTCATCTATAGTTTAAAAAATAAGGATGTAAAAAAGGCC  
 TAAAGAAGATCTTATGGAAACACATCTTGTAG (SEQ ID NO: 298)

#### AOLFR163 sequences:

40 MQRSNHTVTEFILLGFTTDPGMQLGLFVFLGVVSLTVVGNSTLIVLICNDSCSLHTPMYFFTGN  
 LSFLDLWYSSVYTPKILVTCISEDKSISFAGCLCQFFFSAGLAYSECYLLAAVAYDRYVAISKPL  
 LYAQAMSIKLCALLVAVSYCGGFINSIITKKTFSFNFCRENIDDFCDLLPLVELACGEKGGYK  
 IMMYFLLASNVICPAVLILASYLFIITSVLRISSSKGYLKAFSTCSSHLTSVTLYYGSILYIYALPRS  
 SYFDMDDKIVSTFYTVVFPMLNLMYSLRNKDVKEALKKLLP (SEQ ID NO: 299)

45 ATGCAGAGGAGCAATCATAAGTACTGAGTTTATACTGCTGGGCTTCACCACAGACCCA  
 GGAATGCAGCTGGGCTCTTCGTGGTGTTCCTGGGCGTGTACTCTCTCACTGTGGTAGGAA  
 ATAGCACCTCATCGTGTGATCTGTAATGACTCCTGCCTCCACACACCCATGTATTTTTTC  
 ACTGGAAATCTGTCGTTTCTGGATCTCTGGTATTCTTCTGTCTACACCCCAAAGATCCTAGT  
 GACCTGCATCTCTGAAGACAAAAGCATCTCCTTTGCTGGCTGCCTGTGTCAGTTCTTCTTCT  
 50 CTGACGGGCTGGCCTATAGTGAGTGCTACCTGCTGGCTGCCGTGGCTTATGACCGCTACGT  
 GGCCATCTCCAAGCCCCTGCTTTATGCCAGGCCATGTCCATAAAGCTGTGTGCATTGCTG  
 GTAGCAGTCTCATATTGTGGTGGCTTTATTAACCTTTCAATCATCACCAAGAAACGTTTTC  
 CTTTAACTTCTGCCGTGAAAACATCATTGATGACTTTTTCTGTGATTGTGCTTCCCTTGGTGG  
 AGCTGGCCTGTGGCGAGAAGGGCGGCTATAAAATTATGATGTACTTCTGCTGGCCTCCAA  
 55 TGTCATCTGCCCCGAGTGCTCATCCTGGCCTCCTACCTCTTTATCATCACCAGTGTCTTGA  
 GGATCTCCTCCTCCAAGGGCTACCTCAAAGCCTTCTCCACATGCTCCTCCACCTGACCTCT

GTCACTTTATACTATGGCTCCATTCTCTACATCTACGCTCTCCCCAGATCTAGCTATTCTTT  
TGATATGGACAAAATAGTTTCTACATTTTACACTGTGGTATTCCCCATGTTGAATCTCATG  
ATCTACAGCCTAAGGAATAAGGATGTGAAAAGAGGCTCTGAAAAAACTTCTCCCATAA (SEQ  
ID NO: 300)

5

**AOLFR164 sequences:**

MFLTERNTTSEATFTLLGFS DYLELQIPLFFVFLAVYGFSVVGNLGMIVIIKINPKLHTPMYFFLN  
HLSFVDFCYSSIIAPMMLVNLVVEDRTISFSGCLVQFFFFCTFVVTELILFAVMA YDHFAICNP  
LLYTV AISQKLCAMLVVVLYAWGVACSLTLACSALKLSFHGFNTINHHFCELSSLISLSPDSYL  
10 SQLLLFTVATFNEISTLLIILTSYAFIIVTTLKMPASGHRKVFTSCASHLTAITFHGTILFLYCVP  
NSKNSRHTVKVASVFYTVVIPLLNPLIYSLRNKDVKDAIRKIINTKYFHIKHRHWYPFNFVIEQ  
(SEQ ID NO: 301)

ATGTTTCTGACAGAGAGAAATACGACATCTGAGGCCACATTCACTCTCTTGGGCTTCTCAG  
15 ATTACCTGGAAGTCAAATTCCTCTTCTTTGTATTTCTGGCAGTCTACGGCTTCAGTGTG  
GTAGGGAATCTTGGGATGATAGTATCATCAAAAATTAACCCAAAATTGCATACCCCCATGT  
ATTTTTCCTCAACCACCTCTCCTTTGTGGATTTCTGCTATTCTCCATCATTTGCTCCCATGA  
TGCTGGTGAACCTGGTTGTAGAAGATAGAACCATTTCATTCTCAGGATGTTTGGTGCAATT  
CTTTTCTTTTGCACCTTTGTAGTGAAGTGAATTAATTCTATTTGCGGTGATGGCCTATGACC  
20 ACTTTGTGGCCATTTGCAATCCTCTGCTCTACACAGTTGCCATCTCCAGAACTCTGTGCC  
ATGCTGGTGGTTGTATTGTATGCATGGGGAGTCGCATGTTCCCTGACACTCGCGTGCTCTG  
CTTAAAGTTATCTTTTCATGGTTTCAACACAATCAATCATTCTTCTGTGAGTTATCCTCC  
CTGATATCACTCTCTTACCCTGACTCTTATCTCAGCCAGTTGCTTCTTTTCACTGTTGCCAC  
TTTAAAGAGATAAGCACACTACTCATCTTCTGACATCTTATGCATTCATCATTGTCAACA  
25 CCTTGAAGATGCCTTCAGCCAGTGGGCACCGCAAAGTCTTCTCCACCTGTGCCTCCCACT  
GACTGCCATCACCATCTTCCATGGCACCATCCTCTTCTCTACTGTGTACCCAACTCCAAAA  
ACTCCAGGCACACAGTCAAAGTGGCCTCTGTGTTTTACACCGTGGTGTATCCCTTGTGAA  
TCCCTGATCTACAGTCTGAGAAATAAAGATGTAAAGGATGCAATCCGAAAAATAATCAAT  
ACAAAATATTTTCATATTAACATAGGCATTGGTATCCATTTAATTTTGTATTGAACAATA  
30 A (SEQ ID NO: 302)

**AOLFR165 sequences:**

MAVGRNNTIVTKFILLGLSDHPQMKIFL FMLFLGLYLLTLAWNLSLIALIKMDSHLHMPMYFFL  
SNLSFLDICYVSSSTAPKMLS DITEQKTISFVGCA TQYFVFCGMGLTECFLLAAMAYDRYAAICN  
35 PLYTVLISHTLCLKMVVGAYVGGFLSSFIETYSVYQHDFCGPYMNHFFCDLPPVLALSCSDTF  
TSEVVT FIVSVVVGIVSVLVVLISYGYIVA AVVKISSATGRTKAFSTCASHLTA VTLFYGSGFFM  
YMRPSSSYSLNRDKVVSIFYALVIPV VNPPIYSFRNKEIKNAMRKAMERDPGISHGGPFIFMTLG  
(SEQ ID NO: 303)

ATGGCTGTAGGAAGGAACAACACAATTGTGACAAAATTCATTCTCCTGGGACTTTCAGACC  
40 ATCCTCAAATGAAGATTTTCTTTTCATGTTATTTCTGGGGCTCTACCTCCTGACGTTGGCC  
TGGAACCTTAAGCCTCATTGCCCTCATTAAAGATGGACTCTCACCTGCACATGCCCATGTACT  
TCTTCTCAGTAACCTGTCTTCTGACATCTGCTATGTGTCTCCACCGCCCTAAGATG  
CTGTCTGACATCATCACAGAGCAGAAAACCATTTCCTTTGTTGGCTGTGCCACTCAGTACT  
45 TTGTCTTCTGTGGGATGGGGCTGACTGAATGCTTTCTCCTGGCAGCTATGGCCTATGACCG  
GTATGCTGCAATCTGCAACCCCTTGCTTTACACAGTCTCATATCCCATACACTTTGTTTAA  
AGATGGTGGTTGGCGCCTATGTGGGTGGATTCTTAGTTCTTTTCATTGAAACATACTCTGT  
CTATCAGCATGATTTCTGTGGGGCCCTATATGATCAACCCTTTTTCTGTGACCTCCCTCCAG  
TCCTGGCTCTGTCTCTGCTCTGATACCTTCACCAGCGAGGTGGTGACCTTCATAGTCAGTGT  
50 GTCGTGGAATAGTGTCTGTGCTAGTGGTCTCATCTCTTATGGTTACATTGTTGCTGCTGT  
TGTGAAGATCAGCTCAGCTACAGTAGGACAAAGGCCTTCAGCACTGTGCCTCTCACCTG  
ACTGCTGTGACCCTCTTCTATGGTTCTGGATTCTTCATGTACATGCGACCCAGTTCCAGCTA  
CTCCCTAAACAGGGACAAGGTGGTGTCCATATTCTATGCCTTGGTGATCCCGTGGTGAAT  
CCCATCATCTACAGTTTATAGGAATAAGGAGATTAAAAATGCCATGAGGAAAGCCATGGAA  
55 AGGGACCCCGGATTTCTCAGGTGGACCATTCAATTTTATGACCTTGGGCTAA (SEQ ID  
NO: 304)

**AOLFR166 sequences:**

MEMENCTRVKEFIFLGLTQNREVSIVLFLFLLLVYVTTLLGNLLIMVTVTCESRLHTPMYFLLH  
 NLSIADICFSSITVPKVLVDLLSERKTISFNHCFTQMFLFHLIGGVDVFSLSVMALDRYVAISKPL  
 5 HYATIMSRDHCIGLTVAAWLGGFVHSIVQISLLLPFCGPNVLDTFYCDVHRVLKLAHTDIFIL  
 ELLMISNNGLLTTLWFFLLLVSYIVILSLPKSQAGEGRRKAISTCTSHITVVTLHFVPCIYVYARP  
 FTALPMDKAISVTFTVISPLLNPLIYTLRNHEMKSAMRRLKRRLVPSDRK (SEQ ID NO: 305)

ATGGAGATGGAAAAGCTGCACCAGGGTAAAAGAATTTATTTTCCTTGGCCTGACCCAGAATC  
 10 GGGAAGTGAGCTTAGTCTTATTTCTTTTCTACTCTTGGTGTATGTGACAACTTTGCTGGGA  
 AACCTCCTCATCATGGTCACTGTTACCTGTGAATCTCGCCTTCACACGCCCATGTATTTTT  
 GCTCCATAATTTATCTATTGCCGATATCTGCTTCTCTTCCATCACAGTGCCCAAGGTTCTGG  
 TGGACCTTCTGTCTGAAAGAAAGACCATCTCCTTCAATCATTGCTTCACTCAGATGTTTCTA  
 TTCCACCTTATTGGAGGGGTGGATGTATTTTCTCTTTCGGTGATGGCATTGGATCGATATG  
 15 TGGCCATCTCCAAGCCCCTGCACTATGCGACTATCATGAGTAGAGACCATTGCATTGGGCT  
 CACAGTGGCTGCCTGGTTGGGGGGCTTTGTCCACTCCATCGTGCAGATTTCCCTGTTGCTC  
 CCACTCCCTTTCTGCGGACCCAATGTTCTTGACACTTTCTACTGTGATGTCCACCGGGTCT  
 CAAACTGGCCCATACAGACATTTTCATACTTGAAGTACTAATGATTTCCAACAATGGACTG  
 CTCACCACACTGTGGTTTTTCTGCTCCTGGTGTCTACATAGTCATATTATCATTACCCAA  
 20 GTCTCAGGCAGGAGAGGGCAGGAGGAAAGCCATCTCCACCTGCACCTCCACATCACTGT  
 GGTGACCTGCATTTCTGTGCCCTGCATCTATGTCTATGCCCGGCCCTTCACTGCCCTCCCA  
 TGGATAAGGCCATCTCTGTACCTTCACTGTCTATCTCCCTCTGCTCAACCCCTTGATCTAC  
 ACTCTGAGGAACCATGAGATGAAGTCAGCCATGAGGAGACTGAAGAGAAGACTTGTGCT  
 TCTGATAGAAAATAG \*SEQ ID NO: 306)

25

**AOLFR167 sequences:**

MSITKAWNSSSVTMFILLGFTDHPBLQALLFVTFGLGIYLTTLAWNLAFLIRGDTHLHTPMYFF  
 LSNLSFDICYSSAVAPNMLTDFWEQKTISFVGCAAQFFFFVGMGLSECLLTAMAYDRYAAI  
 30 SSPLLYPTIMTQGLCTRMVVGAYVGGFLSSLIQASSIFRLHFHFCGPNINHHFCDLPVLALSCSDT  
 FLSQVNVNLFVVVTVGGTSFLQLLISYGYVSAVLKIPSAEGRWKACNTCASHLMVVVTLFGTAL  
 FVYLRPSSSYLLGRDKVVSFVYSLVPMNLPLIYSLRNKEIKDALWKVLERKKVFS (SEQ ID  
 NO: 307)

ATGTCCATAACCAAAGCCTGGAACAGCTCATCAGTGACCATGTTTCATCCTCCTGGGATTCA  
 35 CAGACCATCCAGAACTCCAGGCCCTCCTCTTTGTGACCTTCCTGGGCATCTATCTTACCACC  
 CTGGCCTGGAACCTGGCCCTCATTTTTCTGATCAGAGGTGACACCCATCTGCACACACCCA  
 TGTACTTCTTCTAAGCAACTTATCTTTTCACTGACATCTGCTACTCTTCTGCTGTGGCTCCC  
 AATATGCTCACTGACTTCTTCTGGGAGCAGAAGACCATATCATTGTGGGCTGTGCTGCTC  
 AGTTTTTTTTCTTTGTGCGCATGGGTCTGTCTGAGTGCCTCCTCCTGACTGCTATGGCATA  
 40 GACCGATATGCAGCCATCTCCAGCCCCCTTCTCTACCCCACTATCATGACCCAGGGCCTCT  
 GTACACGCATGGTGGTTGGGGCATATGTTGGTGGCTTCTGAGCTCCCTGATCCAGGCCAG  
 CTCCATATTTAGGCTTCACTTTTGGCGACCCAACATCATCAACCACTTCTTCTGCGACCTCC  
 CACCAGTCTGCTGTCTTGTCTGACACCTTCTCAGTCAAGTGGTGAATTTCTCCTGCTG  
 GTGGTCACTGTGCGAGGAACATCGTTCCTCCAACCTCTTATCTCCTATGGTTACATAGTGT  
 45 CTGCGGTCTGAAGATCCCTTCAGCAGAGGGCCGATGGAAAGCCTGCAACACGTGTGCT  
 CGCATCTGATGGTGGTGAATCTGCTGTTTGGGACAGCCCTTTTCTGTACTTGGCAGCCAG  
 CTCCAGCTACTTGTAGGCAGGGACAAGGTGGTGTCTGTTTTCTATTGATTGGTGATCCCC  
 ATGCTGAACCTCTCATTTACAGTTTGAGGAACAAAGAGATCAAGGATGCCCTGTGGAAG  
 GTGTTGGAAAGGAAGAAAGTGTCTTCTTAG (SEQ ID NO: 308)

50

**AOLFR168 sequences:**

MEKINNVTETIFWGLSQSPEIEKVCVVFVSFFYIILLGNLLIMLTVCLSNLFKSPMYFFLSFLSFV  
 DICYSSTVAPKMIVDLLAKDKTISYVGCMLQLLGVHFFGCTEIFILTVMAYDRYVAICKPLHYM  
 55 TIMNRETCKMMLGTWVGGFLHSIIQVALVVQLPFCGPNIDHYFCDVHPVLKLACTETYIVG  
 VVVTRANSITIALGSFVILLISYSIILVSLRKQSAEGRRKALSTCGSHIAMVVVIFGPGCTFMYMRPD

TTFSEDKMVAVFYTIITPMLNPLIYTLRNAEVKNAMKKLWGRNVFLEAKGK (SEQ ID NO: 309)

5 ATGGAAAAAATAAACACGTAACCTGAATTCATTTTCTGGGGTCTTTCTCAGAGCCCAGAGA  
TTGAGAAAGTTTGTGTTTGTGGTGTGTTTCTTTCTTCTACATAATCATTCTTCTGGGAAATCTC  
CTCATCATGCTGACAGTTTGCCTGAGCAACCTGTTTAAGTCACCCATGTATTCTTTCTCAG  
CTTCTTGTCTTTTGTGGACATTGTTACTCTTCAGTCACAGCTCCCAAGATGATTGTTGACC  
TGTTAGCAAAGGACAAAACCATCTCCT1ATGTGGGGTGCATGTTGCAACTGCTTGGAGTAC  
10 ATTTCTTTGGTTGCACTGAGATCTTCATCCTTACTGTAATGGCCTATGATCGTTATGTGGCT  
ATCTGTAAACCCCTACATTATATGACCATCATGAACCGGAGACATGCAATAAAATGTTAT  
TAGGGACGTGGGTAGGTGGGTCTTACACTCCATTATCCAAGTGGCTCTGGTAGTCCAACT  
ACCCTTTGTGGACCCAATGAGATAGATCACTACTTTTGTGATGTTACCCTGTGTTGAAA  
CTTGCCCTGCACAGAAACATAACATTGTTGGTGTGTTGTGACAGCCAACAGTGGTACCATTG  
15 CTCTGGGGAGTTTGTATCTTGCTAATCTCCTACAGCATCATCCTAGTTTCCCTGAGAAAAG  
CAGTCAGCAGAAAGGCAGGCGAAAGCCCTCTCCACCTGTGGCTCCCACATTGCCATGGTCG  
TTATCTTTTTCGGCCCCCTGTACTTTTATGTACATGCGCCCTGATACGACCTTTTCAGAGGAT  
AAGATGGTGGCTGTATTTTACACCATATCACTCCCATGTTAAATCCTCTGATTTATACACT  
GAGAAATGCAGAAGTAAAGAATGCAATGAAGAACTGTGGGGCAGAAATGTTTTCTTGGA  
GGCTAAAGGAAATAG (SEQ ID NO: 310)

20

**AOLFR169 sequences:**

MMDNHSSATEFHLLGFPQSQGLHHILFAIFFFYLVTLMGNTVIVIVCVDKRLQSPMYFFLSHL  
STLEILVTIIVPMMLWGLLFLGCRQYLSLHVSINFSCGTMEFALLGVMAVDRYVAVCNPLRY  
NIIMNSSTCIWVVIVSWVFGFLSEIWPIYATFQFTFRKSNSLDHFYCDRGQLKLSCDNTLLTEFI  
25 LFLMAVFILIGSLIPTIVSYTYIISTILKIPSASGRRAKAFSTFASHFTCVVIGYGSCLFLYVKPKQTQ  
GVEYNKIVSLLVSVLTPFLNPFIFTLRNDKVKEALRDGMKRCCQLLKD (SEQ ID NO: 311)

30 ATGATGGACAACCACTCTAGTGCCACTGAATTCACCTTCTAGGCTTCCCTGGGTCCCAAG  
GACTACACCACATTCTTTTGCTATATTCTTTTTCTTCTATTTAGTGACATTAATGGGAAAC  
ACGGTCATCATTGTGATTGTCTGTGTGGATAAACGTCTGCAGTCCCCCATGTATTTCTTCTCCT  
CAGCCACCTCTCTACCCTGGAGATCCTGGTCACAACCATAATTGTCCCCATGATGCTTTGG  
GGATTGCTCTTCTGGGATGCAGACAGTATCTTTCTCTACATGTATCGCTCAACTTTTCTCTG  
TGGGACCATGGAGTTTGCATTACTTGGAGTGATGGCTGTGGACCGTTATGTGGCTGTGTGT  
AACCCTTTGAGGTACAACATCATTATGAACAGCAGTACCTGTATTTGGGTGGTAATAGTGT  
35 CATGGGTGTTTGGATTCTTTCTGAAATCTGGCCCATCTATGCCACATTTACGTTTACCTTC  
CGCAAATCAAATTCATTAGACCATTTTACTGTGACCGAGGGCAATTGCTCAAACCTGTCTT  
CGGATAACACTCTTCTCACAGAGTTTATCCTTTTCTTAAATGGCTGTTTTTATTCCTCATTGGT  
TCTTTGATCCCTACGATTGTCTCCTACACCTACATTATCTCCACCATCCTCAAGATCCCGTC  
AGCCTCTGGCCGGAGGAAAGCCTTCTCCACTTTTGCCTCCCACTTACCTGTGTTGTGATTG  
40 GCTATGGCAGCTGCTTGTCTTCTCTACGTGAAACCCAAGCAAACACAGGGAGTTGAGTACAA  
TAAGATAGTTTCCCTGTTGGTTTCTGTGTTAACCCCTTCTGAATCCTTTTCTCTTACTCT  
TCGGAATGACAAAGTCAAAGAGGCCCTCCGAGATGGGATGAAACGCTGCTGTCAACTCCT  
GAAAGATTAG (SEQ ID NO: 312)

45 **AOLFR170 sequences:**

MSFTSLIPSLCFSLTLPFLFCYLSLLPFLSAFLFITRWLLAFLSLFSVSVPVSSVSSSMVLCYLSVS  
ASPSVFCFSCMQGPILWIMANLSQPSEFVLLGFSSFGELQALLYGPFLMLYLLAFMGNTIIVMVI  
ADTHLHTPMYFFLGNFSLLEILVTMTAVPRMLSDLLVPHKVITFTGCMVQFYHFHSLGSTSFLIL  
TDMALDRFVAICHPLRYGTLMSRAMCVQLAGAAWAAPFLAMVPTVLSRAHLDYCHGDVINH  
50 FFCDNEPLLQLSCSDTRLLEFWDFLMALTFVLSSFLVTLISYGYIVTTVLRIPSASSCQKAFSTCG  
SHLTLVFIGYSSITFLYVRPGKAHSVQVRKVVALVTSVLTLPFLNPFILTFCNQTVKTVLQGMQ  
RLKGLCKAQ (SEQ ID NO: 313)

55 ATGTCTTTCACCTTCTCTCATACCCCTCACTCTGTTTCTCCTTGACTCTCCCATTCCTGTTTTGT  
TATCTTTCTTTATTGCCGTTTCTTTCTGCTTTTCTGTTTATCACTCGCTGGCTACTGCGCTT  
CTCTCTCIATTCTGTCTCTGTCCCTGTTTCTTCTGTTTCAAGTTCAATGGTTCTCTGTCTC

TATCTCTCTGTTTCTGCCTCTCCGTCTGTCTTTTGTTCCTTGCATGCAGGGCCCCATACTG  
 TGGATCATGGCAAATCTGAGCCAGCCCTCCGAATTTGTCCTCTTGGGCTTCTCCTCCTTTGG  
 TGAGCTGCAGGCCCTTCTGTATGGCCCTTCCTCATGCTTTATCTTCTCGCCTTCATGGGAA  
 ACACCATCATCATAGTTATGGTCATAGCTGACACCCACCTACATACACCCATGTACTTCTTC  
 5 CTGGGCAATTTTTCCCTGCTGGAGATCTTGGTAACCATGACTGCAGTGCCAGGATGCTCT  
 CAGACCTGTTGGTCCCCACAAAGTCATTACCTTCACTGGCTGCATGGTCCAGTTCTACTTC  
 CACTTTTCCCTGGGGTCCACCTCCTTCCTCATCTGACAGACATGGCCCTTGATCGCTTTGT  
 GGCCATCTGCCACCCACTGCGCTATGGCACTCTGATGAGCCGGGCTATGTGTGTCCAGCTG  
 GCTGGGGCTGCCTGGGCAGCTCCTTTCTAGCCATGGTACCCACTGTCTCTCCCGAGCTC  
 10 ATCTTGATTACTGCCATGGCGACGTCATCAACCACTTCTTCTGTGACAATGAACCTCTCCTG  
 CAGTTGTCATGCTCTGACACTCGCCTGTTGGAATTTCTGGGACTTCTGATGGCCTTGACCTT  
 TGTCTCAGCTCCTTCTGCTGGTGACCTCATCTCCTATGGCTACATAGTGACCACTGTGCTGC  
 GGATCCCCCTCTGCCAGCAGCTGCCAGAAGGCTTTTCTCCACTTGCGGGTCTCACCTCACACT  
 GGTCTTCATCGGCTACAGTAGTACCATCTTTCTGTATGTCAGGCCTGGCAAAGCTCACTCT  
 15 GTGCAAGTCAGGAAGGTCGTGGCCTTGGTGACTTCAGTTCTCACCCCTTTTCTCAATCCCT  
 TTATCCTTACCTTCTGCAATCAGACAGTTAAAACAGTGCTACAGGGGCAGATGCAGAGGCT  
 GAAAGGCCTTTGCAAGGCACAATGA (SEQ ID NO: 314)

#### AOLFR171 sequences:

20 MVGNLLIWVTTIGSPSLGSLMYFFLAYLSLMDAISTAMSPKLMIDLLCDKIAISLSACMGQLFI  
 EHLLGGAEVFLLVVMAYDRYVAISKPLHYLNIMNRLVCILLVVMAMIGGFVHSVQIVFLYSLP  
 ICGPNVIDHSVCDMYPLELLCLDITYFIGLTVVANGGHCVMVIFLLISCGVILNFLKTYSQEER  
 HKALPTCISHIIVVALVFVPCIFMYVRPVSFPDKLMTVFYSITLMLNPLIYSLRQSEMKNAM  
 KNLWCEKLSIVRKRVSPTLNIPISSKATNRR (SEQ ID NO: 315)

25 ATGGTGGGAAACCTCCTCATTGTTGGGTGACTACTATTGGCAGCCCCCTCCTTGGGCTCCCTAA  
 TGTACTTCTTCTTGCCTACTTGTCACTTATGGATGCCATATATCCACTGCCATGTCACCC  
 AAATTGATGATAGACTTACTCTGTGATAAAATCGCTATTTCTTGTGAGCTTGCATGGGTC  
 AGCTCTTCATAGAACACTTACTTGGTGGTGACAGAGGTCTTCTTTTGGTGGTGATGGCCTA  
 30 TGATCGCTATGTGGCTATCTTAAGCCGCTGCACTATTTGAACATCATGAATCGACTGGTT  
 TGCATCCTTCTGTGTTGGTGGTGCCATGATTGGAGGTTTTGTGCACTCTGTGGTTCAAATTGT  
 CTTTCTGTACAGTCTACCAATCTGTGGCCCCAATGTTATTGACCACTCTGTCTGTGACATGT  
 ACCCATTGTTGGAAGTGTGTGCCCTTGACACCTACTTTATAGGACTCACTGTGGTTGCCAA  
 TGGTGGAAATAATTTGTATGGTCATCTTTACCTTTCTGCTAATCTCCTGTGGAGTCATCCTAA  
 35 ACTTCCTTAAAACTTACAGTCAGGAAGAGAGGCATAAAGCCCTGCCTACCTGCATCTCCCA  
 CATCATTGTGGTTGCCCTCGTTTTTGTTCCTGTATTTTATGTATGTTAGACCCGTTTCCA  
 ACTTTCCCTTTGATAAATTAATGACTGTGTTTTATTCAATTATCACACTCATGTTGAATCCT  
 TTAATATACTCGTTGAGACAATCAGAGATGAAAAATGCTATGAAAAATCTCTGGTGTGAA  
 AAGTTAAGTATAGTTAGAAAAAGAGTATCTCCCACTGAACATATTTATTCCTAGTTCTA  
 40 AGGCAACAAATAGGCGGTAA (SEQ ID NO: 316)

#### AOLFR172 sequences:

MAETLQLNSTFLHPNFFILTGFPGLGSAQTWLTIVFGPIYLLALLGNGALPAVVWIDSTLHQPM  
 FLLAILAATDLGLATSIAPGLLAVLWLGPRSVPYAVCLVQMFFVHALTAMESGVLLAMACDR  
 45 AAAIGRPLHYPVLVTKACVGYAALALALKAVAIIVPFPLLVAKFEHFQAKTIGHTYCAHMAV  
 VELVVGNTQATNLYGLALSLAISGMDILGITGSYGLIAHAVLQLPTREAHAKAFGTCSHICVIL  
 AFYIPGLFSYLAHFRFGHHTVPKPVHILLSNIYLLLPALNPLIYGARTKQIRDRLLETFTFRKSPL  
 (SEQ ID NO: 317)

50 ATGGCAGAACTCTACAACCTCAATTCCACCTTCCTACACCCAACTTCTTCATACTGACTG  
 GCTTTCCAGGGCTAGGAAGTGCCAGACTTGGCTGACACTGGTCTTTGGGCCCATTTATCT  
 GCTGGCCCTGCTGGGCAATGGAGCACTGCCGGCAGTGCTGGATAGAGCTCCACACTGCA  
 CCAGCCCATGTTTCTACTGTTGGCCATCCTGGCAGCCACAGACCTGGGCTTAGCCACATCT  
 ATAGCCCCAGGGTTGCTGGCTGTGCTGTGGCTTGGGCCCCGATCTGTGCCATATGCTGTGT  
 55 GCCTGGTCCAGATGTTCTTTGTACATGCACTGACTGCCATGGAATCAGGTGTGCTTTTGGC  
 CATGGCCTGTGATCGTGCTGCGGCAATAGGGCGTCCACTGCACTACCCTGTCTGGTCACC

AAAGCCTGTGTGGGTTATGCAGCCTTGGCCCTGGCACTGAAAGCTGTGGCTATTGTTGTAC  
 CTTTCCCACTGCTGGTGGCAAAGTTTGAGCACTTCCAAGCCAAGACCATAGGCCATACCTA  
 TTGTGCACACATGGCAGTGGTAGAACTGGTGGTGGGTAACACACAGGCCACCAACTTATA  
 TGGTCTGGCACTTCACTGGCCATCTCAGGTATGGATATTCTGGGTATCACTGGCTCCTAT  
 5 GGACTCATTGCCCATGCTGTGCTGCAGCTACCTACCCGGGAGGCCCATGCCAAGGCCTTTG  
 GTACATGTAGTTCTCACATCTGTGTCATTCTGGCCTTCTACATACCTGGTCTCTTCTCTAC  
 CTCGCACACCGCTTTGGTCATCACACTGTCCCAAAGCCTGTGCACATCCTTCTCTCCAACAT  
 CTAATTGCTGCTGCCACCTGCCCTCAACCCCTCATCTATGGGGCCCGCACCAAGCAGATC  
 AGAGACCGACTCCTGGAAACCTTCACATTAGAAAAAGCCCGTTGTAA (SEQ ID NO: 318)

10

**AOLFR173 sequences:**

MSHTNVTIFHPAVFVLPGLPLEAYHIWLSIPLCLIIYTTAVLGNSILIVVIVMERNLHVPMPYFFLS  
 MLAVMDILLSTTTVPKALAFWLQAHNIAFDACVTQGGFVHMMFVGESAILLAMAFDRFVAIC  
 APLRYTTVLTWPVVGRIALAVITRSFCIFPVIFLLKRLPFCLTNIVPHSYCEHIGVARLACADITV  
 15 NIWYGFSVPVIMVILDVILIAVSYSILRAVFRLPQDARHKALSTCGSHLCVILMFYVPSFFTL  
 THHFRNIPQHVHILLANLYVAVPPMLNPVYGVKTKQIREGVAHRFFDIKTWCCTSPGGS  
 (SEQ ID NO: 319)

ATGAGTCACACCAATGTTACCATCTTCCATCCTGCAGTTTTTGTCTTCTCCTGGCATCCCTGG  
 GTTGGAGGCTTATCACATTTGGCTGTCAATACCTCTTTGCCTCATTACATCACTGCAGTCC  
 TGGGAAACAGCATCCTGATAGTGGTTATTGTTCATGGAACGTAACCTTCATGTGCCCATGTA  
 TTTCTTCTCTCAATGCTGGCCGTCATGGACATCCTGCTGTCTACCACCACTGTGCCCAAGG  
 CCTAGCCATCTTTGGCTTCAAGCACATAACATTGCTTTTGTATGCCTGTGTACCCAAGGC  
 TTCTTTGTCCATATGATGTTTGTGGGGAGTCAGCTATCCTGTTAGCCATGGCCTTTGATCG  
 25 TTTGTGGCCATTTGTGCCCCACTGAGATATACAACAGTGCTAACATGGCCTGTTGTGGGG  
 AGGATTGCTCTGGCCGTCATACCCGAAGCTTCTGCATCATCTTCCCAGTCATATTCTTGCT  
 GAAGCGGCTGCCCTTCTGCCTAACCAACATTGTTCTCCTCACTCCTACTGTGAGCATATTGGA  
 GTGGCTCGTTTAGCCTGTGCTGACATCACTGTAAACATTGGTATGGCTTCTCAGTGCCCAT  
 TGTTCATGGTCATCTTGGATGTTATCCTCATCGCTGTGTCTTACTCACTGATCCTCCGAGCAG  
 30 TGTTTCGTTTGCCCTCCCAGGATGCTCGGCACAAGGCCCTCAGCACTTGTGGCTCCCACCT  
 CTGTGTCATCCTTATGTTTTATGTTCCATCCTTCTTTACCTTATTGACCCATCATTTTGGGCG  
 TAATATTCCTCAACATGTCCATATCTTGTGGCCAATCTTTATGTGGCAGTGCCACCAATGC  
 TGAACCCCATTTGTCTATGGTGTGAAGACTAAGCAGATACGTGAGGGTGTAGCCCAACGGTT  
 CTTTGACATCAAGACTTGGTGCTGTACCTCCCTCTGGGCTCATGA (SEQ ID NO: 320)

35

**AOLFR175 sequences:**

MHFLSQNDLNLNIPHLCLHRHSVIAGAFTIHRHMKIFNSPNSSTFTGFILLGFPCEPREGQILLFV  
 LFTVVYLLTLMGNGSLICAVHWDQRLHAPMYILLANFSLEICYVTSTVPSMLANFLSDTKISF  
 SGCFLOFYFFFLSLGSTECFFLAVMAFDRYLAICRPLRYPTIMTRRLCTNLVNCWVLGFIWFLPI  
 40 VNISQMSFCGSRIIDHFLCDPAPLLTLCKKGPVIELVFSVLSPLPVFMLFLFIVGSYALVRAVL  
 RVPSAAGRRKAFSTCGSHLAVVSLFYGSVLVVMYGSPPSKNEAGKQKTVTLFYSVVTPLLNPVI  
 YSLRNKDMRKALKKFWGT (SEQ ID NO: 321)

ATGCATTTTCTTTCCCAAAATGATTTAAATATAAATCTGATTCCCCATCTATGTTTGCACCG  
 TCATTAGTAATTGCTGGTGCTTTTACAATTACAGGCACATGAAAATCTTCAACAGCCCC  
 AGCAACTCCAGCACCTCACTGGCTTCATCCTCCTGGGCTTCCCTTGCCCCAGGGAGGGGC  
 AGATCCTCCTCTTTGTGCTCTTCACTGTTGTTTACCTCCTGACCCCTCATGGGCAATGGTTCC  
 ATCATCTGTGCTGTGCACTGGGATCAGAGACTCCACGCCCCCATGTACATCCTGCTCGCCA  
 ACTTCTCCTTCTTGGAGATATGTTATGTACCTCCACAGTCCCCAGCATGCTGGCCAACTTC  
 50 CTCTCTGACACCAAGATCATCTCGTTCTCTGGCTGCTTCCCTCCAGTTCTACTTTTCTCTCC  
 TTGGGCTCTACAGAATGCTTTTCTGGCAGTTATGGCATTGATCGATACCTTGCCATCTG  
 TCGGCTCTACGCTATCCAACCATTATGACCAGACGTCTCTGTACCAATCTTGTGGTCAATT  
 GCTGGGTACTTGGTTTCACTGGTTCTTGATTCTATCGTCAACATCTCCCAAATGTCCTTC  
 TGTGGATCTAGGATTATTGACCACTTCTATGTGACCCAGCTCCTCTTCTAACTCTCACTTG  
 55 CAAAAAAGGCCCTGTGATAGAGCTTGTCTTTTCTGTCTTAAGTCTCTGCCTGTCTTTATGC  
 TCTTTCTCTTCAATTGTGGGGTCTATGCTCTGGTCTGTGAGAGCTGTGTTGAGGGTCCCTTCA



GCAGCTGGGAGAAGAAAGGCTTTCTCCACCTGTGGGTCTCACCTGGCTGTGGTTTCACTGT  
TCTACGGCTCAGTACTGGTCATGTATGGGAGCCACCATCTAAGAATGAAGCTGGAAAGC  
AGAAGACTGTGACTCTGTTTTATTCTGTTGTACCCCACTGCTTAACCCTGTGATATATAGT  
CTTAGGAACAAAGATATGAGAAAAGCTCTGAAGAAATTTTGGGGAACATAA (SEQ ID NO:  
5 322)

**AOLFR176 sequences:**

MFFIIHSLVTSVFLTALGPQNRTMHFVTEFVLLGFHGGQREMQSCFFSFLVLYLLTLLGNGAIVC  
AVKLDRLHTPMYILLGNFAFLEIWYISSTVPNMLVNILSEIKTISFSGCFLQFYFFFSLGTTECF  
10 LSV MAYDRYLAICRPLHYPSIMTGKFCILVCVCWVGGLCYPVPIVLISQLPFCGPNIIDHLVCD  
PGPLFALACISAPSTELICYTFNSMIFGPFLSILGSYTLVIRAVLCIPSGAGRTKAFSTCGSHLMV  
VSLFYGTLMVMYVSPTSNGPAGMQKITLVYTAMTFLNPLIYSLRNKDMKDALKRVLGLTVS  
QN (SEQ ID NO: 323)

15 ATGTTCTTTATTATTCACTCTTTGGTTACTTCTGTTTTTCTAACAGCTTTGGGACCCAGAA  
CAGAACAATGCATTTTGTGACTGAGTTTGTCTCCTGGGTTTCCATGGTCAAAGGGAGATG  
CAGAGCTGCTTCTTCTCATTCACTCCTGGTTCTCTATCTCCTGACACTGCTAGGGAATGGAGC  
TATTGTCTGTGCAGTAAAATTGGACAGGCGGCTCCACACACCCATGTACATCCTTCTGGGA  
AACTTTGCCCTTTCTAGAGATCTGGTACATTTCTCCTCACTGTCCCAAACATGCTAGTCAATAT  
20 CCTCTCTGAGATTAAACCCTCTCCTTCTCTGGTTGCTTCTGCAATTCTATTTCTTTTTTTC  
ACTGGGTACAACAGAGTGTCTTTTATCAGTTATGGCTTATGATCGGTACCTGGCCATC  
TGTCGTCCATTACACTACCCCTCCATCATGACTGGGAAGTTCTGTATAATTCTGGTCTGTGT  
ATGCTGGGTAGGCGGATTTCTCTGCTATCCAGTCCCTATTGTTCTTATCTCCCAACTTCCCT  
TCTGTGGGCCCAACATCATTGACCACTTGGTGTGTGACCCAGGCCATTGTTTGCACCTGGC  
25 CTGCATCTCTGCTCCTTCCACTGAGCTTATCTGTTACACCTTCAACTCGATGATTATCTTTG  
GGCCCTTCTCTCCATCTTGGGATCTTACACTCTGGTCATCAGAGCTGTGCTTTGTATTCCC  
TCTGGTGTGGTGAAGCTTTCTCCACATGTGGGTCCCACTAATGGTGGTGTCTC  
TATTCTATGGAACCTTATGGTGATGTATGTGAGCCCAACATCAGGGAACCCAGCAGGAAT  
GCAGAAGATCATCACTCTGGTATACACAGCAATGACTCCATTCTTAAATCCCCTTATCTAT  
30 AGTCTTCGAAACAAAGACATGAAAGATGCTCTAAAGAGAGTCTCTGGGGTTAACAGTTAGC  
CAAACTGA (SEQ ID NO: 324)

**AOLFR177 sequences:**

MSFFFDLRLPMNRSATHIVTEFILLGFPGCWKIQIFLSLFLVIYVLTLLGNGAIYAVRCNPLH  
35 TPMYFLLGNFAFLEIWYVSSTIPNMLVNILSKTKAISFSGCFLQFYFFFSLGTTECLFLAVMAYD  
RYLAICHPLQYPAIMTVRFCKLVSFCWLIGFLGYPIFYISQLPFCGPNIIDHFLCDMDPLMAL  
SCAPAPITECIFYTQSSLVLFSTSMYILRSYILLTAVFQVPSAAGRRKAFSTCGSHLVVVSFLFYG  
TVMVMYVSPTYGIPTLLQKILTVSVTTPFLNPLIYTLRNKDMKLLALRNVLFGMRIRQNS  
(SEQ ID NO: 325)

40 ATGTCTTTCTTCTTTGTAGACTTAAGACCCATGAACAGGTCAGCAACACACATCGTGACAG  
AGTTTATTCTCCTGGGATTCCCTGGTTGCTGGAAGATTCAGATTTTCTCTCTCATTTGTT  
TTGGTGATTTATGTCTTGACCTTGCTGGGAAATGGAGCCATCATCTATGCAAGTGAGATGCA  
ACCCACTACTACACACCCCATGTACTTTCTGCTGGGAAATTTGCCTTCTTGTAGATCTGG  
45 TATGTGTCTCCTCACTATTCTTAACATGCTAGTCAACATTCTCTCAAGACCAAGGCCATCTC  
ATTTTCTGGGTGCTTCTCCTCAGTTCTATTCTTCTTTTCACTGGGAACAAGTGAATGTCTCT  
TTCTGGCAGTAATGGCTTATGATCGATACCTGGCCATCTGCCACCCACTGCAGTACCCCTGC  
CATCATGACTGTAAGGTTCTGTGGTAAGCTGGTGTCTTTCTGTTGGCTTATTGGATTCTTGG  
GATACCCAATTTCCATTTTCTACATCTCCCAACTCCCTTCTGTGGTCCCTAATATCATTGAT  
50 CACTTCTGTGTGACATGGACCCATTGATGGCTCTATCCTGTGCCCCAGCTCCCACTAAGT  
AATGTATTTTCTATACTCAGAGCTCCCTTGCTCTTTTCACTAGTATGTACATTCTTCGA  
TCCTATATCCTGTACTAAACAGCTGTTTTCAGGTCCCTTCTGCAGCTGGTCGGAGAAAG  
CCTTCTCTACCTGTGGTCTCATTGGTTGTGGTATCTCTTTTCTATGGGACAGTCATGGTA  
ATGTATGTAAGTCTACATATGGGATCCCAACTTTATTGCAGAAGATCCTCACACTGGTAT  
55 ATTCAGTAACGACTCCTCTTTTAACTCTGATCTATACTCTTCGTAATAAGGACATGAAA

CTCGCTCTGAGAAATGTCCTGTTTGAATGAGAATTCGTCAAATTCGTGA (SEQ ID NO: 326)

**AOLFR178 sequences:**

5 MVGANHSVVSEFVFLGLTNSWEIRLLLLVFSSMFYMASMMGNSLILLTVTSDPHLHSPMYFLL  
ANLSFIDLGVSSVTSPKMIYDLFRKHEVISFGGCIQIFFIHVIGGVEMVLLIAMAFDRYVAICKP  
LQYLTIMSPRMCMFFLVAAWVTGLIHSVVQLVFVNLPCGPNVSDSFYCDLPRFIKLACTDSY  
RLEFMVTANSFISLGSFFILIISYVVILTVLKHSSAGLSKALSTLSAHVSVVVLFPGPLIFVYTW  
PSPSTHLDKFLAIFDAVLTPVLNPIYTFRN (SEQ ID NO: 327)

10 ATGGTTGGGGCAAATCACTCCGTGGTGTGACAGTTTGTGTTCCCTGGGACTCACCAATTCCT  
GGGAGATCCGACTTCTCCTCCTTGTGTTCTCCTCCATGTTTACATGGCCAGTATGATGGGA  
AACTCTCTCATTTTGTCTACTGTGACTTCTGACCCCTCACTTGCACTCCCCCATGTATTTTCT  
GTTAGCCAACCTCTCCTTCATTGACCTGGGTGTTTCTCTGTCACTTCTCCCAAAATGATTT  
15 ATGACCTGTTTCAAGAACGACGAAGTCATCTCCTTTGGAGGCTGCATCGCTCAAATCTTCTT  
CATCCACGTCAATTGGCGGTGTGGAGATGGTGTCTCATAGCCATGGCCTTTGACAGATAT  
GTGGCCATATGTAAGCCCTCCAGTACCTGACCATTAAGAGCCCAAGAATGTGCATGTTCT  
TCTTAGTGGCTGCTGGGTGACCGGCCCTTATCCACTCTGTAGTTCAATTGGTTTTTGTAGTA  
AACTTGCCCTTCTGTGGTCTAATGTATCGGACAGCTTTTACTGTGACCTTCTCGGTTTCT  
20 CAAACTTGCTGCACAGACAGCTACCGACTGGAGTTCATGGTTACAGCCAACAGTGGATTC  
ATCTCTCTGGGCTCCTTCTTCATACTGATCATTTCTATGTGGTCATCATTCTCACTGTTCT  
GAAACACTCTTCAGCTGGTTTATCCAAGGCTCTGTCCACCCTTTAGCTCACGTCACTGTG  
GTAGTTTTGTTCTTTGGTCTTTGATTTTTGTCTATACGTGGCCATCTCCCTCCACACACCT  
GGATAAGTTTCTGGCCATCTTTGATGCAGTTCTCACTCCTGTTTTAAATCCTATCATCTACA  
25 CATTCAAGGAATTGA (SEQ ID NO: 328)

**AOLFR179 sequences:**

MNGMNHHSVVSEFVFMGLTNSREIQLLLVFVSLFYFASMMGNLVIVFTVTMDAHLHSPMYFLL  
ANLSIIDMAFCSITAPKMICDIFKKHKAISFRGCITQIFFSHALGGTEMVLLIAMAFDRYMAICKP  
30 LHYLTIMSPRMCLYFLATSSIIGLIHSVLVQLVFVDLPFCGPNIFDSFYCDLPRLLRLACTNTQEL  
EFMVTVNSGLISVGSFVLLVISYIFLFTVWKHSSGGLAKALSTLSAHVTVVILFFGPLMFFYTW  
PSPTSHLDKYLAFDAFITPFLNPVIYTFRNKDMKVAMRRLCSRLAHFTKIL (SEQ ID NO: 329)

35 ATGAATGGAATGAATCACTCTGTGGTATCAGAATTTGTATTTCATGGGACTCACCAACTCAC  
GGGAGATTACGCTTCTACTTTTTGTTTTCTCTTTGTTGTTCTACTTTGCGAGCATGATGGGA  
AACCTTGTCATTGTATTCACTGTAAACCATGGATGCTCATCTGCACTCCCCCATGTATTTCT  
CCTGGCTAACCTCTCAATCATTGATATGGCATTTTGTCTCAATTACAGCCCCTAAGATGATTT  
GTGATATTTTCAAGAAACACAAGGCCATCTCCTTTGCGGGATGTATTACTCAGATCTTCTT  
TAGCCATGCTCTTGGGGGCACTGAGATGGTGTCTCATAGCCATGGCCTTTGACAGATAC  
40 ATGGCCATATGTAAACCTCTCCACTACCTGACCATCATGAGCCCAAGAATGTGTCTATACT  
TTTTAGCCACTTCTCTATCATTGGCCTTATCCACTCATTGGTCCAATTAGTTTTTGTGGTA  
GATTACCTTTTTGTGGTCTTAATATCTTTGACAGTTTTTACTGTGATCTCCCTCGGCTCCT  
CAGACTTGCTGTACCAACACCCAAGAAGTGGAGTTCATGGTCACTGTCAATAGTGGACTC  
ATTTCTGTGGGCTCCTTTGTCTTGCTGGTAATTTCTACATCTTCATTCTGTTCACTGTTTG  
45 GAAACATTCTTCTGGTGGTCTAGCCAAGGCCCTCTCTACCCTGTGAGCTCATGTCACTGTG  
GTCATCTTGTCTTTGGGCCACTGATGTTTTTCTACACATGGCCTTCTCCACATCACACCT  
GGATAAATATCTTGCTATTTTGTATGCATTTATTACTCCTTTTCTGAATCCAGTTATCTACA  
CATTCAAGGAACAAAGACATGAAAGTGGCAATGAGGAGACTGTGCAGTCGTCTTGCGCATT  
TTACAAAGATTTTGTA (SEQ ID NO: 330)

50

**AOLFR180 sequences:**

MTNKMAYAIYIKNLNYFSFLIVQCLQPTMAIFNNTTSSSNFLLTAFPGLECAHVWISIPVCCLYTI  
ALLGNSMFLVIITKRRLHKPMYYFLSMLAAVDLCLTTTLPTVLGVLFHAREISFKACFIQMF  
FVHAFSLLESSVLVAMAFDRFVAICNPLNYATILTDRMVLVIGLVICIRPAVFLPLLVAINTVSF  
55 HGGHELSHPFYHPEVIKYTYSKPWISSFWGLFLQLYLNGTDVLFILFSYVLILRTVLGIVARKK

QQKALSTCVCHICAVTIFYVPLISLSLAHRLFHSTPRVLCSTLANIYLLPPVLNPIIYSLKTKTIR  
QAMFQLLQSKGSWGFNVRGLRGRWD (SEQ ID NO: 331)

5 ATGACTAATAAAATGTATGCTATATATATAAAGAATCTTAATTATTTTTCTTTCCTCATAGT  
TCAGTGTCTTCAACCAACCATGGCAATATTCAATAACACCACTTCGTCTTCCTCAAACCTTCC  
TCCTCACTGCATTCCCTGGGCTGGAATGTGCTCATGTCTGGATCTCCATTCCAGTCTGCTGT  
CTCTACACCAATTGCCCTCTTGGGAAACAGTATGATCTTTCTTGTCATCATTACTAAGCGGA  
GACTCCACAAACCCATGTATTATTTCTCTCCATGCTGGCAGCTGTTGATCTATGTCTGACC  
ATTACGACCCCTTCCCACTGTGCTTGGTGTCTCTGGTTTCATGCCCGGGAGATCAGCTTTAA  
10 AGCTTGCTTCATTCAAATGTTCTTTGTGCATGCTTTCTCCTTGCTGGAGTCTCGGTGCTGG  
TAGCCATGGCCTTTGACCGCTTCGTGGCTATCTGTAACCCACTGAACTATGCTACTATCCTC  
ACAGACAGGATGGTCTGCTGATAGGGCTGGTCATCTGCATTAGACCAGCAGTTTTCTTAC  
TTCCCTTCTTGTAGCCATAAACACTGTGTCTTTTCATGGGGGTACGAGCTTTCCCATCCA  
TTTTGCTACCACCCAGAAGTGATCAAATACACATATTCCAAACCTTGGATCAGCAGTTTTT  
15 GGGGACTGTTTCTTCAGCTCTACCTGAATGGCACTGACGTATTGTTTATTCTTTCTCCTAT  
GTCCTGATCCTCCGTACTGTTCTGGGCAATTGTGGCCCGAAAGAAGCAACAAAAAGCTCTCA  
GCACCTGTGTCTGCACATCTGTGCAGTCACTATTTCTATGTGCCACTGATCAGCCTCTCT  
TTGGCACACCGCCTCTTCCACTCCACCCCAAGGGTGCTCTGTAGCACTTTGGCCAATATTTA  
TCTGCTCTTACCACCTGTGCTGAACCCTATCATTTACAGCTTGAAGACCAAGACAATCCGC  
20 CAGGCTATGTTCCAGCTGCTCCAATCCAAGGGTTCATGGGGTTTAAATGTGAGGGGTCTTA  
GGGAAGATGGGATTGA (SEQ ID NO: 332)

**AOLFR181 sequences:**

25 MSVLNNSEVKLFLLIGIPGLEHAHIWFSIPICLMYLLAIMGNCTILFIKTEPSLHEPMYYFLAML  
AVSDMGLSLSSLPTMLRVFLFNAMGISPNACFAQEFFIHGFTVMESSVLLIMSLDRFLAIHNPLR  
YSSILTSNRVAKMGLILAIRSILLVIPFPFTLRRLKYCQKNLLSHSYCLHQDTMKLACSDNKTNV  
IYGFIALCTMLDLALIVLSYVLILKTLISLASLAERLKAINTCVSHICAVLTFYVPITLAAMHHF  
AKHKSPLVVILIADMFLVPLMNPVIVYCVKTRQIWEKILGKLLNVCGR (SEQ ID NO: 333)

30 ATGTCTGTTCTCAATAACTCCGAAGTCAAGCTTTTCCTTCTGATTGGGATCCCAGGACTGG  
AACATGCCACATTTGGTTCTCCATCCCCATTTGCCTCATGTACCTGCTTGCCATCATGGGC  
AACTGCACCATTTCTCTTTATTATAAAGACAGAGCCCTCGCTTCATGAGCCCATGTATTATT  
CCTTGCCATGTTGGCTGTCTCTGACATGGGCCTGTCCCTCTCCTCCCTTCCATACCATGTTGA  
GGGTCTTCTTGTTCAATGCCATGGGAATTTACCTAATGCCTGCTTTGCTCAAGAATTCCTC  
35 ATTCATGGATTCATGTCATGGAATCCTCAGTACTTCTAATTATGTCTTTGGACCGCTTTCT  
TGCCATTACAATCCCTTAAGATACAGTTCTATCCTCACTAGCAACAGGGTTGCTAAAAATG  
GGACTTATTTTAGCCATTAGGAGCATTCTCTTAGTGATTCCATTTCCCTTACCTTAAGGAG  
ATTAATAATATTGTCAAAAGAATCTTCTTTCTCACTCATACTGTCTTCATCAGGATACCATGA  
AGCTGGCCTGCTCTGACAACAAGACCAATGTCATCTATGGCTTCTTCATTGCTCTCTGTACT  
40 ATGCTGGACTTGGCACTGATTGTTTTGTCTTATGTGCTGATCTTGAAGACTATACTCAGCAT  
TGCATCTTTGGCAGAGAGGCTTAAGGCCCTAAATACCTGTGTCTCCCACATCTGTGCTGTG  
CTCACCTTCTATGTGCCCATCATCACCTGGCTGCCATGCATCACTTTGCCAAGCACAAAA  
GCCCTCTTGTTGTGATCCTTATTGCAGATATGTTCTTGTGGTGCCGCCCTTATGAACCCC  
ATTGTGTACTGTGTAAAGACTCGACAAATCTGGGAGAAGATCTTGGGGAAGTTGCTTAAT  
45 GTATGTGGGAGATAA (SEQ ID NO: 334)

**AOLFR182 sequences:**

50 MTLGSLGNSSSVSATFLLSGIPGLERMHIWISIPCFMYLVSIPGNCTILFIKTERSLHEPMYFL  
SMLALIDLGLSLCTLPTVLGIFWVGAREISHDACFAQLFFIHCFSFLESSVLLSMAFDRFVAICHP  
LHYVSILTNTVIGRIGLVSLGRSVALIFPLPFMLKRFPCGSPVLSHSYCLHQEVMKLACADMK  
ANSIYGMFVIVSTVGIDSLILFSYALILRTVLSIASRAERFKALNTCVSHICAVLLFYTPMIGLSV  
IHRFGKQAPHLVQVVMGFMYLLFPPVMNPVIVSVKTKQIRDRVTHAFY (SEQ ID NO: 335)

55 ATGACCCTGGGATCCCTGGGAAACAGCAGCAGCAGCGTTTCTGCTACCTTCTGCTGAGTG  
GCATCCCTGGGCTGGAGCGCATGCACATCTGGATCTCCATCCCACTGTGCTTCATGTATCT  
GGTTTCCATCCCGGGCAACTGCACAATCTTTTTATCATTAAAAACAGAGCGCTCACTTCAT

GAACCTATGTATCTCTTCCTGTCCATGCTGGCTCTGATTGACCTGGGTCTCTCCCTTTGCAC  
 TCTCCCTACAGTCCTGGGCATCTTTTGGGTGGAGCACGAGAAATTAGCCATGATGCCTGC  
 TTTGCTCAGCTCTTTTTTCACTGCTTCTCCTTCCTCGAGTCCTCTGTGCTACTGTCTATG  
 GCCTTTGACCGCTTTTGTGGCTATCTGCCACCCCTTGCACTATGTTTCCATTCTCACCAACAC  
 5 AGTCATTGGCAGGATTGGCCTGGTCTCTCTGGGTGCTAGTGTAGCACTCATTTTTCCATTA  
 CCTTTTATGCTCAAAAGATTCCCCTATTGTGGCTCCCCAGTTCTCTCACATTCTTATTGTCT  
 CCACCAAGAAAGTGATGAAATTGGCCTGTGCCGACATGAAGGCCAACAGCATCTACGGCAT  
 GTTTGTCATCGTCTCTACAGTGGGTATAGACTCACTGCTCATCCTCTTCTCTTATGCTCTGA  
 TCCTGCGCACCGTGCTGTCCATCGCCTCCAGGGCTGAGAGATTCAAGGCCCTTAACACCTG  
 10 TGTTCACCATCTGTGCTGTGCTGCTCTTCTACACTCCCATGATTGGCCTCTCTGTCTATCC  
 ATCGCTTTGGAAAGCAGGCACCCACCTGGTCCAGGTGGTTCATGGGTTTCATGTATCTTCT  
 CTTTCTCCTGTGATGAATCCCATTTGTCTACAGTGTGAAGACCAACAGATCCGGGATCGA  
 GTGACGCATGCCTTTTGTACTAA (SEQ ID NO: 336)

15 **AOLFR183 sequences:**

MTNLNASQANHRNFILTGIPGTPDKNPWLAFPLGFLYTLTLLGNGTILAVIKVEPSLHEPTYFYFL  
 SILALTDVLSMSLPSMLSIYWFNAPQIVFDACIMQMFFIHVFGIVESGVLVSMADFDRFVAIRN  
 PLHYVSILTHDVIRKGTISVLTRA VCVVPFPFLIKCLPFCHSNVLSHSYCLHQNMMLACASTR  
 20 INSLYGLIVIFTLGLDVLLTLLSYVLTKTVLGIVSRGERLKTLSLCLSHMSTVLLFYVPMGA  
 ASMHRFWHEHLSPVVHVMADIYLLLPVLNPIVYSVKTKQI (SEQ ID NO: 337)

ATGACGAACTTGAATGCATCACAGGCCAACCACCGTAACTTCATTCTGACAGGTATCCCAG  
 GAACGCCAGACAAGAACCCATGGTTGGCCTTTCCCTGGGATTTCTCTACACACTCACACT  
 CCTGGGAAATGGTACCATCCTAGCTGTCATCAAGGTGGAGCCAAGTCTCCATGAGCCACG  
 25 TATTACTTCCTTTCTATCTTGGCTCTCACTGACGTTAGTCTCTCCATGTCCACCTTGCCCTCC  
 ATGCTCAGCATCTACTGGTTTAATGCCCTCAGATTGTTTTTGATGCATGCATCATGCAGAT  
 GTTCTTCATCCATGTATTTGGAATAGTAGAATCAGGAGTCCTAGTGTCCATGGCCTTTGAC  
 AGATTGTGGCCATCCGAAACCCATTACACTATGTTTCCATCCTCACTCACGATGTTATTG  
 AAAGACTGGAATATCTGTCTCACCCTGGGAGTCTGTGTGGTATTCCCTGTGCCCTTCCTT  
 30 ATAAAGTGCTACCCCTCTGCCATTCCAATGTCTTGTCTCATTACACTGTCTTCACCAAAA  
 CATGATGCGGCTAGCTTGTGCCAGCACCCGCATCAACAGCCTCTACGGCCTCATCGTCGTC  
 ATCTTACACTGGGGCTCGATGTTCTCTCACTCTACTGTCTTATGTACTACCCTGAAGAC  
 TGTGCTGGGCATTGTCTCCAGAGGTGAAAGGCTGAAAACCCTCAGCACATGCCTCTCTCAC  
 ATGTCTACCGTGCTCCTCTTCTATGTTCCCTTTTATGGGTGCTGCCCTCCATGATCCACAGATT  
 35 TTGGGAGCATTTATCACCAGTAGTGCACATGGTCATGGCTGATATACCTACTGCTCCCG  
 CCTGTGCTAAACCCCATTTGTCTACAGTGTGAAGACCAAGCAAATTTGA (SEQ ID NO: 338)

**AOLFR184 sequences:**

MSTLPTQIAPNSSTSMAPTFLLVGMPGLSGAPSWWTLPLIAVYLLSALGNGTILWIALQPALHR  
 40 PMHFFLFLLSVSDIGLVTALMPTLLGIALAGAHTVPASACLLQMVFHVFVSMESSVLLAMSID  
 RALAICRPLHYPALLTNGVISKISLAISFRCLGLHLPLPFLLAYMPYCLPQVLTHSYCLHPDVARL  
 ACPEAWGAAYSLFVLSAMGLDPLLIFFSYGLIGKVLQGVESREDRWKAGQTCAAHLAVLLF  
 YIPMILLALINHPPLPITQHTHTLLSYVHFLPLPLINPLYSVKMKEIRKRLNRLQPRKVGGAQ  
 (SEQ ID NO: 339)

45 ATGTCAACATTACCAACTCAGATAGCCCCAATAGCAGCACTTCAATGGCCCCCACCTTCT  
 TGCTGGTGGGCATGCCAGGCCTATCAGGTGCACCCTCCTGGTGGACATTGCCCTCATTGC  
 TGTCTACCTTCTCTGCACTGGGAAATGGCACCATCCTCTGGATCATTGCCCTGCAGCCC  
 GCCCTGCACCGCCCAATGCACTTCTTCTCTTCTTGTCTAGTGTGTCTGATATTGGATTGGT  
 50 CACTGCCCTGATGCCACACTGCTGGGCATCGCCCTTGTGGTGCTCACACTGCTCCCTGCC  
 TCAGCCTGCCCTTCTACAGATGGTTTTTATCCATGTCTTTCTGTCTATGGAGTCTCTGTCTT  
 GCTCGCCATGTCCATTGATCGGGCACTGGCCATCTGCCGACCTCTCCACTACCCAGCGCTC  
 CTCACCAATGGTGTAATTAGCAAAATCAGCCTGGCCATTTCTTTTCGATGCCTGGGTCTCC  
 ATCTGCCCTGCCATTCTGTGCTGGCCTACATGCCCTACTGCCTCCCACAGGTCCTAACCCAT  
 55 TCTTATTGCTTGCATCCAGATGTGGCTCGTTTGGCCTGCCCAGAAGCTTGGGGTGCAGCCT  
 ACAGCCTATTTGTGGTTCTTTCAGCCATGGGTTTGGACCCCTGCTTATTTCTTCTCCTAT

GGCCTGATTGGCAAGGTGTTGCAAGGTGTGGAGTCCAGAGAGGATCGCTGGAAGGCTGGT  
CAAACCTGTGCTGCCACCTCTCTGCAGTGCTCCTCTTCTATATCCCTATGATCCTCCTGGC  
ACTGATTAACCATCCTGAGCTGCCAATCACTCAGCATACCCATACTCTTCTATCCTATGTCC  
ATTTCCCTTCTCCTCCATTGATAAACCCCTATTCTCTATAGTGTCAGATGAAGGAGATTAGA  
5 AAGAGAATACTCAACAGGTTGCAGCCCAGGAAGGTGGGTGGTGTCTCAGTGA (SEQ ID NO:  
340)

**AOLFR185 sequences:**

MFYPILNDISTKNNNSNIMSCCNILFIKTVEILVYNQTSQSPWYPIVPSKSLVYNNNTCFDCYHLQR  
10 VDCVPSRDHINQSMVLASGNSSSHPVSEILLGIPGLESQLWIAFPFCATYAVAVVGNITLLHVIR  
IDHTLHEPMYFLAMLATDLVLSSTQPKMLAIFWFHAHEIQYHACLIQVFFIHFSSVESGVL  
MAMALDCYVATCFPLRHSSILTPSVVIKLGTTVMRLRGLLVVSPFCFMVSRMPFCQHQAIPQSYC  
EHMAVLKLVCAOTSISRGYGLFVAFSVAGFDMIVIGMSYVMILRAVLQLPSGEARLKAFSTRA  
SHICVILALYIPALFSFLTFRFGHDVPRVVHILFANLYLLPPMLNPIYGVRTKQIGDRVIQGCCG  
15 NIP (SEQ ID NO: 341)

ATGTTCTACCCCATTTTGAATGACATAAGTACGAAAAACAACAGTAACATCATGTCTGTT  
GTAACATATTATTTATTAACAGTTGAAATATTCTAGTTTATAATCAAACCAATCACC  
20 CTGGTATCCAATAGTCCCATCCAAAAGCCTTGATATAATAAATAACACTTGTTTTGATTGTT  
ATCATCTGCAGAGAGTAGATTGCGTTCCAGCAGAGACCATATTAACAGTCCATGGTGCT  
GGCTTCAGGGAACAGCTCTTCTCATCCTGTGTCCTTCATCCTGCTTGGAATCCAGGCCTG  
GAGAGTTTCCAGTTGTGGATTGCCTTTCCGTTCTGTGCCACGTATGCTGTGGCTGTTGTTGG  
AAATATCACTCTCCTCCATGTAATCAGAATTGACCACACCCTGCATGAGCCCATGTACCTC  
TTTCTGGCCATGCTGGCCATCACTGACCTGGTCTCTCCTCCTCCACTCAACCTAAGATGTT  
25 GGCCATAATTCTGGTTTCATGCTCATGAGATTAGTACCATGCCTGCCTCATCCAGGTGTTCT  
TCATCCATGCCTTTTCTTCTGTGGAGTCTGGGGTGCTCATGGCTATGGCCCTGGACTGCTAC  
GTGGCTACCTGCTTCCCACTCCGACACTCTAGCATCCTGACCCCATCGGTCTGTATCAAAC  
TGGGGACCATCGTGATGCTGAGAGGGCTGCTGTGGGTGAGCCCTTCTGCTTCATGGTGTC  
TAGGATGCCCTTCTGCCAACACCAAGCCATTCCCCAGTCATACTGTGAGCACATGGCTGTG  
30 CTGAAGTTGGTGTGTGCTGATACAAGCATAAGTCGTGGGTATGGGCTCTTTGTGGCCTTCT  
CTGTGGCTGGCTTTGATATGATTGTCTAGTATGTCATACGTGATGATTTGAGAGCTGT  
GCTTCAGTTGCCCTCAGGTGAAGCCCGCTCAAAGCTTTTAGCACACGTGCCTCCCATATC  
TGTGTCTCTTGGCTCTTTATATCCAGCCCTTTTTTCTTCTCCTCACCTACCGCTTTGGCCAT  
GATGTGCCCCGAGTTGTACACATCCTGTTTGCTAATCTCTATCTACTGATACCTCCCATGCT  
35 CAACCCCATCATTTATGGAGTTAGAACCAAACAGATCGGGGACAGGGTTATCCAAGGATG  
TTGTGGAAACATCCCCTGA (SEQ ID NO: 342)

**AOLFR186 sequences:**

MSNASLVTAFLITGLPHAPGLDALLFGIFLVVYVLTVLGNLLILLVIRVDSHLHTPMYYFLTNL  
40 FIDMWFSTVTVPKMLMTLVSPSGRAISFHSCVAQLYFFHFLGSTECFLYTVMSYDRYLAI  
RYTSMMSGSRCALLATGTWLSGLHSAVQTILTFHLPYCGPNQIQHYFCDAPPILKLACADTSA  
NVMVIFVDIGIVASGCFVLIVLSYVSIVCSILRIRTS DGRRRAFQTCASHCIVVL CFFVPCVVIYLR  
PGSMDAMDGVVAIFYTVLTPLLNPVVYTLRNKEVKKA VLKLRDKVAHPQRK (SEQ ID NO:  
343)

45 ATGTCCAACGCCAGCCTCGTGACAGCATTATCCTCACAGGCCTTCCCCATGCCCCAGGGC  
TGGACGCCCTCCTCTTTGGAATCTTCTGGTGGTTTACGTGCTCACTGTGCTGGGGAACCT  
CCTCATCCTGCTGGTGATCAGGGTGGATTCTACCTCCACACCCCATGTACTACTTCTCA  
CCAACCTGTCCTTCATTGACATGTGGTTCTCCACTGTACGGTGCCCAAAATGCTGATGAC  
50 CTGGTGTCCCCAAGCGGCAGGGCTATCTCCTTCCACAGCTGCGTGGCTCAGCTCTATTTT  
TCCACTTCTGGGGAGCACCGAGTGTCTTCTCTACACAGTCATGTCTATGATCGCTACTTG  
GCCATCAAGTTACCCGCTCAGGTACACCAGCATGATGAGTGGGAGCAGGTGTGCCCTCCTGG  
CCACCGGCACTTGGCTCAGTGGCTCTCTGCACTCTGCTGTCCAGACCATATTGACTTTCCAT  
TTGCCCTACTGTGGACCCAACCAGATCCAGCACTACTTCTGTGACGCACCGCCCATCCTGA  
55 AACTGGCCTGTGCAGACACCTCAGCCAACGTGATGGTCATCTTTGTGGACATTGGGATAGT  
GGCCTCAGGCTGCTTTGTCTGATAGTGCTGTCTATGTGTCCATCGTCTGTTCCATCCTGC

GGATCCGCACCTCAGATGGGAGGCGCAGAGCCTTTCAGACCTGTGCCTCCCACTGTATTGT  
GGTCCTTTGCTTCTTTGTTCCCTGTGTTGTCAATTTATCTGAGGCCAGGCTCCATGGATGCCA  
TGGATGGAGTTGTGGCCATTTTCTACACTGTGCTGACGCCCCCTTCTCAACCCTGTTGTGTAC  
ACCCTGAGAAACAAGGAGGTGAAGAAAGCTGTGTTGAAACTTAGAGACAAAGTAGCACAT  
5 CCTCAGAGGAAATAA (SEQ ID NO: 344)

**AOLFR187 sequences:**

MAQVRALHKIMALFSANSIGAMNNSDTRIAGCFLTGPGLLEQLHIWLSIPFCIMYIAALEGNGLI  
CVILSQAILHEPMYIFLSMLASADVLLSTTTMPKALANLWLGYSHSIFDGCCTQKFFIHFLFIHSA  
10 VLLAMAFDRYVAICSPLRYVTILTSKVIKIVTATLSRSFIIMFPSIFLLEHLHYCQINIIAHTFCEH  
MGIAHLSCSDISINVWYGLAAALLSTGLDIMLITVSYIHILQAVFRLLSQDARSKALSTCGSHICV  
ILLFYVPALFSVFAYRFGGRSIPCYVHILLASLYVIPPMLNPVIYGVRTKPILEGAKQMPFSLAK  
GSK (SEQ ID NO: 345)

15 ATGGCACAGGTGAGGGCGCTGCATAAAATCATGGCCCTTTTTTCTGCTAACAGCATAGGTG  
CTATGAACAACCTCTGACACTCGCATAGCAGGCTGCTTCCTCACTGGCATCCCTGGGCTGGA  
GCAACTACATATCTGGCTGTCCATCCCCCTTCTGCATCATGTACATCGCTGCCCTGGAAGGC  
AATGGCATCCTAATTTGTGTATCCTCTCCCAGGCAATCCTGCATGAGCCCATGTACATAT  
TCTTATCTATGCTGGCCAGTGTGTATGTCTTGTCTCTACCACCACCATGCCTAAGGCCCTG  
20 GCCAATTTGTGGCTAGGTTATAGCCACATTTCTTTGATGGCTGCCTCACTCAAAGTTCTT  
CATTCACCTTCTCTTCACTTCACTCTGCTGTCTGCTGGCCATGGCCTTTGACCGCTATGTGG  
CCATCTGCTCCCCCTGCGATATGTCACAATCCTCACAAGCAAGGTCATTGGGAAGATCGT  
CACTGCCACCCTGAGCCGCAGCTTCATCATTATGTTTCCATCCATCTTTCTCCTTGAGCACC  
TGCACATTTGCCAGATCAACATCATTGCACACACATTTTGTGAGCACATGGGCATTGCCCA  
25 TCTGTCTGTTCTGATATCTCCATCAATGTCTGGTATGGGTGGCAGCTGCTCTTCTCTCCA  
CAGGCCTGGACATCATGCTTATTACTGTTTCTACATCCACATCCTCCAAGCAGTCTTCCGC  
CTCCTTTCTCAAGATGCCCGCTCCAAGGCCCTGAGTACCTGTGGATCCCATATCTGTGTAT  
CCTACTCTTCTATGTCCCTGCCCTTTTCTGTCTTTGCTTACAGGTTTGGTGGGAGAAGCA  
TCCCATGCTATGTCCATATTCTCTGGCCAGCCTCTACGTTGTCACTTCTCTATGCTCAAT  
30 CCCGTTATTTATGGAGTGAGGACTAAGCCAATACTGGAAGGGGCTAAGCAGATGTTTCA  
AATCTTGCCAAAGGATCTAAATAA (SEQ ID NO: 346)

**AOLFR188 sequences:**

MFPSLCPVLLVQLPLMNENMQCFVFCSDSLRMMVSRFIHVFPVKMKRIIVGGYSKHFFSN  
35 ELLCVRPWSGKTWSIRHHIFDMELLTNNLKFITDPFVCLRLHLSPTPSEEHMKNKNNVTEFILL  
GLTQNPGEQKVLVFTFLLIYMTIMGNLLIIVTIMASQSLGSPMYFFLASLSFIDTVYSTAFAPK  
MIVDLLSEKKTISFQGCMAQLFMDHLFAGAEVILLVVMAYDRYMAICKPLHELITMNRRCVIL  
MLLAAWIGGFLHSLVQFLFIYQLPFCGPNVIDNFLCDLYPLLKLACTNTYVTLKSMANGGAIC  
AVTFFTILLSYGVILHSLKTQSLEGRKAFYTCASHVTVVILFFVPCIFLYARPNSTFPIDKSMTV  
40 VLTFTTMLNPLIYTLKNAEMKSAMRKLWSKKVSLAGKWLYHS (SEQ ID NO: 347)

ATGTTCCCCTCCCTGTGTCCATGTGTTCTCCTTGTTCAACTCCCCTTATGAATGAGAACAT  
GCAGTGTTTTGTCTTCTGTGATAGTTTGTGAGAATGATGGTTTCCCGCTTCATCC  
ATGTCCCATTTGTAAAAATGAAAAGGATAATTGTGGGAGGATATTCTAAACACTTCTTTTC  
45 TAATGAGCTGCTCTGTGTGAGGCCCTGGTCAGGGAAAACGTGGTCGATAAGGCATCACAT  
TTTTGACATGGAGCTTCTGACAAATAATCTCAAATTTATCACTGACCCCTTTGTTTGTAGGC  
TCCGACACCTGAGTCCAACACCTTCAGAAGAACACATGAAAAATAAGAACAAATGTGACTG  
AATTTATCCTCTTAGGGCTCACACAGAACCTGAGGGGCAAAAGGTTTATTTGTCACATT  
CTTACTAATCTACATGGTGACGATAATGGGCAACCTGCTTATCATAGTGACCATGATGGCC  
50 AGCCAGTCCCTGGGTTCCTCCCTGACTTTTTTCTGGCTTCTTATCATTATCATAGATACCGT  
CTATTCTACTGCATTTGCTCCCAAAATGATTGTTGACTTGCTCTCTGAGAAAAAGACCATIT  
CCTTTCAGGGTTGTATGGCTCAACTTTTTATGGATCATTTATTTGCTGGTGTGAAGTCATT  
CTTCTGGTGGTAATGGCCTATGATCGATACATGGCCATCTGTAAGCCTCTTCATGAATTGA  
TCACCATGAATCGTCGAGTCTGTGTTCTTATGCTGTTGGCGGCCTGGATTGGAGGCTTTCT  
55 TCACTCATGGTTCAATTTCTCTTTATTTATCAGCTCCCTTTCTGTGGACCCAATGTCAATG  
ACAACTTCCTGTGTGATTTGTATCCCTTATTGAAACTTGCTTGACCAATACCTATGTCACT

GGGCTTTCTATGATAGCTAATGGAGGAGCGATTGTGCTGTCACCTTCTTCACTATCCTGC  
 TTTCTATGGGGTCATATTACACTCTCTTAAGACTCAGAGTTTGGAAGGGAAACGAAAAGC  
 TTTCTACACCTGTGCATCCACGTCACCTGTGGTCATTTTATTCTTTGTCCCCTGTATCTTCTT  
 GTATGCAAGGCCCAATTCTACTTTTCCCATTGATAAATCCATGACTGTAGTTCTAACTTTTA  
 5 TAACTCCCATGCTGAACCCACTAATCTATACCCTGAAGAATGCAGAAATGAAAAGTGCCAT  
 GAGGAACTTTGGAGTAAAAAAGTAAGCTTAGCTGGGAAATGGCTGTATCACTCATGA  
 (SEQ ID NO: 348)

**AOLFR189 sequences:**

10 MQQNNVPEFILLGLTQDPLRQKIVFVIFLYMGTVVGNMLIIVTIKSSRTLGSMPYFFLFYLSF  
 ADSCFSTSTAPRLIVDALSEKKIITYNECMTQVFALHLFGCMEIFVLILMAVDYVAICKPLRYP  
 TIMSQQVCHLIVLAWIGSLIHSTAQIILALRLPFCGPYLDHYCCDLQPLLKLACMDTYMINLLL  
 VSNSSGAICSSSMILHSYIVLHSLRNHSAKGKKKALSACTSHIIVVILFFGPCIFYTRPPTTFPMD  
 KMOVAVFYTIGTPFLNPLIYTSEECRSEKCHEK (SEQ ID NO: 349)

15 ATGCAGCAAAATAACAGTGTGCCTGAATTCATACTGTTAGGATTAACACAGGATCCCTTGA  
 GGCAGAAAATAGTGTGTTGTAATCTTCTTAATTTTCTATATGGGAACTGTGGTGGGGAATAT  
 GCTCATTATTGTGACCATCAAGTCCAGCCGGACACTAGGAAGCCCCATGTACTTCTTTCTA  
 TTTTATTTGTCTTTGTCAGATTCTTGCTTTTCAACTTCCACAGCCCCCTAGATTAATTGTGGA  
 20 TGCTCTCTCTGAAAAGAAAATTATAACCTACAATGAGTGCATGACACAAGTCTTTGCACTA  
 CATTTATTTGGCTGCATGGAGATCTTTGTCTCATTTCTCATGGCTGTTGATCGCTATGTGGC  
 CATCTGTAAGCCCTTGCGTTACCCAACCATCATGAGCCAGCAGGTCTGCATCATCCTGATT  
 GTTCTTGCCCTGGATAGGGTCTTTAATACACTCTACAGCTCAGATTATCCTGGCCTTAAGATT  
 GCCTTTCTGTGGACCCTATTTGATTGATCATTATTGCTGTGATTGTCAGCCCTTGTTGAAAC  
 25 TTGCCTGCATGGACACTTACATGATCAACCTGCTGTTGGTGTCTAACAGTGGGGCAATTTG  
 CTCAAGTAGTTTTCATGATTTTGATAATTTTCATATATTGTCATCTTGCATTCACTGAGAAACC  
 ACAGTGCCAAAGGGAAGAAAAAGGCTCTCTCCGCTTGACAGTCTCACATAATTGTAGTCAT  
 CTTATTCTTTGGCCCATGTATATTTCATATATACACGCCCCCGACCACCTTCCCCATGGACA  
 AGATGGTGGCAGTATTTTATACTATTGGAACACCCTTTCTCAATCCACTCATCTACACATCT  
 30 GAGGAATGCAGAAGTGAAAAATGCCATGAGAAAG (SEQ ID NO: 350)

**AOLFR190 sequences:**

MQRSNHTVTEFILLGFTTDPGMQLGLFVFLGVYCLTVVGSSTLIVLICNDSRLHTPMYFVIGN  
 LSLDLWYSSVHTPKILVTCISEDKISIFAGCLCQFFSARLAYSECYLLAAMAYDHYVAISKPLL  
 35 YAQTMPPRLCICLVLYSYTGGFVNAILTSNTFTLDFCGDNVIDDFCDVPPLVKLACSVRESYQ  
 AVLHFLLASNVISPTVLILASYLSIITILRIHSTQGRIKVFSTCSSHLISVTLYYGSILYNYSRPS  
 YSLKRDKMVSTFYTMLFPMNLNPMIYSLRSKDMKDALKKFFKSA (SEQ ID NO: 351)

ATGCAGAGGAGCAATCACACAGTGAAGTTCATCCTGCTGGGCTTCACCACAGATCCAG  
 40 GGATGCAACTGGGCCTCTTTGTGGTGTTCCTGGGTGTGTAAGTGTGACTGTGCTGAGTGTGGTAGGAAG  
 TAGCACCTCATCGTGTGATCTGTAATGACTCCCGCTACACACACCCCATGTATTTGTCA  
 TTGGAAATCTGTCATTTCTGGATCTCTGGATTCTTCTGTCCACACCCCAAAGATCCTAGTG  
 ACCTGCATCTCTGAAGACAAAAGCATCTCCTTTGCTGGCTGCCTGTGTGTCAGTTCTTCTCTGC  
 CAGGCTGGCCTATAGTGAGTGCTACCTACTGGCTGCCATGGCTTATGACCACTACGTGGCC  
 45 ATCTCCAAGCCCCTGCTTTATGCTCAGACCATGCCAAGGAGATTGTGCATCTGTTTGGTTTT  
 ATATTCTATACTGGGGGTTTTGTCAATGCAATAATATTAACCAGCAACACATTCACATTG  
 GATTTTTGTGGTGACAATGTCATTGATGACTTTTTCTGTGATGTTCCACCCCTCGTGAAGCT  
 GGCATGCAGTGTGAGAGAGAGCTACCAGGCTGTGCTGCACTTCCTTCTGGCCTCCAATGTC  
 ATCTCCCCTACTGTGCTCATCCTTGCTCTTACCTCTCCATCATCACCACCATCCTGAGGAT  
 50 CCACTCTACCCAGGGCCGCATCAAAGTCTTCTCCACATGCTCCTCCCACCTGATCTCCGTTA  
 CCTTATACTATGGCTCCATTCTCTACAACACTCTCCCGCCAAGTCCAGCTACTCCCTCAAG  
 AGGCAAAAATGGTTTCTACCTTTTATACTATGCTGTTCCCATGTTGAATCCCATGATCTA  
 CAGTCTGAGGAGTAAAGACATGAAAGACGCTCTGAAAAAATTCTTCAAGTCAGCATAA  
 (SEQ ID NO: 352)

55

**AOLFR191 sequences:**

MTGGGNITEITYFILLGFSDFPRIKVLFTIFLVITYTSLAWNLSLIVLIRMDSHLHTPMYFFLSNLS  
 FIDVCYISSVTPKMLSNLLQEQTTTFVGCIIQYFIFSTMGLSESLMTAMAYDRYAAICNPLLYS  
 SIMSPTLCVWMVLGAYMTGLTASLFQIGALLQLHFCGSNVIRHFFCDMPQLLLSCTDTFFVQV  
 5 MTAILTMFFGIASALVIMISYGYIGISIMKITSAGSPKAFNTCASHLTAVSLFYTSYGIFVYLRSSS  
 GGSSSFDRFASVFYTVVIPMLNPLIYSLRNKEIKDALKRLQKRKCC (SEQ ID NO: 353)

ATGACTGGGGGAGGAAATATTACAGAAATCACCTATTTTCATCCTGCTGGGATTCTCAGATT  
 TTCCCAGGATCATAAAAGTGCTCTTCACTATATTCCTGGTGATCTACATTACATCTCTGGCC  
 10 TGGAACCTCTCCCTCATTGTTTTAATAAGGATGGATTCCCACCTCCATACACCCATGTATTT  
 CTTCTCAGTAACCTGTCCTTCATAGATGTCTGCTATATCAGCTCCACAGTCCCCAAGATGC  
 TCTCCAACCTCTTACAGGAACAGCAAACATCACTTTTGTGGTTGTATTATTTCAGTACTTT  
 ATCTTTTCAACGATGGGACTGAGTGAGTCTTGTCTCATGACAGCCATGGCTTATGATCGTT  
 ATGCTGCCATTTGTAACCCCTGCTCTATTTCATCCATCATGTCAACCCACCTCTGTGTTTGG  
 15 ATGGTACTGGGAGCCTACATGACTGGCCTCACTGCTTCTTTATTCCAAATGGTGCTTTGCT  
 TCAACTCCACTTCTGTGGGTCTAATGTCATCAGACATTTCTTCTGTGACATGCCCCAAGTGT  
 TAATCTTGTCTGTACTGACACTTTCTTTGTACAGGTCATGACTGCTATATTAACCATGTTT  
 TTTGGGATAGCAAGTGCCCTAGTTATCATGATATCCTATGGCTATATTGGCATCTCCATCA  
 TGAAGATCACTTCAGCTAAAGGCAGTCCAAAGGCATTCAACACCTGTGCTTCTCATCTAAC  
 20 AGCTGTTTCCCTCTTCTATACATCAGGAATCTTTGTCTATTTGAGGTCCAGCTCTGGAGGTT  
 CTTCAAGCTTTGACAGATTTGCATCTGTTTTCTACACTGTGGTCATTCCCATGTTAAATCCC  
 TTGATTTACAGTTTGAGGAACAAAGAAATTAAGATGCCTTAAAGAGGTTGCAAAAGAGA  
 AAGTGCTGCTGA (SEQ ID NO: 354)

**AOLFR192 sequences:**

MENNTEVTEFILVGLTDDPELQIPLFVFLFYILITLVGNLGMIELILLDSCLHTPMYFFLSNLSLV  
 DFGYSSAVTPKVMVGFLTGDKFILYNACATQFFFFVAFITAESFLLASMA YDRYAALCKPLHY  
 TTTMTTNVCACLAIGSYICGFLNASIHTGNTFRLSFCRSNVVEHFFCDAPLLTLSCSDNYISEM  
 VIFFVVGFNDFLSILVILISYLFIFITIMKMRSPEGRQKAFSTCASHLTAVSIFYGTGIFMYLRPNSS  
 30 HFMGTDKMASVFYAIVIPMLNPLVYSLRNKEVKSFAFKKTVGKAKASIGFIF (SEQ ID NO: 355)

ATGGAGAACAACACAGAGGTGACTGAATTCATCCTTGTGGGGTTAACTGATGACCCAGAA  
 CTGCAGATCCCACTCTTCATAGTCTTCTTTTCATCTACCTCATCACTCTGGTTGGGAACCT  
 GGGGATGATTGAATTGATTCTACTGGACTCCTGTCTCCACACCCCCATGTACTTCTTCTCTCA  
 35 GTAACCTCTCCCTGGTGGACTTTGGTTATTCCTCAGCTGTCACTCCCAAGGTGATGGTGGG  
 GTTCTCACAGGAGACAAATTCATATTATATAATGCTTGTGCCACACAATCTTCTTCTTTG  
 TAGCCTTTATCACTGCAGAAAGTTTCTCCTGGCATCAATGGCCTATGACCGCTATGCAGC  
 ATTGTGTAACCCCTGCATTACACCACCACCATGACAACAAATGTATGTGCTTGCCTGGCC  
 ATAGGCTCCTACATCTGTGGTTTCTGAATGCATCCATTCACTGCGGAACACTTTCAGGC  
 40 TCTCCTTCTGTAGATCCAATGTAGTTGAACACTTTTTCTGTGATGCTCCTCCTCTCTTGACT  
 CTCTCATGTTTCAGACAACACTACATCAGTGAGATGGTTATTTTTTTTGTGGTGGGATTCAATG  
 ACCTCTTTTCTATCCTGGTAATCTTGATCTCCTACTTATTTATATTTATCACCATCATGAAG  
 ATGCGCTCACCTGAAGGACGCCAGAAGGCCTTTTCTACTTGTGCTTCCCACCTTACTGCAG  
 TTTCCATCTTTATGGGACAGGAATCTTTATGTACTTACGACCTAACTCCAGCCATTTTCATG  
 45 GGCACAGACAAAATGGCATCTGTGTTCTATGCCATAGTCATTCCCATGTTGAATCCACTGG  
 TCTACAGCCTGAGGAACAAAGAGGTTAAGAGTGCCTTTAAAAAGACTGTAGGGAAGGCAA  
 AGGCCTCTATAGGATTCATATTTTAA (SEQ ID NO: 356)

**AOLFR193 sequences:**

MENKTEVTQFILLGLTNDSELQVPLFTTFPIYIITLVGNLGIIVLIFWDSCLHNPMYFFLSNLSLV  
 DFCYSSAVTPIVMAGFLIEDKVISYNACAAQMYFVAFATVENYLLASMA YDRYAAVCKPLHY  
 TTTMTTTVCARLAIGSYLCGFLNASIHTGDTFSLFCKSNVEVHHFFCDIPAVMVLSCSDRHISEL  
 VLIYVVSFNIFIALLVILISYTFIFITILKMHSASVYQKPLSTCASHFIADVGYGTIFMYLQPSSSH  
 SMDTDKMAPVFYTMVIPMLNPLVYSLRNKEVKSFAFKKVVEKAKLSVGWSV (SEQ ID NO:  
 55 357)



ATGGAAAATAAGACAGAAGTAACACAATTTCATTCTTCTAGGACTAACCAATGACTCAGAA  
 CTGCAGGTTCCCTCTTTATAACGTTCCCTTCATCTATATTATCACTCTGGTTGGAAACCT  
 GGGAATTATTGTATTGATATTCTGGGATTCCTGTCTCCACAATCCCATGTACTTTTTCTCA  
 5 GTAACCTTGTCTCTAGTGGACTTTTGCTACTCTTCAGCTGTCACTCCCATCGTCATGGCTGGA  
 TTCCTTATAGAAGACAAGGTCATCTCTTACAATGCATGTGCTGCTCAAATGTATATCTTTGT  
 AGCTTTTGCCACTGTGGAAAATTACCTCTTGGCCTCAATGGCCTATGACCGCTATGCAGCA  
 GTGTGCAAAACCCCTACATTACACCACAACCATGACAACAACCTGTGTGTGCTCGTCTGGCCA  
 TAGGCTCCTACCTCTGTGGTTTCCTGAATGCCTCCATCCACACTGGGGACACATTTAGTCTC  
 10 TCTTTCTGTAAAGTCCAATGAAGTCCATCACTTTTCTGTGATATTCCAGCAGTCATGGTTCT  
 CTCTTGCTCTGATAGACATATTAGCGAGCTTGTTCTTATTTATGTTGTGAGCTTCAATATCT  
 TTATAGCTCTCCTGGTTATCTTGATATCCTACACATTCATTTTTATCACCATCCTAAAGATG  
 CACTCAGCTTCAGTATACCAGAAGCCTTTGTCCACCTGTGCCTCTCATTTTCATTGCAGTCGG  
 CATCTTCTATGGGACTATTATCTTCATGTACTTACAACCCAGCTCCAGTCACTCCATGGACA  
 CAGACAAAATGGCACCTGTGTTCTATACAATGGTCATCCCCATGCTGAACCCCTCTGGTCTA  
 15 TAGTCTGAGGAACAAGGAAGTGAAGAGTGCATTCAAGAAAGTTGTTGAGAAGGCAAAATT  
 GTCTGTAGGATGGTCAGTTTAA (SEQ ID NO: 358)

#### AOLFR194 sequences:

20 MERQNQSCVVEFILLGFSNYPELQGQLFVAFVLVYLVTLIGNAIIIVIVSLDQSLHVPMYLFLNL  
 SVVDLSFSAVIMPEMLVVLSTKTTISFGGCFQMYFILLFGGAECFLLGAMAYDRFAAICHPL  
 NYQMIMNKGVFMKLIIFSWALGFMLGTVQTSWVSSFPFCGLNEINHISCETPAVLELACADTF  
 FEIYAFTGTFLIILVPFLILLSYIRVLFKMPSTTGRQKAFSTCAHLTSVTLFYGTASMTYLO  
 PKSGYSPETKKVMSLSYSLTPLLNLIIYSLRNSEMKRALMKLWRRRVVLHTI (SEQ ID NO:  
 359)

25 ATGGAAAGACAAAATCAAAGCTGTGTGGTTGAATTCATCCTCTTGGGCTTTTCTAACTATC  
 CTGAGCTCCAGGGCAGCTCTTTGTGGCTTTCCTGGTTATTTATCTGGTGACCCTGATAGG  
 AAATGCCATTATTATAGTCATCGTCTCCCTAGACCAGAGCCTCCACGTTCCCATGTACCTGT  
 30 TTCTCCTGAACTTATCTGTGGTGGACCTGAGTTTCAGTGCAGTTATTATGCCTGAAATGCT  
 GGTGGTCTCTCTACTGAAAAAACTACAATTTCTTTTGGGGGCTGTTTTGCACAGATGTAT  
 TTCATCCTTCTTTTGGTGGGGCTGAATGTTTTCTTCTGGGAGCAATGGCTTATGACCGATT  
 TGCTGCAATTTGCCATCCTCTCAACTCAAAATGATTATGAATAAAGGAGTTTTATGAAA  
 TTAATTATATTTTCATGGGCCTTAGGTTTTATGTTAGGTACTGTTCAAACATCATGGGTATC  
 TAGTTTTCCCTTTTGTGGCCTTAATGAAATTAACCATATATCTTGTGAAACCCAGCAGTGT  
 35 TAGAACTTGCATGTGCAGACACGTTTTTGTGTTGAAATCTATGCATTACAGGCACCTTTTTG  
 ATTATTTTGGTTCCTTTCTTGTGATACTCTTGTCTTACATTTCGAGTTCTGTTTGCCATCCTG  
 AAGATGCCATCAACCACTGGGAGACAAAAGGCCTTTTCCACCTGTGCCGCTCACCTCACAT  
 CTGTGACCCTATTCTATGGCACAGCCAGTATGACTTATTTACAACCCAAATCTGGCTACTC  
 ACCGGAACCAAGAAAGTGATGTCTTACTCACTTCTGACACCACTGCTGAATCTG  
 40 CTTATCTACAGTTTGCAGAAATAGTGAGATGAAGAGGGCTTTGATGAAATTATGGCGAAGG  
 CGAGTGGTTTTACACACAATCTGA (SEQ ID NO: 360)

#### AOLFR195 sequences:

45 MIVQLICTVCFILAVNTFHVRSFDFLKADDMGEINQTLVSEFLLGLSGYPKIEIVYFALILVMY  
 LVILIGNGVLIHASFDSHFHTPMYFFLGNLFLDICYTSSSVPSLTVSLISKRNISFSGCAVQMFF  
 GFAMGSTECLLLGMMAFDTRYVAICNPLRYPILSKVAYVLMASVSWLSGGINSVQTLAMRL  
 PFCGNNIINHFACEILAVLKLACADISLNIITMVISNMAFLVPLMVIFFSYMFILYTILOMNSATG  
 RRKAFSTCSAHLTVVIIFYGTIFFMYAKPKSQDLIGEEKLQALDKLISLFYGVVTPMLNPILYSLR  
 NKDVKAAVKYLLNKKPIH (SEQ ID NO: 361)

50 ATGATTGTTTCAGTTAATTTGTACTGTTTGTCTTGGCAGTAAATACATTTTCATGTTAGATC  
 TTCTTTTGATTTCCTGAAAGCAGATGACATGGGTGAGATTAACCAAGACACTTGTGTCAGAA  
 TTCTTCTTCTGGGTCTTTCTGGATACCCAAAGATTGAGATTGTTTACTTTGCTCTCATCT  
 AGTTATGTACCTAGTGATTCTAATTGGCAATGGTGTCTAATCATAGCCAGCATCTTTGATT  
 55 CTCATTTTCACACACCAATGTACTTCTTCTGGGCAACCTCTCTTCTGGATATCTGCTAT  
 ACATCCTCCTCTGTTCCCTCAACATTGGTGAGCTTAATCTCAAAGAAAAGAAACATTTCT

TCTCTGGATGTGCAGTGCAGATGTTCTTTGGGTTTGCAATGGGGTCAACAGAATGTCTGCT  
 TCTTGGCATGATGGCATTGATCGTTATGTGGCCATCTGCAACCCACTGAGATACCCCATC  
 ATCCTGAGCAAGGTGGCGTATGTATTGATGGCTTCTGTGTCCTGGCTGTCCGGTGAATAA  
 ATTCAGCTGTGCAAAACATTACTTGCCATGAGACTGCCTTTCTGTGGGAATAATATTATCAA  
 5 TCATTTTCGCATGTGAAATATTAGCTGTCTCAAGCTGGCCTGTGCTGATATATCCCTCAATA  
 TTATCACCATGGTGATATCAAATATGGCCTTCCTGGTTCTTCCACTGATGGTCATTTTTC  
 TCCTATATGTTTCATCCTCTACACCATCTTGCAAATGAATTCAGCCACAGGAAGACGCAAGG  
 CATTITTCACGTGCTCAGCTCACCTGACTGTGGTGATCATATTTTACGGTACCATCTTCTTT  
 ATGTATGCGAAACCGAAGTCTCAAGACCTGATTGGGGAAGAAAAATTGCAAGCATTAGAC  
 10 AAGCTCATTTCTCTGTTTTATGGGGTAGTGACACCCATGCTGAATCCTATACTCTATAGCTT  
 GAGAAATAAGGATGTAAAAGCTGCTGTAAAATATTTGCTGAACAAAAAACCAATTCATA  
 A (SEQ ID NO: 362)

# **AOLFR196 sequences:**

15 MLESNYTMPTEFLFVGFTDYLPLRVTLFLVFLVYTLTMVGNILLILVNINSSLQIPMYFSLNL  
 SFLDISCSTAITPKMLANFLASRKSISPYGCALQMFFAFADAECLILAAMAYDRYAICNPLL  
 YTTILMSRRVCVFVLAIFYSGSTTSLVHVLTFRLSFCGSNIVNHFFCDIPLLALSCTDTQINQL  
 LLFALCSFIQTSTFVVFISYFCILITVLSIKSSGGRSKTFSTCASHLIAVTLFYGALLFMYLQPTTS  
 20 YSLDTDKVVAVFYTVVFPMPFNPIIYSFRNKDVKNALKKLLERIGYSNEWYLNRLRIVNI (SEQ  
 ID NO: 363)

ATGTTGGAGAGTAATTACACCATGCCAACTGAGTTCCTATTTGTTGGATTACAGATTATC  
 TACCTCTCAGAGTCACACTGTTCTTGGTATTCCTTCTGGTATATACATTAACATGGTGGGA  
 AATATACTCTTAATAATTCTAGTTAATATTAATTCAAGCCTTCAAATTCCTATGATTATTT  
 25 TCTTAGCAACTTATCTTTCTTAGACATCAGCTGTTCTACAGCAATCACTCCTAAATGCTGG  
 CAAACTTCTTGGCATCCAGGAAAAGCATCTCTCCTTATGGGTGTGCACTACAAATGTTTTT  
 CTTGCTTCTTTTGTGCTGATGCTGAGTGCCTTATCCTGGCAGCAATGGCTTATGACCGCTATG  
 CAGCCATCTGCAACCCACTGCTCTATACTACACTGATGTCTAGGAGAGTCTGTGTCTGCTT  
 CATTGTGTTGGCATATTTCACTGGAAGTACAACATCACTGGTCCATGTGTGCTCACATTC  
 30 AGGCTGTCATTTTGTGGCTCCAATATCGTCAATCATTTTTTCTGTGATATCCCACCTCTTCT  
 GGCTTTATCATGTACAGACACTCAGATCAACCAGCTTCTGCTCTTTGCTTTGTGCACTTCA  
 TCCAGACCAGCACTTTGTGGTAATATTTATTTCTTACTTCTGCATCCTCATCACTGTGTTG  
 AGCATCAAGTCCTCAGGTGGCAGAAGCAAAACATTCTCCACTTGTGCTTCCCACCTCATAG  
 CAGTCACCTTATTCTATGGAGCGCTCCTGTTTATGTACTTACAGCCACCAGTCTATTCC  
 35 CTAGACACTGATAAGGTGGTGGCAGTGTTTTATACTGTTGTATTTCCCATGTTTAATCCAA  
 TAATTTATAGTTTTCAGAAACAAGGATGTGAAAAATGCTCTCAAAAAGCTATTAGAAAGAA  
 TTGGATATTCAAATGAATGGTATTTAAATCGTTTAAGAATAGTCAATATCTAA (SEQ ID NO:  
 364)

# **AOLFR197 sequences:**

40 MCYLSQLCLSLGEHTLHMGMRHTNESNLAGFILLGFSYDYPQLQKVLFLILLYLLTILGNTTI  
 ILVSRLEPKLHMPMYFFLSHLSFLYRCFTSSVIPQLLVNLWEPMTIAIYGGCLVHLVNSHALGS  
 TECVLLALMSCDRYVAVCRPLHYTVLMHIHLCMALASMAWLSGIATTLVQSTLTLQLPFCGH  
 RQVDHFICEVPVLIKLA CVGTFNEABLFVASILFLIVPVSPILVSSGYIAHAVLRIKSATRRQKAF  
 45 GTCFSLTLTVVTIFYGTIIFMYLQPAKSRSDQKGFVSLFYTVVTRMLNPLIYTLRIKEVKGALKK  
 VLAKALGVNII (SEQ ID NO: 365)

ATGTGTTATCTTTCTCAGCTATGCCTCAGCCTTGGGGAACACACTTTACATATGGGGATGG  
 TGAGACATACCAATGAGAGCAACCTAGCAGGTTTCATCCTTTTAGGGTTTTCTGATTATCC  
 50 TCAGTTACAGAAGGTTCTATTTGTGCTCATATTGATTCTGTATTTACTAACTATTTTGGGGA  
 ATACCAACCATCATTCTGGTTTCTCGTCTGGAACCAAGCTTCATATGCCAGTATTTCTTC  
 CTTTCTCATCTCTCCTTCCTGTACCGCTGCTTCACCAGCAGTGTTATTTCCCACTCCTGGT  
 AAACCTGTGGGAACCCATGAAAACTATCGCCTATGGTGGCTGTTTGGTTACCTTTACAAC  
 TCCCATGCCCTGGGATCCACTGAGTGCGTCTCTTGGCTCTGATGTCCTGTGACCGCTATGT  
 55 GGCTGTCTGCCGTCCTCTCCATTACACTGTCTTAATGCATATCCATCTCTGCATGGCCTTGG  
 CATCTATGGCATGGCTCAGTGAATAGCCACCACCCTGGTACAGTCCACCTCACCTGCA

GCTGCCCTTCTGTGGGCATCGCCAAGTGGATCATTTTCATCTGCGAGGTCCCTGTGCTCATC  
 AAGCTGGCTTGTGTGGGCACACGTTTAAACGAGGCTGAGCTTTTTGTGGCTAGTATCCTTT  
 TCCTTATAGTGCCTGTCTCATTTCATCCTGGTCTCCTCTGGCTACATTGCCACGCAAGTGTG  
 AGGATTAAGTCAGCTACCAGGAGACAGAAAGCATTTCGGGACCTGCTTCTCCACCTGACA  
 5 GTGGTCACCATCTTTTATGGAACCATCATCTTCATGTATCTGCAGCCAGCCAAGAGTAGAT  
 CCAGGGACCAGGGCAAGTTTGTCTCTCTTCTACACTGTGGTAACCCGCATGCTTAACCC  
 TCTTATTTATACCTTGAGGATCAAGGAGGTGAAAGGGGCATTAAAGAAAGTTCTAGCAAA  
 GGCTCTGGGAGTAAATATTTTATGA (SEQ ID NO: 366)

10 **AOLFR198 sequences:**

MENCTEVTKFILLGLTSVPBLQIPLFILFTFIYLLTLGNNLGMMLLILMDSCLHTPMYFFLSNLSL  
 VDFGYSSAVTPKVMAGFLRGDKVISYNACAVQMFFVALATVENYLLASMAVDYAAVCKP  
 LHYTTTMTASVGACLALGSYVCGFLNASFHIGGIFSLSFCKSNLVHHFFCDVPAVMALSCSDKH  
 TSEVILVFMSSFNIFVLLVIFISYLFIFITLKMHSAGHQAALSTCASHFTAVSVFYGTVFIFYLQ  
 15 PSSSHSMDTDKMASVIFYAMIIPMLNPVVYSRLNREVQNAFKKVLRRQKFL (SEQ ID NO: 367)

ATGGAGAATTGTACGGAAGTGACAAAGTTCATTCTTCTAGGACTAACCAGTGTCCCAGAAC  
 TACAGATCCCCCTCTTATCTTGTTCACCTTCATCTACCTCCTCACTCTGTGTGGGAACCTG  
 GGGATGATGTTGCTGATCCTGATGGACTCTTGTCTCCACACCCCATGTACTTTTCTCTCAG  
 20 TAACCTGTCTCTGGTGGACTTTGGATACTCCTCAGCTGTCACTCCCAAGGTTCATGGCTGGG  
 TTCCTTAGAGGAGACAAGGTTCATCTCCTACAATGCATGTGCTGTTTCTCTCTTTGT  
 AGCCTTGGCCACGGTGGAAAATTACTTGTGTCCTCAATGGCCTATGACCGCTATGCAGCA  
 GTGTGCAAACCCCTACACTACACCACCACCATGACGGCCAGTGTAGGTGCCTGTCTGGCCC  
 TAGGCTCATATGTCTGTGGCTTCCTAAATGCCTCATTCCACATTGGGGGCATATTCAAGTCTC  
 25 TCTTTCTGTAAATCCAATCTGGTACATCACTTTTTCTGTGATGTTCCAGCAGTCATGGCTCT  
 GTCTTGCTCTGATAAACACACTAGTGAGGTGATTCTGGTTTTTATGTCAAGCTTTAATATCT  
 TTTTGTCTCTTAGTTATCTTTATCTCCTACTTGTTCATATTTCATACCATCTTGAAGATGC  
 ATTCAGCTAAGGGACACCAAAAAGCATTGTCCACCTGTGCCTCTCACTTCACTGCAGTCTC  
 CGTCTTCTATGGGACAGTAATCTTCATCTACTTGCAGCCAGCTCCAGCCACTCCATGGAC  
 30 ACAGACAAAATGGCATCTGTGTTCTATGCTATGATCATCCCCATGCTGAACCTGTGGTCT  
 ACAGCCTGAGGAACAGAGAAGTCCAGAATGCATTCAAGAAAGTGTGAGAAGGCAAAAAT  
 TTCTATAA (SEQ ID NO: 368)

**AOLFR199 sequences:**

35 MDTGNKTLPQDFLLGFPQSQTQLSLFMLFLVMYILTVSGNVAILMLVSTSHQLHTPMYFFLS  
 NLSFLEIWTYTTAAVPAKALAILGRSQTISFTSCLLQMYFVFSLGCTEYFLAAMAYDRCLAICY  
 LHYGAIMSSLLSAQLALGSWVCGFVAIAVPTALISGLSFCGPRAINHHFCDIAPWIALACTNTQA  
 VELVAFVIAVVILSSCLITFVSYYVYIISTILRIPSAAGRSKAFSTCSSHLTVVLIWYGSTVFLHVR  
 TSIKDALDLIKA VHLNTPVTPVLNPFYTLRNEKVRRETLKKWKWK (SEQ ID NO: 369)

40 ATGGACACAGGCAACAAAACCTCTGCCCCAGGACTTTCTCTTACTGGGCTTTCTCTGTTCTC  
 AAACCTCTTCAGCTCTCTCTTTATGCTTTTTCTGGTGATGTACATCCTCACAGTTAGTGGT  
 AATGTGGCTATCTTGATGTTGGTGAGCACCTCCCATCAGTTGCATACCCCATGTACTTCTT  
 TCTGAGCAACCTCTCCTTCTGGAGATTTGGTATACCACAGCAGCAGTGCCCAAAGCACTG  
 45 GCCATCCTACTGGGGAGAAAGTCAGACCATATCATTTACAAGCTGTCTTTTGCAGATGTACT  
 TTGTTTTCTCATTAGGCTGCACAGAGTACTTCTCCTGGCAGCCATGGCTTATGACCGCTGT  
 CTGCCATCTGCTATCCTTTACACTACGAGCCATCATGAGTAGCCTGCTCTCAGCGCAGC  
 TGGCCCTGGGCTCCTGGGTGTGTGGTTTCGTGGCCATTGCAGTGCCACAGCCCTCATCAG  
 TGGCCTGTCTTCTGTGGCCCCCGTGCCATCAACCACTTCTTCTGTGACATTGCACCCTGGA  
 50 TTGCCCTGGCCTGCACCAACACACAGGCAGTAGAGCTTGTGGCCTTTGTGATTGCTGTTGT  
 GGTATCTCTGAGTTTCATGCCTCATCACTTTGTCTCCTATGTGTACATCATCAGCACCATCC  
 TCAGGATCCCCCTCTGCCAGTGGCCGGAGCAAAGCCTTCTCCACGTGCTCCTCGCATCTCAC  
 CGTGGTGCTCATTTGGTATGGGTCCACAGTTTTCTTCCAGTCCGCACCTCTATCAAAGAT  
 GCCTTGGATCTGATCAAAGCTGTCCACGTCTGAACACTGTGGTGACTCCAGTTTAAACC  
 55 CCTTCATCTATACGCTTCGTAATAAGGAAGTAAGAGAGACTCTGCTGAAGAAATGGAAGG  
 GAAAATAA (SEQ ID NO: 370)

**AOLFR200 sequences:**

MTRKNYTSLEFVLLGLADTLELQILFLFFLVIYTLTVLGNLGMILLIRIDSQ LHTPMYFFLANL  
 SFVDVCNSTTTTPKMLADLLSEKKTISFAGCFLQMYFFISLATTECILFGLMAYDRYAAICRPLL  
 5 YSLMSRVTYVKMAAGAFAGLLNFMVNTSHVSSLFCDSNVIIHFFCDSPPLFKLSCSDTILKE  
 SISSILAGVNIVGTLLVILSSYSYVLFISFMSHSGEGRHRAFSTCASHLTAIIFYATCIYTYLRPSS  
 SYSLNQDKVASVFYTVVIPMLNPLIYSLRSKEVKKALANVISRKRTSSFL (SEQ ID NO: 371)

ATGACCAGAAAAAATTATACCTCACTGACTGAGTTCGTCCTATTGGGATTAGCAGACACGC  
 10 TGGAGCTACAGATTATCCTCTTTTTGTTTTTCTTGTTGATTATACACTTACAGTACTGGGA  
 AATCTCGGGATGATCCTCTTAATCAGGATCGATTCCCAGCTTCACACACCCATGTATTTCTT  
 CCTGGCTAACCTGTCCTTTGTGGACGTTTGTAACCTCAACTACCATCACCCCAAAGATGCTG  
 GCAGATTTATTATCAGAGAAGAAAACCATCTCTTTTGTGGCTGCTTCTTACAGATGTACT  
 TCTTTATCTCCCTGGCGACAACCGAATGCATCCTCTTTGGGTAAATGGCCTATGACAGGTA  
 15 TGCGGCCATATGTGCGCCGCTGCTTTACTCCTTGATCATGTCCAGGACCGTCTACCTAAAA  
 ATGGCAGCCGGGGCTTTGCTGCAGGGTTGCTGAACTTCATGGTCAACACAAGCCATGTCA  
 GCAGCTTGTCATTCTGTGACTCCAATGTCATCCATCACTTCTTCTGTGACAGTCCCCACIT  
 TTCAAGCTCTCTTGTCTGACACAATCCTGAAAGAAAGCATAAGTTCTATTTTGGCTGGTG  
 TGAATATTGTGGGGACTCTGCTTGTATCCTCTCCTCTACTCCTACGTTCTCTTCTCCATT  
 20 TTTTCTATGCATTGGGGGAGGGGAGGCACAGAGCTTTCTCCACGTGTGCCTCTCACCTGA  
 CAGCCATAATTCTGTTCTATGCCACCTGCATCTATACTTACCTGAGACCTAGTTCCAGCTAC  
 TCCCTGAATCAGGACAAAGTGGCTTCTGTGTTCTACACAGTGGTGTATCCCATGTTGAATC  
 CTCTGATCTACAGCCTCAGGAGTAAGGAAGTAAAGAAGGCTTTAGCGAATGTAATTAGCA  
 GGAAAAGGACCTCTTCCTTTCTGTGA (SEQ ID NO: 372)

**AOLFR201 sequences:**

MEWENHTILVEFFLKGLSGHPRELLFFVLIFIMYVVILLGNGLILISILDPHLHTPMYFFLGNL  
 SFLDICYTTTSIPSTLVSLSERKTISLSCAVQMFLGLAMGTTECVLLGMMAFDRYVAICNPLR  
 30 YPIIMSKDAYVPMAGSWIIGAVNSAVQSVFVQLPFCRNINNHFTCEILAVMKLACADISDN  
 EFIMLVATTLFILPLLIIVSYTLIIVSIFKISSSEGRSKASSTCSAHLTVVIIIFYGTILFMYMKPKS  
 KETLNSDDL DATDKHSMFYGVMTMPMNPLIYSLRNKDVKEAVKHLLNRRFFSK (SEQ ID NO:  
 373)

ATGGAATGGGAAAACACACCATCTGGTGGAATTTTTTCTGAAGGGACTTTCTGGTCACC  
 35 CAAGACTTGAGTTACTCTTTTTGTGCTCATCTTCATAATGTATGTGGTCATCCTTCTGGGG  
 AATGGTACTCTCATTTAATCAGCATCTTGGACCCCTCACCTTCACACCCCTATGTACTTCTT  
 TCTGGGGAACCTCTCCTTCTTGGACATCTGCTACACCACCACTCTATTCCCTCCACGCTAG  
 TGAGCTTCTTTTCAAGAAAGAACCATTTCCCTTTCTGGCTGTGCAGTGCAGATGTTCTT  
 CGGCTTGGCCATGGGGACAACAGAGTGTGCTTCTGGGCATGATGGCCTTTGACCGCTAT  
 40 GTGGCTATCTGCAACCCTCTGAGATATCCCATCATCATGAGTAAGGATGCCTATGTACCCA  
 TGGCAGCTGGGTCTGGATCATAGGAGCTGTCAATTCTGCAGTACAATCAGTGTTTGTGGT  
 ACAATTGCCTTTCTGCAGGAATAACATCATCAATCATTTACCTGTGAAATTCTGGCTGTC  
 ATGAAACTGGCCTGTGCTGACATCTCAGACAATGAGTTCATCATGCTTGTGGCCACAACAT  
 TGTTCATATTGACACCTTTGTTATTAATCATTGTCTCTTACACGTTAATCATTTGTGAGCATC  
 45 TTCAAAATTAGCTCTTCCGAGGGGAGAAGCAAAGCTTCCTCTACCTGTTACGCCCATCTGA  
 CTGTGGTCATAATATTCTATGGGACCATCCTCTTCATGTACATGAAGCCCAAGTCTAAAGA  
 GACACTTAATTGGATGACTTGGATGCTACCGACAAAATTATATCCATGTTCTATGGGGTG  
 ATGACTCCCATGATGAATCCTTTAATCTACAGTCTTAGAAACAAGGATGTGAAAGAGGCA  
 GTAAAACACCTACTGAACAGAAGGTTCTTTAGCAAGTGA (SEQ ID NO: 374)

**AOLFR202 sequences:**

MEWENHTILVEFFLKGLSGHPRELLFFVLIFIMYVVILLGNGLILISILDPHLHTPMYFFLGNL  
 SFLDICYTTTSIPSTLVSLSERKTISLSCAVQMFLSLAMGTTECVLLGVMAFDRYVAICNPLR  
 55 YPIIMSKDAYVPMAGSWIIGAVNSAVQTVFVQLPFCRNINNHFTCEILAVMKLACADISGN  
 EFILLVTTLFLLTPLLIIIVSYTLIILSIFKISSSEGRSKPSSTCSARLTVVITFCGTIFLMYMKPKSQ

ETLNSDDLDATDKLIFIFRVMTPMMNPLIYSLRNKDVKEAVKHLRRKNFNK (SEQ ID NO: 375)

5 ATGGAATGGGAAAACCAACACCATTTCTGGTGGAAATTTTTCTGAAGGGACTTTCTGGTCACC  
CAAGACTTGAGTTACTCTTTTTGTGCTCATCTTCATAATGTATGTGGTCATCCTTCTGGGG  
AATGGTACTCTCATTTTAATCAGCATCTTGGACCCTCACCTTCACACCCCTATGTACTTCTT  
TCTGGGGAACCTCTCCTTCTTGGACATCTGCTACACCAACCACTCTATTCCCTCCACGCTAG  
TGAGCTTCCTTTTCAAGAAAGAAAGACCATTTCCCTTTCTGGCTGTGCAGTGCAGATGTTTCT  
10 CAGCTTGGCCATGGGGACAACAGAGTGTGTGCTTCTGGGCGTGATGGCCTTTGACCGCTAT  
GTGGCTATCTGCAACCTCTGAGATATCCCATCATCATGAGTAAGGATGCCTATGTACCCA  
TGGCAGCTGGGTCTGGATCATAGGAGCTGTCAATTCTGCAGTACAAACAGTGTGTTGTGGT  
ACAATTGCCTTTCTGCAGGAATAACATCATCAATCATTTACCTGTGAAATTCTAGCTGTC  
ATGAAACTGGCCTGTGCTGACATCTCAGGCAATGAGTTCATCCTGCTTGTGACCACAACAT  
TGTTCTTATTGACACCTTTGTTATTAATTATTGTCTCTTACACGTTAATCATTTTGAGCATC  
15 TTCAAAATTAGCTCTTCGGAGGGGAGAAGCAAACCTTCCTCTACCTGCTCAGCTCGTCTGA  
TTGTGGTGATAACATTCTGTGGGACCATCTTCCTCATGTACATGAAGCCCAAGTCTCAAGA  
GACACTTAATTCAGATGACTTGGATGCCACTGACAACTTATATTCATATTCTACAGGGTG  
ATGACTCCCATGATGAATCCTTTAATCTACAGTCTTAGAAACAAGGATGTGAAGGAGGCA  
GTAAACACCTACTGAGAAGAAAAAATTTAACAAGTAA (SEQ ID NO: 376)

20

**AOLFR203 sequences:**

25 MKRQNSQCVVEFILLGFSNFPBLQVQLFGVFLVTVVVTLMGNAITVIISLNQSLHVPMYLFLN  
LSVVEVSFSAVITPEMLVVLSTEKTMSFVGCFAQMYFILLFGGTECFLLGAMAYDRFAAICHPL  
NYPVIMNRGVFMKLVIFSWISGIMVATVQTTWVFSFPFCGPNEINHLFCETPPVLELVCADTFLF  
EYAFGTILIVMVPFLILLSYIRVLFALIKMPSTTGRQKAFSTCASHLTSVTLFYGTANMTYLQ  
PKSGYSPETKKLISLAYTLLTPLLNPLIYSLRNSEMKTLLIKLWRRKVILHTF (SEQ ID NO: 377)

30 ATGAAAAGACAAAATCAAAGCTGTGTGGTTGAATTCATCCTCCTGGGCTTTTCTAACTTTC  
CTGAGCTCCAGGTGCAGCTCTTTGGGGTTTTCTAGTTATTTATGTGGTGACCCTGATGGG  
AAATGCCATCATTACAGTCATCATCTCCTTAAACCAGAGCCTCCACGTTCCCATGTACCTGT  
TCCTCCTGAACCTATCTGTGGTGGAGGTGAGTTTCAGTGCAGTCATTACGCCTGAAATGCT  
GGTGGTGCTCTCTACTGAGAAAATATGATTCTTTTGTGGGCTGTTTGCACAGATGTAT  
TTCATCCTTCTTTTTGGTGGGACTGAATGTTTTCTCCTGGGAGCGATGGCTTATGACCGATT  
TGCTGCAATTTGCCATCCTCTGAACTACCAAGTGATTATGAACAGAGGGGTTTTATGAAA  
35 TTAGTAATATTCTCATGGATCTCAGGGATCATGGTGGCTACTGTGCAGACCACTTGGGTAT  
TTAGTTTTCCATTTTGTGGCCCCAATGAAATTAATCATCTCTTCTGTGAGACTCCCCCGGTA  
CTAGAGCTTGTGTGTGCAGACACCTTCTTATTTGAAATCTATGCCTTCACAGGCACCATTTT  
GATTGTTATGGTTCCCTTTCTTGTGATCCTCTTGTCTTACATTGAGTTCTGTTTGCCATCCT  
GAAGATGCCATCAACTACTGGGAGACAAAAGGCCTTTCCACCTGTGCCTCTCACCTCACA  
40 TCTGTGACCCTGTTCTATGGCACAGCCAATATGACTTATTTACAACCCAAATCTGGCTACTC  
ACCCGAAACCAAGAAACTGATCTCATTGGCTTACACGTTGCTTACCCCTCTGCTCAATCCG  
CTCATCTATAGCTTACGAAACAGTGAGATGAAGAGGACTTTGATAAACTATGGCGAAGA  
AAAGTGATTTTACACACATTCTGA (SEQ ID NO: 378)

45

**AOLFR204 sequences:**

MEKKKNVTEFILIGLTQNPIMEKVTFVFLVLYMITLSGNLLIVVTITTSQALSSPMYFFLTHLSL  
IDTVYSSSSAPKLIVDSFQEKKISFNGCMAQAYABHIFGATEILLTVMACDCYVAICKPLNYTT  
IMSHSLCILLVAVAVWVGFLHATIQILFTVWLPFCGPNVIGHFMCDLYPLLKLVCIDTHTLGLFV  
AVNSGFICLLNFLILVVSIVILRLSKNNSLEGRCKALSTCISHIIVVLFVFCIFVYLRSVTTLP  
50 DKAVAVFYTMVVPMLNPVYTLRNAEVKSAIRKLWRKKVTSND (SEQ ID NO: 379)

55 ATGGAGAAGAAAAAGAATGTGACTGAATTCATTTTAATAGGTCTTACACAGAACCCCATATA  
ATGGAGAAAGTCACGTTTGTAGTATTTTTGGTTCTTTACATGATAACACTTTCAGGCAACC  
TGCTCATTGTGGTTACCATACCACAGCCAGGCTCTGAGCTCCCCCATGTACTTCTTCCTG  
ACCCACCTTTCTTTGATAGACACAGTTTATTCTTCTTCTCAGCTCCTAAGTTGATTGTGGA  
TTCTTTCAAGAGAAGAAAATCATCTCCTTTAATGGGTGTATGGCTCAAGCCTATGCAGAA

CACATTTTTGGTGCTACTGAGATCATCCTGCTGACAGTGATGGCCTGTGACTGCTATGTGG  
 CCATCTGCAAACCTCTGAACTACACAACCATATGAGCCACAGCCTGTGCATTCTCCTGGT  
 GGCAGTGGCCTGGGTGGGAGGATTTCTTCATGCAACTATTGAGATTCTCTTTACAGTATGG  
 CTGCCCTTCTGTGGCCCCAATGTCATAGGCCACTTCATGTGTGACTTGTACCCATTGTTAAA  
 5 ACTTGTTTGCATAGACACTCATACCCTTGGTCTCTTTGTTGCTGTGAACAGTGGGTTTATCT  
 GCTTATTAACCTTCCTTATCTTGGTGGTATCCTATGTGATCATCTTGAGATCTTTAAAGAAC  
 AATAGCTTGGAGGGGAGGTGTAAAGCCCTCTCCACCTGTATTTCTCACATCATAGTAGTTG  
 TCTTATTCTTTGTGCCCTGTATATTTGTGTATCTGCGCTCAGTGACCACTCTGCCATTGAT  
 10 AAAGCTGTTGCTGTATTTTATACTATGGTGGTCCCAATGTAAATCCCGTGGTCTACACAC  
 TCAGAAATGCTGAGGTAAAAAGTGCAATAAGGAAGCTTTGGAGAAAAAAAGTGACTTCAG  
 ATAATGATTAA (SEQ ID NO: 380)

#### AOLFR205 sequences:

MESENRTVIREFILLGLTQSQDIQLLVFVLVLIFYFIILPGNFLIIFTIKSDPGLTAPLYFFLGNLAFL  
 15 DASYSFTVAPRMLVDFLSAKKIISYRGCTQLFHLHFLGGEGLLLVVMAFDRIAICRPLHYPT  
 VMNPRTCYAMMLALWLGGFVHSIIQVVLRLPFCGPNQLDNFFCDVPQVIKLACTDITFVVEL  
 LMVFNGLMTLLCFLGLLASAYAVILCRIRGSSSEAKNKAMSTCITHIIVIFMFGPGIFITRPFRA  
 FPADKVVSLFHTVIFPLLPVITYTLRNQEVKASMKKVFNKHIA (SEQ ID NO: 381)  
 20 ATGGAAAGCGAGAACAGAACAGTGATAAGAGAATTCATCCTCCTTGGTCTGACCCAGTCT  
 CAAGATATTCAGCTCCTGGTCTTTGTGCTAGTTTAAATATCTACTTCATCATCCTCCCTGG  
 AAATTTTCTCATTATTTTACCATAAAGTCAGACCCTGGGCTCACAGCCCCCTCTATTTCT  
 TTCTGGGCAACTTGGCCTTCTGGATGCATCCTACTCCTTCACTGTGGCTCCCCGGATGTTG  
 GTGGACTTCTCTCTGCGAAGAAGATAATCTCCTACAGAGGCTGCATCACTCAGCTCTTTT  
 25 TCTTGCACTTCTTGGAGGAGGGGAGGGATTACTCCTTGTGTGATGGCCTTTGACCGCTA  
 CATCGCCATCTGCCGGCCTCTGCACTATCCTACTGTCATGAACCCTAGAACCTGCTATGCA  
 ATGATGTTGGCTCTGTGGCTTGGGGGTTTTGTCCACTCCATTATCCAGGTGGTCTCATCTC  
 CCGCTTGCCTTTTTGTGGCCCAAACCAGCTGGACAACCTTCTTCTGTGATGTCCACAGGTC  
 ATCAAGCTGGCCTGCACCGACACATTTGTGGTGGAGCTTCTGATGGTCTTCAACAGTGGCC  
 30 TGATGACACTCCTGTGCTTCTGGGGCTTCTGGCCTCCTATGCAGTCATTCTTTGTGCATA  
 CGAGGGTCTTCTTCTGAGGCAAAAAACAAGCCATGTCCACGTGCATCACCATATCATTTG  
 TTATATTCTTCATGTTTGGACCTGGCATCTTCACTACACGCGCCCTTCAGGGCTTTCCCA  
 GCTGACAAGGTGGTTTCTCTCTTCCACACAGTGATTTTTCTTTGTTGAATCCTGTCAATTA  
 TACCTTCGCAACCAGGAAGTGAAAGCTTCCATGAAAAAGGTGTTAATAAGCACATAGC  
 35 CTGA (SEQ ID NO: 382)

#### AOLFR206 sequences:

MANRNNVTEFILLGLTENPKMQKIIFVVSIVYINAMIGNVLIVVTITASPSLRSPMYFFLAYLSFI  
 40 DACYSSVNTPKLITDSLKENKTLFNGCMTQVFEHFFRGVEVILLTVMAYDHYVAICKPLHYT  
 TIMKQHVCSLLVGVSWVGGFLHATIQILFICQLPFCGPNVIDHFMCDLYTLINLACTNHTLGLF  
 IAANSFGICLLNCLLLLVS CVVILYSLKTHSLEARHEALSTCVSHITVVILSFIPCIFVYMRPPATL  
 PIDKAVAVFYTMITSMLNPLYTLRNAQMKNAIRKLCRKAISSVK (SEQ ID NO: 383)  
 45 ATGGCGAATAGAAACAATGTGACAGAGTTTATTCTATTGGGGCTTACAGAGAATCCAAAA  
 ATGCAGAAAATCATATTTGTGTGTTTTCTGTCTATCATCAACGCCATGATAGGAAATG  
 TGCTCATTGTGGTCACCATCACTGCCAGCCCATCACTGAGATCCCCCATGTACTTTTCTCTG  
 GCCTATCTCTCCTTTATTGATGCCTGCTATTCTCTGTCAATACCCCTAAGCTGATCACAGA  
 TTCACTCTATGAAAACAAGACTATCTTATTCAATGGATGTATGACTCAAGTCTTTGGAGAA  
 CATTTTTTCAGAGGTGTTGAGGTCACTCTACTGTAAATGGCCTATGACCACTATGTGTG  
 50 CCATCTGCAAGCCCTTGCACTATACCACCATGAAGCAGCATGTTTGTAGCTGTAGT  
 GGGAGTGTGATGGGTAGGAGGCTTCTTCATGCAACCATAACAGATCCTCTTCATCTGTCAA  
 TTACCTTTCTGTGGTCCTAATGTCATAGATCACTTTATGTGTGATCTCTACACTTTGATCAA  
 TCTTGCTGCACTAATAACCCACACTCTAGGACTCTTCATTGCTGCCAACAGTGGGTTTATAT  
 GCCTGTAAACTGTCTCTTGTCTCCTGGTCTCCTGCGTGGTCATACTGTACTCCTTAAAGACC  
 55 CACAGCTTAGAGGCAAGGCATGAAGCCCTCTTACCTGTGTCTCCACATCACAGTTGTCA  
 TCTTATCCTTTATACCCTGCATATTTGTGTACATGAGACCTCCAGCTACTTTACCCATTGAT

AAAGCAGTTGCTGTATTCTACACTATGATAACTTCTATGTTAAACCCCTTAATCTACACCTT  
GAGGAATGCTCAAATGAAAAATGCCATTAGGAAATTGTGTAGTAGGAAAGCTATTTCAAG  
TGTCAAATAA (SEQ ID NO: 384)

5 **AOLFR207 sequences:**

MERTNDSTSTEFFLVGLSAHPKLQTVFFVLILWMYLMILLGNGVLISVIIFDLSHLHTPMYFFLCN  
LSFLDVCTSSSVPLILASFLAVKKVVSFSGCMVQMFISFAMGATECMILGTMALDRYVAICY  
LRYPVIMSKGAYVAMAAGSWVTGLVDSVVQTAFAMQLPFCANNVIKHFVCEILAILKLACADI  
SINVISM TGSNLIVLVIPLLVISISYIFIVATILRIPSTEGKHKAFTSCSAHLTVVIIIFYGTIFFMYAKP  
10 ESKASVDSGNEDEALISLFYGVMTPLNPLIYSLRNKDVKAAVKNILCRKNFSDGK (SEQ ID  
NO: 385)

ATGGAAAGGACCAACGATTCCACGTCGACAGAATTTTCTCCTGGTAGGGCTTTCTGCCACC  
CAAAGCTCCAGACAGTTTCTTCGTTCTAATTTTGTGGATGTACCTGATGATCCTGCTTGGGA  
15 AATGGAGTCCTTATCTCAGTTATCATCTTTGATTCTCACCTGCACACCCCATGTATTTCTT  
CCTCTGTAATCTTCTCCTCGACGTTTGCTACACAAGTTCCTCTGTCCCACTAATCTTG  
CCAGCTTTCTGGCAGTAAAGAAAAAGGTTTCTCTCTGGGTGTATGGTGCAAATGTTTAT  
TTCTTTTGCCATGGGGGCCACGGAGTGCATGATCTTAGGCACGATGGCACTGGACCGCTAT  
GTGGCCATCTGCTACCCACTGAGATACCCTGTCTCATCATGAGCAAGGGTGCTATGTGGCCA  
20 TGGCAGCTGGGTCTGGGTCACTGGGCTTGTGGACTCAGTAGTGCAGACAGCTTTTGCAAT  
GCAGTTACCATCTGTGCTAATAATGTCATTAAACATTTTGTCTGTGAAATTCTGGCTATCT  
TGAAACTGGCCTGTGCTGATATTTCAATCAATGTGATTAGTATGACAGGGTCGAATCTGAT  
TGTTCTGGTTATTCCATTGTTAGTAATTTCCATCTCTTACATATTTATTGTTGCCACTATTCT  
GAGGATTCCTTCCACTGAAGGAAACATAAGGCCTTCTCCACCTGCTCAGCCACCTGACA  
25 GTGGTGATTATATTCTATGGAACCATCTTCTTCATGTACGCAAAGCCTGAGTCTAAAGCCT  
CTGTTGATTCAAGTAATGAAGACATCATTGAGGCCCTCATCTCCCTTTTCTATGGAGTGAT  
GACTCCCATGCTTAATCCTCTCATCTATAGTCTGCGAAACAAGGATGTAAAGGCTGCTGTC  
AAAAACATACTGTGTAGGAAAAACTTTTCTGATGGAAAATGA (SEQ ID NO: 386)

30 **AOLFR208 sequences:**

MFPANWTSVKVFFFLGFFHYPKVQVIIFAVCLLMYLITLLGNIFLISITILDSHLHTPMYFLSNL  
SFLDIWYSSSALSPMLANFVSGRNTISFSGCATQMYLSLAMGSTECVLLPMMAYDRYVAICNP  
LRYPVIMNRRTCVQIAAGSWMTGCLTAMVEMMSVLPLSLCGNSIINHFTCEILAILKLVCVDT  
LVQLIMLVISVLLPMPMLLICISYAFILASILRISSVEGRSKAFSTCTAHLMVVVLFGTALSMH  
35 LKPSAVDSQEIDKFMALVYAGQTPMLNPIIYSLRNKEVKVALKKLLIRNHFNTAFISILK (SEQ  
ID NO: 387)

ATGTTCCCGGCAAATTGGACATCTGTAAAAGTATTTTCTTCTCCTGGGATTTTTTCACTACCC  
CAAAGTTCAGGTCATCATATTTGCGGTGTGCTTGCTGATGTACCTGATCACCTTGCTGGGC  
40 AACATTTTTCTGATCTCCATCACCATTCTAGATTCACCTGCACACCCCTATGTACCTCTT  
CCTCAGCAATCTCTCCTTTCTGGACATCTGGTACTCCTCTTCTGCCCTCTCTCCAATGCTGG  
CAAACCTTTGTTTCAGGGAGAAACACTATTTTCACTCTCAGGGTGCGCCACTCAGATGTACCT  
CTCCCTTGCCATGGGCTCCACTGAGTGTGTGCTCCTGCCCATGATGGCATATGACCGGTAT  
GTGGCCATCTGCAACCCCTGAGATACCCTGTCTCATCATGAATAGGAGAACCTGTGTGCAGA  
45 TTGCAGCTGGCTCCTGGATGACAGGCTGTCTCACTGCCATGGTGGAATGATGTCTGTGCT  
GCCACTGTCTCTGTGGTAATAGCATCATCAATCATTTCACTTGTGAAATTCTGGCCATCT  
TGAAATTGGTTTGTGTGGACACCTCCCTGGTGCAAGTAATCATGCTGGTGATCAGTGTACT  
TCTTCTCCCATGCCAATGCTACTCATTTGTATCTCTTATGCATTTATCCTCGCCAGTATCC  
TGAGAATCAGCTCAGTGGAAGGTGCAAGTAAAGCCTTTTCAACGTGCACAGCCACCTGA  
50 TGGTGGTAGTTTTGTTCTATGGGACGGCTCTCTCCATGCACCTGAAGCCCTCCGCTGTAGA  
TTCACAGGAAATAGACAAATTTATGGCTTTGGTGTATGCCGGACAAACCCCATGTTGAAT  
CCTATCATCTATAGTCTACGGAACAAAGAGGTGAAAGTGGCCTTGAAAAAATGTCTGATTA  
GAAATCATTTTAATACTGCCTTCATTTCCATCCTCAAATAA (SEQ ID NO: 388)

**AOLFR209 sequences:**

MDKINQTFVREFILLGLSGYPKLEIIFALILVMYVVILIGNGVLIASILDSRLHMPMYFFLGNLS  
 FLDICYTTSSIPSTLVSLISKRNISFSGCAVQMFFGFAMGSTECFLGMMAFDTRYVAICNPLRY  
 5 PIIMNKVVYVLLTSVSWLSGGINSTVQTSLAMRWPF CGNNIINHFLCEILAVLKLACSDISVNIV  
 TLA VSNIAFLVLP LLVIFFSYMFILY TILRTNSATGRHKAFSTCSAHLTVVIFYG TIFFM YAKPKS  
 QDLLGKDNLQATEGLVSMFYGVVTPMLNPIIYSLRNKDVKAAIKYLLSRKAINQ (SEQ ID NO:  
 389)

10 ATGGACAAGATAAACCAGACATTTGTGAGAGAATTCATTCTTCTGGGACTCTCTGGTTACC  
 CCAAACCTTGAGATCATTTTCTTGGCTCTGATTCTAGTTATGTACGTAGTGATTCTAATTGGC  
 AATGGTGTTCTGATCATAGCAAGCATCTTGGATTCTCGTCTTCACATGCCCATGTACTTCTT  
 CCTGGGCAACCTCTCTTCTCTGGATATCTGCTATACAACCTCCTCCATCCCTCAACACTGG  
 TGAGCTTAATCTCAAAGAAAAGAAACATTTCTTCTCTGGATGTGCAGTGCGAGATGTTCTT  
 15 TGGGTTTGCAATGGGGTCAACAGAATGTTTCTCTTGGCATGATGGCATTGATCGTTAT  
 GTGGCCATCTGTAACCCCTCTGAGATAACCCATCATCATGAACAAGGTGGTGTATGTACTGC  
 TGACTTCTGTATCATGGCTTCTGGTGGAATCAATTCAACTGTGCAAACATCACTTGCCAT  
 GCGATGGCCTTCTGTGGGAACAATATTATTAATCATTTCTTATGCGAGATCTTAGCTGTCC  
 TAAAAATTAGCTTGTTCTGATATATCTGTCAATATTGTTACCCTAGCAGTGTCAAAATATTGCT  
 20 TTCCTAGTTCTTCTCTGCTCGTGATTTTTTCTCCTATATGTTTCATCCTCTACACCATCTTG  
 CGAACGAACTCGGCCACAGGAAGACACAAGGCATTTTCTACATGCTCAGCTCACCTGACTG  
 TGGTGATCATATTTTATGGTACCATCTTCTTATGTATGCAAAACCTAAGTCCAGGACCTC  
 CTTGGGAAAGACAACCTTGCAAGCTACAGAGGGGCTTGTTTCCATGTTTTATGGGGTTGTGA  
 CCCCCATGTAAACCCATAATCTATAGCTTGAGAAATAAAGATGTAAAAGCTGCTATAAA  
 25 ATATTTGCTGAGCAGGAAAGCTATTAACCAGTAA (SEQ ID NO: 390)

**AOLFR210 sequences:**

MMGRRNDNTNVADFILTGLSDSEEVQMALEFMLFLLIYLTMLGNVGMILLIRLDLQLHTPMYFFL  
 THLSFIDLSYSTVVPKTLANLLTSNYISFTGCF AQMF CFVFLGTAECYLLSSMAYDRYAAICSP  
 30 LHYTVIMPKRLCLALITGPYVIGFMDSFVNVVSMSRLHFCD SNIIHHFFCDTSPILALSCTD TDN  
 TEMLIPIAGSTLMVSLITISASYVSILSTILKINSTSGKQKAFSTCVSHLLGVTIFYGTMIIFYLKP  
 RKSYSLGRDQVAPVFYTIVIPMLNPLIYSLRNREVKNALIRVMQRRQDSR (SEQ ID NO: 391)

35 ATGATGGGTAGAAGGAATGACACAAATGTGGCTGACTTCATCCTTACGGGACTGTCAGAC  
 TCTGAAGAGGTCCAGATGGCTCTGTTTATGCTATTTCTCCTCATATACCTAATTACTATGCT  
 GGGGAATGTGGGGATGCTATTGATAATCCGCCTGGACCTCCAGCTTCACACTCCCATGTAT  
 TTTTCTTACTCACCTGTCAATTTATTGACCTCAGTTACTCAACTGTGCTCACACCTAAAAC  
 CTTAGCGAACTTACTGACTTCCAATATATTTCTTACGGGCTGCTTTGCCAGATGTTCT  
 GTTTTGTCTTCTGGGTACTGCTGAATGTTATCTTCTCTCTCAATGGCCTATGATCGCTAT  
 40 GCAGCGATCTGCAGTCCTCTACACTACAGTATTATGCCCCAAAGGCTCTGCCTC  
 TCATCACTGGGCCTTATGTGATTGGCTTTATGGACTCCTTTGTCAATGTGGTTTCCATGAGC  
 AGATTGCATTTCTGTGACTCAAACATAATTCATCACTTTTCTGTGACACTTCCCCAATTTT  
 AGCTCTGTCTGCACTGACACAGACAACACTGAAATGCTGATATTCATTATCGCTGGTTCC  
 ACCCTGATGGTGTCCCTTATCACAATATCTGCATCCTATGTGTCCATTCTCTTACCATCCT  
 45 GAAAAATTAATTCCACTTCAGGAAAGCAGAAAGCTTTCTCTACTTGCGTCTCTCATCTCTTG  
 GGAGTCACCATCTTCTATGGAATATGATTTTACTTACTTAAAGCCAAAGAAAGTCTTATT  
 CTTGGGAAGAGATCAAGTGGCTCCTGTGTTTTATACTATTGTGATTCCCATGCTGAATCC  
 ACTCATTTATAGTCTTAGAAACAGAGAAGTGAAAAATGCTCTCATTAGAGTCATGCAGAG  
 AAGACAGGACTCCAGGTAG (SEQ ID NO: 392)

50

**AOLFR211 sequences:**

MMGRRNNTNVADFILMGLTLSEEQMALFMLFLLIYLTMLGNVGMILLIRLDLQLHTPMYFFL  
 THLSFIDLSYSTVVPKTLANLLTSNYISFTGCF AQMF FFAFLGTAECYLLSSMAHDYAAICSP  
 LHYTVIMSKRLCLALITGPYVIGFIDSFVNVVSMSRLHFYDSNVIHHFFCDTSPILALSCTD TYNT  
 55 EILIFIIVGSTLMVSLFTISASYVFILFTILKINSTSGKQKAFSTCVSHLLGVTIFYSTLIFTYLPKPK  
 SYSLGRDQVASVFYTIVIPVLNPLIYSLRNKEVKNAVIRVMQRRQDSR (SEQ ID NO: 393)



ATGATGGGTTAGAAGGAATAACACAAATGTGGCTGACTTCATCCTTATGGGACTGACACTTT  
 CTGAAGAGATCCAGATGGCTCTGTTTATGCTATTTCTCCTGATATACCTAATTACTATGCTG  
 GGAATGTGGGGATGATATTGATAATCCGCCTGGACCTCCAGCTTCACACTCCCATTGATT  
 5 TTTTCCTTACTCACCTGTCATTTATTGACCTCAGTTACTCAACTGTCGTCACACCTAAACC  
 TTAGCGAACTTACTGACTTCCAATAATTTTCTTTACGGGCTGCTTTGCCAGATGTTCTT  
 TTTTGCTTCTTGGGTACTGCTGAATGTTACCTTCTCTCCTCAATGGCCCATGATCGCTATG  
 CAGCGATCTGCAGTCCTTACACTACACAGTTATTATGTCCAAAAGGCTCTGCCTCGCTCT  
 CATCACTGGGCCTTATGTGATTGGCTTTATAGACTCCTTTGTCAACGTGGTTTCCATGAGCA  
 10 GATTGCATTTCTACGACTCAAACGTAATTCATCACTTTTTCTGTGACACTTCCCCAATTTTA  
 GCTCTGTCCTGCACTGATACATAACAACCCGAAATCCTGATATTCAATTATTGTTGGTTCCAC  
 CCTGATGGTGTCCCTTTTCACAATATCTGCATCCTATGTGTTTATTCTCTTTACCATCCTGA  
 AAATTAATTCCACTTCAGGAAAGCAGAAAGCTTTCTTACTTGGCTCTCTCATCTCTTGGG  
 AGTCACCATCTTTTATAGCACTCTGATTTTACTTATTTAAAACCAAGAAAGTCTTATTCCT  
 15 TGGGAAGAGATCAAGTGGCTTCTGTTTTTTATATACTATTGTGATTCCCGTGCTGAATCCACT  
 CATTTATAGTCTTAGAAACAAAGAGGTGAAAAATGCTGTCATCAGAGTCATGCAGAGAAG  
 ACAGGACTCCAGGTAA (SEQ ID NO: 394)

**AOLFR212 sequences:**

20 MAGNNFTEVTVFILSGFANHPQLVSLFLMFLFIYFTVLGNLGLITLIRMDSQLHTPMYFFLSN  
 LAFIDIFYSSVTPKALVNFQSNRRSISFVGCFFVQMYFFVGLVCCCEFLGSMAYNRYAICNPL  
 LYSVVMQKVSNNWLGVMFYVIGFTSSLSVWVISSLAFCDSINHHFCDTALLALSCVDTFGT  
 EMVSFVLGFTLLSSLLITVTYHHSAILRIQSAAGRQKAFSTCASHLMAVTIFYGSLIFTYLQPD  
 NTSSLTQAQVASVFYTVIPMLNPLIYSLRNKDVKNALLRVIHRKLF (SEQ ID NO: 395)

25 ATGGCTGGCAACAATTTCACTGAGGTTACCGTCTTCATCCTCTCTGGATTTGCAAAATCACC  
 CTGAATTACAAGTCAGTCTTTTCTTGATGTTTCTCTTCAATTTATCTATTCACTGTTTTGGGA  
 AACCTGGGACTGATCACGTTAATCAGAATGGATTCTCAGCTTCACACCCCTATGTACTTTT  
 TCCTGAGCAATTTAGCATTTATTGACATATTTTACTCCTCTACTGTAACACCTAAGGCATTG  
 30 GTGAATTTCCAATCCAATCGGAGATCCATCTCCTTTGTTGGCTGCTTTGTTCAAATGTACTT  
 TTTTGTGGATTGGTGTGTTGTGAGTGTTTCTTCTGGGATCAATGGCCTACAATCGCTACA  
 TAGCAATCTGCAATCCCTTACTGTATTCAAGTAGTCATGTCCAAAAAGTGTTCAACTGGCT  
 GGGAGTAATGCCATATGTGATAGGCTTCAAGCTCGCTGATATCTGTCTGGGTGATAAGC  
 AGTTTGGCGTTCTGTGATTCCAGCATCAATCATTTTTTTGTGACACCACAGCTCTTTTAGC  
 35 ACTCTCTGTGTAGATACATTCCGGCACAGAAATGGTGAGCTTTGTCTTAGCTGGATTCACT  
 CTTCTTAGCTCTCTCCTTATCATCACAGTCACCTTATATCATCATCATCTCAGCCATCCTGAG  
 GATCCAGTCAGCAGCAGGCAGGCAGAAAGGCTTCTCCACCTGCGCATCCACCTCATGGCT  
 GTAACATATCTTTTATGGGTCTCTGATTTTACCTATTTGCAACCTGATAACACATCATCGCT  
 GACCCAGGCGCAGGTGGCATCTGTATTCTATACGATTGTCAATCCCATGCTGAATCCACTC  
 40 ATCTACAGTCTGAGGAACAAAGATGTGAAAAATGCTCTTCTGAGAGTCATACATAGAAAA  
 CTTTTTCCATGA (SEQ ID NO: 396)

**AOLFR213 sequences:**

45 MNSLGKLVSMILSAHVFCYKFNCFGCTHSIPALGADPPGGMGLGNESSLMDFILLGFSDHPRL  
 EAVLFVFFVLLFYLLTLVGNFTIHSYLDPLHTPMYFFLSNLSLLDICFTTSLAPQTLVNLQRPKK  
 TITYGGCVAQLYISLALGSTECILLADMDLRYIAVCKPLHYVVMNPRLCQQLASISWLSGLA  
 SSLIHATFTLQPLCGNHRDLHFICEVPALLKLACVDTTVNELVLFVVSFLFVVPALISISYGF  
 TQAVLRIKSVEARHKAFSTCSSHLTVVIIFYGTIHYVYLQPSDSYAQDQKGFIISLFYTMVTPILNP  
 IYTLRNKDMKEALRKLLSGKL (SEQ ID NO: 397)

50 ATGAATAGTTTGGGAAAGTTGGTCTCCATGATCCTCTCAGCTCATGTGTTCTGTTATTCTAA  
 ATTTAATTGTTTTGGATGTACCCATTCCATTCTGCCTTAGGTGCGGATCCCCCTGGAGGG  
 ATGGGATTGGGCAATGAGAGTTCCCTAATGGATTTTCATCCTTCTAGGCTTCTCAGACCACC  
 CTCGTCTGGAGGCTGTTCTCTTTGTATTTGTCTTTTCTTCTACCTCCTGACCCCTTGTGGGA  
 55 AACTTCACCATAATCATCATCTCATATCTGGATCCCCCTCTTCATACCCCAATGTACTTTTT  
 TCTCAGCAACCTCTCTTTACTGGACATCTGCTTCACTACTAGCCTTGCTCCTCAGACCTTAG

TTAACTTGCAAAGACCAAAGAAGACGATCACTTACGGTGGTTGTGTGGCGCAACTCTATAT  
 TTCTCTGGCACTGGGCTCCACTGAATGTATCCTCTTGGCTGACATGGCCTTGGATCGGTAC  
 ATTGCTGTCTGCAAACCCCTCCACTATGTAGTCATCATGAACCCACGGCTTTGCCAACAGC  
 TGGCATCTATCTCCTGGCTCAGTGGTTTGGCTAGTTCCTAATCCATGCAACTTTTACCTTG  
 5 CAATTGCCTCTCTGTGGCAACCATAGGCTGGACCAATTTATTTGCGAAGTACCAGCTCTTCT  
 CAAGTTGGCTTGTGTGGACACCACTGTCAATGAATTGGTGCTTTTTGTGTAGTGTCTGT  
 TTGTGTCAATCCACCAGCACTCATCTCCATCTCCTATGGCTTCATAACTCAAGCTGTGCTG  
 AGGATCAAATCAGTAGAGGCAAGGCATAAAGCCTTCAGCACCTGCTCCTCCACCTTACAG  
 TGGTGATTATATTCTATGGCACCATAATCTACGTGTACCTGCAACCTAGTGACAGCTATGC  
 10 CCAGGACCAAGGGAAGTTTATCTCCCTCTTCTACACCATGGTGACCCCCACTTTAAATCCT  
 ATCATCTATACTTTAAGGAACAAGGATATGAAAGAGGCTCTGAGGAAACTTCTCTCGGGA  
 AAATTGTGA (SEQ ID NO: 398)

**AOLFR214 sequences:**

15 MDKSNSSVVSEFVLLGLCSSQKLQLFYCFPSVLYTVIVLGNLLIILTVTSDTSLHSPMYFLLGN  
 LSFVDICQASFATPKMIADFLSAHETISFSGCIAQIFFIHLFTGGEMVLLVSMAYDRYVAICKPLY  
 YVVMISRRRTCTVLVMISWAVSLVHTLSQLSFTVNLPCGPNVVDSEFFCDLPRVTKLACLDSEYIE  
 ILIVVNSGILSLSTFSLLVSSYIILVTVWLKSSAAMAKAFSTLASHIAVVILFFGPCIFYVWPFTIS  
 20 PLDKFLAIFYTVFIPVLNPIIYTLNRNMDKAAVRKIVNHYLRPRRISEMSLVVRTSFH (SEQ ID  
 NO: 399)

ATGGATAAGTCCAATTCTTCAGTGGTGTCTGAATTTGTAAGTGTGGGACTCTGTAGTTCTC  
 AAAAAGTCCAGCTTTTCTATTTTGTCTCTCTGTGTGTATACAGTCAITGTGCTGGGA  
 AATCTTCTCATTATCCTCACAGTGACTTCTGATACCAGCCTGCACTCCCTATGTACTTTCT  
 25 CTGGGAAACCTTTCTTTGTGTGACATTTGTGAGGCTTCTTTTGCTACCCCTAAAATGATTG  
 CAGATTTTCTGAGTGACACGAGACCATATCTTTCAGTGGCTGCATAGCCCAAATTTTCTTT  
 ATTCACCTTTTTACTGGAGGGGAGATGGTGCTACTTGTTCGATGGCCTATGACAGGTATG  
 TAGCCATATGCAAACCTTATACTATGTGGTCATCATGAGCCGAAGGACATGCACTGTCTT  
 GGTAATGATCTCCTGGGCTGTGAGCTTGGTGACACATTAAAGCCAGTTATCATTTACTGTG  
 30 AACCTGCCTTTTTGTGGACCTAATGTAGTAGACAGCTTTTTTTGTGATCTTCTCGAGTCAC  
 CAAACTTGCTGCCTGGACTCTTACATCATTGAAATACTAATTGTGGTCAATAGTGGAATT  
 CTTTCCCTAAGCACTTCTCTCTTGGTCACTCCTACATCATTATTTCTTGTACAGTTTG  
 GCTCAAGTCTTCAAGTGCATGCAATGGCAAAGGCAATTTCTACGCTGGCTTCCCATATTGCAGTA  
 GTAATAATTATTCTTTGGACCTTGCATCTTCATCTATGTGTGGCCCTTTACCATCTCTCCTTT  
 35 GGATAAATTTCTTGCCATATTTTACACTGTTTTACCCCCGTCCTAAACCCATTATTTATA  
 CACTAAGGAATAGGGATATGAAGGCTGCCGTAAGGAAAATTGTGAACCATTACCTGAGGC  
 CAAGGAGAATTTCTGAAATGTCACTAGTAGTGAGAACTTCCTTTCATTAA (SEQ ID NO:  
 400)

**AOLFR215 sequences:**

40 MAHTNESMVSEFVLLGLSNSWGLQLFFFAIFSIVYVTSVLGNVLIIVISFDSHLNMPMYFLLSNL  
 SFIDICQSNFATPKMLVDFFIERKTISFEGCMAQIFVLHSFVGSEMMMLLVAMAYDRFIAICKPLH  
 YSTIMNRRLCVIFVSISWAVGVLSVSHLAFTVDLPFCGPNEVDSEFFCDLPLVIELACMDTYEM  
 EIMTLTNSGLISLSCFLALIISYTHLIGVRCRSSSGSSKALSTLTAHTTVVILFFGPCIFYFIWPFPSRL  
 45 PVDKFLSVFYTVCTPLLNPIIYSLRNEDVKAAMWKLNRNHHVNSWKN (SEQ ID NO: 401)

ATGGCTCACACAAATGAATCGATGGTGTCTGAGTTTGTACTTTTGGGACTCTCTAATTCCT  
 GGGGACTTCAACTTTTCTTTTTCGCCATCTTCTCTATAGTCTATGTGACATCAGTGCTAGGC  
 AATGTCTTAATTATTGTCATTATTTCTTTTGACTCCCATTTGAACTCTCCTATGTACTTCTTG  
 50 CTCAGTAATCTTTCTTTCATTGATATCTGTCACTTAACCTTTGCCACCCCCAAGATGCTTGT  
 AGACTTTTTTATTGAGCGCAAGACTATCTCCTTTGAGGGTTGCATGGCCAGATATTTCGTT  
 CTTACAGTTTTGTGGGAGTGAGATGATGTTGCTTGTAGCTATGGCATATGACAGATTTA  
 TAGCCATATGTAAGCCTCTGCACTACAGTACAATTATGAACCGGAGGCTCTGTGTAATTTT  
 TGTGTCTATTTCTGGGCGGTGGGCGTTCTTCATTCTGTGAGCCACTTGGCTTTTACAGTGG  
 55 ACCTGCCATTCTGTGGTCCCAATGAGGTGGATAGCTTCTTTGTGACCTTCCCTTGGTGATA  
 GAGCTGGCTTGCATGGATACATATGAAATGGAAATTATGACCCTAACGAACAGTGGCCTG

ATATCATTGAGCTGTTTCCTGGCTTTAATTATTTCTACACCATCATTTTGATCGGTGTCGG  
 ATGCAGGTCCTCCAGTGGGTCATCTAAGGCTCTTTCTACATTAACTGCCACATCACAGTG  
 GTCATTCTTTCTTCGGGCTTGCAATTTATTTCTATATATGGCCTTTTAGCAGACTTCCTGT  
 GGACAAATTTCTTTCTGTGTTCTACACTGTTTGTACTCCCTTGTTGAACCCCATCATCTACT  
 5 CTTTGAGGAATGAAGATGTTAAAGCAGCCATGTGGAAGCTGAGAAACCATCATGTGAACT  
 CCTGGAATACTAG (SEQ ID NO: 402)

**AOLFR216 sequences:**

MDVGNKSTMSEFVLLGLSNSWELQMFFFMVFSLLYVATMVGNLIVITVIVDPHLHSPMYFLL  
 10 TNLSIIDMSLASFATPKMITDYLTHGKTISFDGCLTQIFFLHLFTGTEILLMAMSFDRYIAICKPL  
 HYASVISPVQCVVALVVASWIMGVMHMSQVIFALTFPCGPYEVDSEFFCDLPVVFQLACVDTY  
 VLGLFMISTSGIALSCFIVLFNSYVIVLVTVKHSSRGSSKALSTCTAHFIVVFLFFGPCIFTYMW  
 PLSSFLTDKILSVFYTIFTPTLNPITYTLRNQEVKIAMRKLKNRFLNFKAMPS (SEQ ID NO: 403)

15 ATGGATGTGGGCAATAAGTCTACCATGTCTGAATTTGTTTTGCTGGGGCTCTCTAATTCCT  
 GGGAACCTACAGATGTTTTCTTTATGGTGTTTTTCATTGCTTTATGTGGCAACAATGGTGGG  
 TAACAGCCTCATAGTCATCACAGTTATAGTGGACCCTCACCTACACTCTCCTATGTATTTCC  
 TGCTTACCAATCTTTCAATCATTGATATGTCTCTTGCTTCTTTCGCCACCCCAAAGATGATT  
 ACAGATTACCTAACAGGTCACAAAACCATCTCTTTTGATGGCTGCCTTACCCAGATATTCT  
 20 TTCTCCACCTTTTCACTGGAACCTGAGATCATCTTACTCATGGCCATGTCCTTTGATAGGTAT  
 ATTGCAATATGCAAGCCCCTGCACTATGCTTCTGTCTATTAGTCCCCAGGTGTGTGTTGCTCT  
 CGTGGTGGCTTCTCTGGATTATGGGAGTTATGCATTCAATGAGTCAGGTCATATTTGCCCTC  
 ACGTTACCATTTCTGTGGTCCCTATGAGGTAGACAGCTTTTCTGTGACCTTCTGTGGTGT  
 CCAGTTGGCTTGTGTGGATACTTATGTTCTGGGCCTCTTTATGATCTCAACAAGTGGCATA  
 25 ATTGCGTTGTCCTGTTTTATTGTTTTATTAAATTCATATGTTATTGTCCTGGTTACTGTGAA  
 GCATCATTCTTCCAGAGGATCATCTAAGGCCCTTTCTACTTGTACAGCTCATTTTCATTGTTG  
 TCTTCTTGTCTTTGGGCCATGCATCTTCATCTACATGTGGCCACTAAGCAGCTTTCTCACA  
 GACAAGATTCTGTCTGTGTTTTATACCATCTTTACTCCCACTCTGAACCCAATAATCTATAC  
 TTTGAGGAATCAAGAAGTAAAGATAGCCATGAGGAAACTGAAAAATAGGTTTCTAAATTT  
 30 TAATAAGGCAATGCCTTCATAG (SEQ ID NO: 404)

**AOLFR217 sequences:**

MLESFQKSEQMAWSNQSAVTEFILRGLSSSLELQIFYFLFFSIVYAATVLGNLLIVVTIASEPHLH  
 SPTYFLLGNLSFIDMSLASFATPKMIADFLREHKAI SFEGCMTQMFFLHLLGGAEIVLLISMSFD  
 35 RYVAICKPLHYLTMSRRMCVGLVILSWIVGIFHALSQLAFTVNLFPFCGPNEVDSEFFCDLPVLIK  
 LACVDTYILGVFMISTSGMIALVCFILLVISYTHLVTVRQRSSGGSSKALSTCSAHFTVVTLLFGP  
 CTFIYVWPFTNFPIDKVLVSVFYTTYTPLLNPVIYTVRNKDVKYSMRKLSSHIFKSRKTDHTP  
 (SEQ ID NO: 405)

40 ATGCTAGAGTCCTTCCAGAAATCAGAGCAAATGGCCTGGAGCAATCAGTCTGCGGTAACC  
 GAATTCATACTACGGGTCTGTCCAGTTCTTTAGAACTCCAGATTTTCTACTTCTGTTTTT  
 CTCCATAGTCTATGCAGCCACTGTGCTGGGGAACCTTCTTATTGTGGTCACCATTGCATCA  
 GAGCCACACCTTCATTCCCCTACGTACTTTCTGCTGGGCAATCTCTCCTTCATTGACATGTC  
 CCTGGCCTCATTTGCCACCCCAAAATGATTGCAGACTTCCTTAGAGAACACAAAGCCATC  
 45 TCTTTTGAAGGCTGCATGACCCAGATGTTCTTCTACATCTCTTAGGGGGTGCTGAGATTG  
 TACTGCTGATCTCCATGTCTTTGATAGGTACGTGGCTATCTGTAAGCCTCTACATTACCTA  
 ACAATCATGAGCCGAAGAATGTGTGTTGGGCTTGTGATACTTCTCTGGATTGTGCGCATCT  
 TCCATGCTCTGAGTCAGTTAGCATTACAGTGAATCTGCCCTTCTGTGGACCCAATGAAGT  
 AGACAGTTTCTTTTGTGACCTCCCTTTGGTGATTAACTTGCTTGTGTGCGACACATATATTC  
 50 TGGGGGTGTTTCATGATCTCAACCAGTGGCATGATTGCCCTGGTGTGCTTCATCTCTTGGT  
 GATCTCTTACACTATCATCTGGTCAACCGTTCGGCAGCGTTCCTCTGGTGGATCCTCCAAA  
 GCCCTCTCCACGTGCAGTGCCCACTTACTGTTGTGACCCTTTTCTTTGGCCCATGCATTT  
 CATTTATGTGTGGCCTTTCACAAATTTCCCAATAGACAAAGTACTCTCAGTATTTTATACCA  
 TATACACTCCCCTCTTGAATCCAGTGATCTATACCGTTAGGAATAAAGATGTCAAGTATTC  
 55 CATGAGGAACTAAGCAGCCATATCTTTAAATCTAGGAAGACTGATCATACTCCTTAA  
 (SEQ ID NO: 406)

**AOLFR218 sequences:**

METANYTKVTEFVLTGLSQTREVQLVLFVIFLSFYLFILPGNLIICTIRLDPHLTSPMYFLLANLA  
 LLDIWYSSITAPKMLIDFFVERKIIISFGGCCIAQLFFLHFVGASEMFLIVMAYDRYAAICRPLHYA  
 5 TIMNRRLCCILVALSWMGGFIHSIIQVALIVRLPFCGPNELDSYFCDITQVVRJACANTFPEELVM  
 ICSSGLISVVCFTALLMSYAFLLALLKKHSGSDENTNRAMSTCYSHITIVVLMFGPSIYTYARPF  
 SFSLDKVVSVFHTVIFLLNPITYTLRNKEVKAAMRKVVTKYILCEEK (SEQ ID NO: 407)

ATGGAAACTGCAAATTACACCAAGGTGACAGAATTTGTTCTCACTGGCCTATCCCAGACTC  
 10 GGGAGGTCCAACTAGTCCTATTTGTTATATTTCTATCCTTCTATTTGTTTCATCCTACCAGGA  
 AATATCCTTATCATTGTCACCATCAGGCTAGACCCCTCATCTGACTTCTCCTATGTATTTCT  
 GTTGGCTAATCTGGCCCTCCTTGATATTTGGTACTCTTCCATTACAGCCCCTAAAATGCTCA  
 TAGACTTCTTTGTGGAGAGGAAGATAATTTCTTTGGTGGATGCATTGCACAGCTCTTCTT  
 CTTACACTTTTGTGGGGCTTCGGAGATGTTCTTGTCTCATAGTGTATGGCCTATGACCGCTAT  
 15 CTTGCTATCTGCCGACCCCTCCACTATGCTACCATCATGAATCGACGCTCTGTCTGTATCCT  
 GGTGGCTCTCTCCTGGATGGGGGGCTTCATTCACTTCTATAATACAGGTGGCTCTCATTGTT  
 CGACTTCTTTCTGTGGGCCCAATGAGTTAGACAGTTACTTCTGTGACATCACACAGGTTG  
 TCCGGATTGCCTGTGCCAACACCTTCCCAGAGGAGTTAGTGATGATCTGTAGTAGTGGTCT  
 GATCTCTGTGGTGTGTTTCATTGCTCTGTTAATGTCTATGCCTTCTTCTGGCCTTGCTCA  
 20 AGAAACATTACAGGCTCAGATGAGAATACCAACAGGGCCATGTCCACCTGCTATTCCCACAT  
 TACCATTGTGGTGCTAATGTTTGGGCCATCCATCTACATTTATGCTCGCCCATTTGACTCAT  
 TTTCCCTAGATAAAGTGGTGTCTGTGTTTCATACTGTAATATTCCCTTTACTTAATCCCATT  
 ATTTACACATTGAGAAACAAGGAAGTAAAGGCAGCCATGAGGAAGGTGGTCACCAAATAT  
 ATTTTGTGTGAAGAGAAAGTGA (SEQ ID NO: 408).

25

**AOLFR219 sequences:**

MLTSLDLCFSPIQVAEIKSLPKSMNETNHSRVTEFVLLGLSSSRELQPFLLTFSLLYLAILLGNF  
 LILTVTSDSRLHTPMYFLLANLSFIDVCVASFATPKMIADFLVERKTISFDACLAQIFFVHLFTGS  
 EMVLLVSMAYDRYVAICKPLHYMTVMSSRRVCVVLVLISWVFGFIHTTSQLAFTVNLPCGPN  
 30 KVDSEFFCDLPLVTKLACIDTYVVSLLIVADSGFLSLSSFLLLVVSYTVILVTVRNRSSASMAKAR  
 STLTAHITVVTLFFGPCIFIYVWPFSSYSVDKVLAVFYTIFTLILNPVIYTLRNKEVKAAMSKLKS  
 RYLKPSQVSVIRNVLFLETK (SEQ ID NO: 409).

ATGCTCACTTCATTAACTGATCTCTGTTTCTCTCCTATTCAGGTAGCTGAAATTAAGTCCCT  
 35 TCCAAAATCGATGAATGAGACAAATCATTCTCGGGTGACAGAATTTGTGTTGCTGGGACTG  
 TCTAGTTCAAGGGAGCTCCAACCTTCTTGTGTTCTTACATTTTCACTACTTTATCTAGCAAT  
 TCTGTGTTGGCAACTTCTCATCATCCTCACTGTGACCTCAGATTCCCGCCTTCACACCCCCA  
 TGTACTTCTGCTTGCAAACCTGTCATTTATAGACGTATGTGTTGCCTCTTTTGCTACCCCT  
 AAAATGATTGCAGACTTTCTGGTTGAGCGCAAGACTATTTCTTTTGATGCCTGCCTGGCCC  
 40 AGATTTTCTTTGTTTCATCTCTTCACTGGCAGTGAAATGGTGCTCCTAGTTTCCATGGCCTAT  
 GACCGTTATGTTGCTATATGCAAACCTCTCCACTACATGACAGTCATGAGCCGTCGTGTAT  
 GTGTTGTGCTCGTCCTCATTTCATGGTTTGTGGGCTTCATCCATACTACCAGCCAGTTGGCA  
 TTCACTGTTAATCTGCCATTTTGTGGTCCTAATAAGGTAGACAGTTTTTTCTGTGACCTTCC  
 TCTAGTGACCAAGTTAGCCTGCATAGACACTTATGTTGTCAGCTTACTAATAGTTGCAGAT  
 45 AGTGGCTTTCTTTCTGAGTTCCCTTCTCCTCTTGGTGTCTCCTACACTGTAATACTTGTT  
 ACAGTTAGGAATCGCTCCTCTGCAAGCATGGCGAAGGCCCGCTCCACATTGACTGCTCACA  
 TCACTGTGGTCACTTTATTTCTTTGGACCATGCATTTTCATCTATGTGTGGCCCTTCAGCAGT  
 TACTCAGTTGACAAAGTCCTTGCTGTATTCTACACCATCTTCACGCTTATTTTAAACCTGT  
 AATCTACACGCTAAGAAACAAAGAAGTGAAGGCAGCTATGTCAAACTGAAGAGTCGGTA  
 50 TCTGAAGCCTAGTCAGGTTTCTGTAGTCATAAGAAATGTTCTTTTCCCTAGAAACAAAGTAA  
 (SEQ ID NO: 410).

**AOLFR220 sequences:**

MKQYSVGNQHSNYRSLLPFLCSQMTQLTASGNQTMVTEFLFSMFPHAHRGGLLFFIPLLLIYG  
 55 FILTGNLIMFIVIQVGMALHTPLYFFISVLSFLEICYTTTTIPKMLSCLISEQKSISVAGCLLQMYFF  
 HSLGITESCVLTAIDRYAICNPLRYPTIMIPKLCIQLTVGSCFCGFLVLPEIAWISTLPFCGS

NQIHQIFCDFTPVLSLACTDTFLVVIVDAIHAAEIVASFLVIALSYIRIIVILGMHSAEGHHKAFST  
CAAHLAFLVFLFFGSVAVMYLRFSATYSVFWDTAIAVTFVILAPFFNPITYSLKNKDMKEAIGRLF  
HYQKRAGWAGK (SEQ ID NO: 411).

- 5 ATGAAGCAATATTTCAGTGGGTAATCAACATTCCAATTATAGGAGTCTCTGTTTCCTTTTCT  
GTGTTACAGATGACACAGTTGACGGCCAGTGGGAATCAGACAATGGTGACTGAGTTCCT  
CTTCTCTATGTTCCCGCATGCGCACAGAGGTGGCCTCTTATTCTTTATTCCCTTGCTTCTCA  
TCTACGGATTTATCCTAACTGGAAACCTAATAATGTTTCATTGTCATCCAGGTGGGCATGGC  
CCTGCACACCCCTTTGTATTTCTTTATCAGTGTCTCTCTCTCTGGAGATCTGCTATACCA  
10 CAACCACCATCCCCAAGATGCTGTCTGCCTAATCAGTGAGCAGAAGAGCATTTCGGTGGC  
TGGCTGCCTCCTGCAGATGTACTTTTTCCACTCACTTGGTATCACAGAAAGCTGTGTCTCTG  
ACAGCAATGGCCATTGACAGGTACATAGCTATCTGCAATCCACTCCGTTACCCAACCATCA  
TGATTCCCAAACCTTTGTATCCAGCTGACAGTTGGATCCTGCTTTTGTGGCTTCTCTCTTGTG  
CTTCTGAGATTGCATGGATTTCACCTTGCCTTTCTGTGGCTCCAACCAGATCCACCAGAT  
15 ATTCTGTGATTTACACCTGTGCTGAGCTTGGCCTGCACAGATACATTCTAGTGGTCATT  
GTGGATGCCATCCATGCAGCGGAAATTGTAGCCTCCTTCTCTGGTCATTGCTCTATCCTACA  
TCCGGATTATTATAGTGATTCTGGGAATGCACTCAGCTGAAGGTCATCACAAGGCCTTTTC  
CACCTGTGCTGCTCACCTTGTGTGTTCTTGTATTTTTTGGCAGTGTGGCTGTCATGTATT  
TGAGATTCTCAGCCACCTACTCAGTGTTTTGGGACACAGCAATTGCTGTCACTTTTGTATC  
20 CTTGCTCCCTTTTCAACCCCATCATCTATAGCCTGAAAAACAAGGACATGAAAGAGGCTA  
TTGGAAGGCTTTTCCACTATCAGAAGAGGGCTGGTTGGGCTGGGAAATAG (SEQ ID NO:  
412).

**AOLFR221 sequences:**

- 25 MRNLSGGHVEEFVLVGFPTTPPLQLLLFVLFFAIYLLTLENALIVFTTWLAPSLHRPMYFFLGH  
LSFLELWYINVTIPRLAFLTQDGRVSYVGCMTQLYFFIALACTECVLLAVMAYDRYLAICGP  
LLYPSLMPSSLATRLAAASWGSFGFFSSMMKLLFISQLSYCGPNINHFCDISPLLNLTCSDKEQA  
ELVDLLALVMILLPLLAVVSSYTAIAAILRIPTSRGRHKAFSTCAHHLAVVVITYSSTLFTYAR  
PRAMYTFNHNKIISVLYTIIVFFNPAYICLRNKEVKEAFRKTVMGRCHYPRDVQD (SEQ ID  
30 NO: 413).

- ATGAGAAATTTGAGTGGAGGCCATGTGCGAGGAGTTTGTCTTGGTGGGTTTCCCTACCACGC  
CTCCCCTCCAGCTGCTCCTCTTTGTCTTTTTTTTGAATTTACCTTCTGACATTGTTGGAGA  
ATGCACTTATTGTCTTCAATATGGCTTGTCTCAAGCCTTCATCGTCCCAGTACTTTTTTC  
35 ATTGGCCATCTCTCTTTCCTGGAGCTATGGTACATCAATGTCAACCTTCCCTCGGCTCTTGGC  
AGCCTTTCTTACCCAGGATGGTAGAGTCTCCTACGTAGGTTGCATGACCCAACTGTACTTC  
TTTATTGCCTTAGCCTGTACTGAATGTGTGCTGTTGGCAGTTATGGCCTATGATCGCTACCT  
GGCCATCTGTGGACCCCTCCTTTACCCTAGTCTCATGCCITCCAGTCTGGCCACTCGCCTTG  
CTGCTGCCTCTTGGGGCAGTGGCTTCTTCAGCTCCATGATGAAGCTTCTTTTTATTTCCCAA  
40 TTGTCTACTGTGGACCCAACATTATCAACCACITTTTCTGTGATATTTCCCACTACTCAA  
CCTCACCTGCTCTGACAAGGAGCAAGCAGAGCTAGTAGACTTCCTTCTGGCCCTGGTGATG  
ATTCTACTCCCTCTATTGGCTGTGGTTTCATCATACACTGCCATCATTGCAGCCATCCTGAG  
GATCCCTACGTCCAGGGGACGCCACAAAGCCTTTTCCACTTGTGCCGCTCATCTGGCAGTG  
GTTGTTATCTACTACTCCTCCACTCTCTTCACCTATGCACGGCCCCGGGCCATGTACACCTT  
45 CAACCACAACAAGATTATCTCTGTGCTCTACACTATCATTGTACCATTCTTCAACCCAGCCA  
TCTACTGCCTGAGGAACAAGGAGGTGAAGGAGGCCTTCAGGAAGACAGTGATGGGCAGAT  
GTCATATCTAGGGATGTTTCAGGACTGA (SEQ ID NO: 414).

**AOLFR222 sequences:**

- 50 MGQTNVTSWRDFVFLGFSSSGELQLLLFALFLSLYLVTLSNVFIIAIRLDSHLHTPMYFLSFL  
SFSETCYTLGHIIPRLSGLAGDQAISYVGCQAQMFFSASWACTNCFLLAAMGFDRYVAICAPL  
HYASHMNPILCAQLVITSFLTGYLFLGMLTVIFHLSFCSSEIHFCDTPPVLSLACGDTGPS  
BLRIFILSLVLLVSFFFITISYAYILAILRIPSAEGQKKAFTSCASHLTVVIIIHYGCASFVYLRPK  
ASYSLERDQLIAMTYTVVTPLLNPVYSLRTRAIQTALRNAFRGRLLGKG (SEQ ID NO: 415).

55

ATGGGGCAGACCAACGTAACCTCCTGGAGGGATTTTGTCTTCCTGGGCTTCTCCAGTTCTG  
 GGGAGTTGCAGCTCCTTCTCTTTGCCTTGTTCTCTCTGTATCTAGTCACTCTGACCAGC  
 AATGTCTTCATTATCATAGCCATCAGGCTGGATAGCCATCTGCACACCCCATGTACCTCTT  
 CCTTCTCCTATCCTTCTCTGAGACCTGCTACACTTTGGGCATCATCCCTAGAATGCTCT  
 5 CTGGCCTGGCTGGGGGGGACCAGGCTATCTCCTATGTGGGCTGTGCTGCCAGATGTTCTT  
 TTCTGCCTCATGGGCTGTACTAACTGCTTCCTTCTGGCTGCCATGGGCTTTGACAGATATG  
 TGGCCATCTGTGCTCCACTCCACTATGCCAGCCACATGAATCCTACCCTCTGTGCCAGCT  
 GGTCACTTCTCCTTCTGACTGGATACCTCTTTGGACTGGGAATGACACTAGTTATTTTCC  
 ACCTCTCATTCTGCAGCTCCCATGAAATCCAGCACTTTTTTTGTGACACGCCACCTGTGCTG  
 10 AGCCTAGCCTGTGGAGATACAGGCCCGAGTGAGCTGAGGATCTTTATCCTCAGTCTTTTGG  
 TCCTCTTGGTCTCCTTCTTCTTCATCACCATCTCCTACGCCTACATCTTGGCAGCAATACTG  
 AGGATCCCCTCTGCTGAGGGGCAGAAGAAGGCCTTCTCCACTTGTGCCTCGCACCTTACAG  
 TGGTCATTATTATTATGGCTGTGCTTCTTCGTGTACCTGAGGCCCAAAGCCAGCTACTCT  
 CTTGAGAGAGATCAGCTTATTGCCATGACCTATACTGTAGTGACCCCCCTCCTTAATCCCA  
 15 TTGTTATAGTCTAAGGACTAGGGCTATACAGACAGCTCTGAGGAATGCTTTCAGAGGGAG  
 ATTGCTGGGTAAAGGATGA (SEQ ID NO: 416).

**AOLFR223 sequences:**

MEANESSEGISFVLLGLTSPGQQRPLFVLFLLLYVASLLGNGLIVAAIQASPALHAPMYFLLA  
 20 HLSFADLCFASVTVPKMLANLLAHDHSISLAGCLTQMYFFALGVTDSCLLAAMAYDCYVAIR  
 HPLPYATRMSRAMCAALVGMWLVSHVHSLLYILLMARLSFCASHQVPHFFCDHQPILLRLSC  
 SDTHHIQLLIFTEGA AVVVT PFLILASYGAIAAAVLQLPSASGRLRAVSTCGSHLAVVSLFYGT  
 VIAVYFQATSRREA EWGRVATVMYTVVTPMLNPIIYSLWNRDVQGALRALLIGRRISASDS  
 (SEQ ID NO: 417).

ATGGAGGCTGCCAATGAGTCTTCAGAGGGAATCTCATTCTGTTTTATTGGGACTGACAACAA  
 GTCTTGACAGCAGCGGCTCTCTTTGTGCTGTTCTTGCTCTTGTATGTGGCCAGCCTCCTG  
 GGTAATGGACTCATTGTGGCTGCCATCCAGGCCAGTCCAGCCCTTCATGCACCCATGTACT  
 TCCTGCTGGCCCACTGTCTTTGCTGACCTCTGTTTCGCCTCCGTCAGTGTGCCCAAGATG  
 30 TTGGCCAACTTGTTGGCCCATGACCACTCCATCTCGCTGGCTGGCTGCCTGACCCAAATGT  
 ACTTCTTCTTTGCCCTGGGGGTAAGTGATAGCTGTCTTCTGGCGGCCATGGCCTATGACTG  
 CTACGTGGCCATCCGGCACCCCTCCCTATGCCACGAGGATGTCCCGGCCATGTGCGCA  
 GCCCTGGTGGGAATGGCATGGCTGGTGTCCACGTCCTCCCTCCTGTATATCCTGTCTCA  
 TGGCTCGCTTGCTCTTCTGTGCTTCCCACCAAGTGCCCCACTTCTTCTGTGACCACCAGCCT  
 35 CTCTTAAGGCTCTCGTGCTCTGACACCCACCACATCCAGCTGCTCATCTTACCGAGGGCG  
 CCGCAGTGGTGGTCACTCCCTTCTGCTCATCCTCGCCTCCTATGGGGCCATCGCAGCTGC  
 CGTGCTCCAGCTGCCCTCAGCCTCTGGGAGGCTCCGGGCTGTGTCCACCTGTGGCTCCAC  
 CTGGCTGTGGTGAGCCTCTTCTATGGGACAGTCATTGCAGTCTACTTCCAGGCCACATCCC  
 GACGCGAGGCAGAGTGGGGCCGTGTGGCCACTGTATGTACACTGTAGTACCCCCATGC  
 40 TGAACCCCATCATCTACAGCCTCTGGAATCGCGATGTACAGGGGGCACTCCGAGCCCTTCT  
 CATTGGGCGAAGGATCTCAGCTAGTGA CTCTGA (SEQ ID NO: 418).

**AOLFR224 sequences:**

MGSFNTSFEDGFILVGFSDWPQLEPILFVFIFIFYSLTFLGNTIIIALSWLDRRLHTPMYFFLSHLSL  
 45 LDLCFTTSTVPQLLINLCGVDRITTRGGCVAQLFIYLALGSTECVLLVVMADFRIA AVCRPLHY  
 MAIMHPHLCQTLAIASWGAGFVNSLIQTGLAMAMPLCGHRLNHFFCEMPVFLKLACADTEGT  
 EAKMFVARVIVVAVPAALILGSYVHIAHAVLRVKSTAGRRKAFGTCSHLLVVFLFYGSAIYT  
 YLQSIHNYSEREGKFVALFYTIITPILNPLIYTLRNKDVKGALWKVLWRGRDSG (SEQ ID NO:  
 419).

ATGGGAAGTTTCAACACCAGTTTTGAAGATGGCTTCATTTTGGTGGGATTCTCAGATTGGC  
 CGCAACTGGAGCCCATCCTGTTTGTCTTTATTTTATTTTCTACTCCCTAACTCTCTTTGGC  
 AACACCATCATCATCGCTCTCTCCTGGCTAGACCTTCGGCTGCACACACCTATGTACTTCTT  
 TCTCTCTCATCTGTCCCTCCTGGACCTCTGCTTACCACCAGCACCGTGCCCCAGCTCCTGA  
 55 TCAACCTTTGCGGGGTGGACCGCACCATCACCCGTGGAGGGTGTGTGGCTCAGCTCTTCAT  
 CTACCTAGCCCTGGGCTCCACAGAGTGTGTGCTCCTGGTGGTGTATGGCCTTTGACCGCTAT

GCTGCTGTCTGTCTGCTCCACTCCACTACATGGCCATCATGCACCCCCATCTCTGCCAGACCCCT  
 GGCTATCGCCTCCTGGGGTGCGGGTTTCGTGAACCTCTCTGATCCAGACAGGTCTCGCAATG  
 GCCATGCCTCTCTGTGGCCATCGACTGAATCACTTCTTCTGTGAGATGCCTGTATTTCTGAA  
 GTTGGCTTGTGCGGACACAGAAGGAACAGAGGCCAAGATGTTTGTGGCCCCGAGTCATAGT  
 5 CGTGGCTGTTTCTGAGCACTTATTCTAGGCTCCTATGTGCACATTGCTCATGCAGTGCTG  
 AGGGTGAAGTCAACGGCTGGGCGCAGAAAGGCTTTTGGGACTTGTGGGTCCCACCTCCTA  
 GTAGTTTTCTTTTTTATGGCTCAGCCATCTACACATATCTCCAATCCATCCACAATTATTC  
 TGAGCGTGAGGGAAAATTTGTTGCCCTTTTTTATACTATAATTACCCCCATCTCAATCCTC  
 TCATTTATACACTAAGAAACAAGGACGTGAAGGGGGCTCTGTGGAAAGTACTATGGAGGG  
 10 GCAGGGACTCAGGGTAG (SEQ ID NO: 420).

**AOLFR225 sequences:**

MENYNQSTDFILLGLFPSSIIDLFFFILIVFIFLMALIGNLSMILLIFLDTHLHTPMYFLLSQLSLID  
 LNYISTIVPKMASDFLHGNKSISFTGCGIQSFFFLALGGAEALLASMAYDRYIAJCFPLHYLIRM  
 15 SKRVCVLMITGWSWIGSINACAHTVYVLHIPYCRSRAINHFFCDVPAMVTLACMDTWVYEGTV  
 FLSATIFLVFPFIGISCSYGQVLFVYHMKSAEGRKKAYLTCSTHLTVVTFYAPFVYTYLRPRS  
 LRSPTEDKVLAVFYTLTPMLNPITYSLRNKEVMGALTRVSQRICSVKM (SEQ ID NO: 421).

ATGGAAAATTACAATCAAACATCAACTGATTTTCATCTTATTGGGGCTGTTTCCACCATCAA  
 20 TAATTGACCTTTTCTTCTTCATTCTCATTTGTTTCATTTTCTGATGGCTCTAATTGGAAACC  
 TGTCCATGATTCTTCTCATCTTCTTGGACACCCATCTCCACACACCCATGTATTTCTACTG  
 AGTCAGTCTCCCTCATTGACCTAAATTACATCTCCACCATTTGTTCTAAGATGGCATCTGA  
 TTTTCTGCATGGAAACAAGTCTATCTCCTTCACTGGGTGTGGGATTCCAGAGTTTCTTCTTCT  
 TGGCATTAGGAGGTGCAGAAGCACTACTTTTGGCATCTATGGCCTATGATCGTTACATTGTC  
 25 TATTTGCTTTCTCTCCACTATCTCATCCGCATGAGCAAAAGAGTGTGTGTGCTGATGATA  
 ACAGGGTCTTGGATCATAGGCTCGATCAATGCTTGTGCTCACACTGTATATGTACTCCATA  
 TTCCTTATTGCCGATCCAGGGCCATCAATCATTTCTTCTGTGATGTCCCAGCAATGGTGACT  
 CTGGCCTGCATGGACACCTGGGTCTATGAGGGGCACAGTGTTTTTGTAGTGCCACCATCTTTC  
 TCGTGTTTTCCCTTCATTGGTATTTTCATGTTTCTATGGCCAGGTTCTCTTTGCTGTCTACCAC  
 30 ATGAAATCTGCAGAAGGGAGGAAGAAAGCCTATTTGACCTGCAGCACCCACCTCACTGTA  
 GTAACITTTCTACTATGCACCTTTTGTCTACACTTATCTACGTCCAAGATCCCTGCGATCTCC  
 AACAGAGGACAAGGTTCTGGCTGTCTTACACCATCCTCACCCCAATGCTCAACCCCATC  
 ATCTATAGCCTGAGGAACAAGGAGGTGATGGGGGCCCTGACACGAGTGAGTCAGAGAATC  
 TGCTCTGTGAAAATGTAG (SEQ ID NO: 422).

35

**AOLFR226 sequences:**

MEWRNHSGRVSEFVLLGFAPAPLQVLLFALLLLAYVLVLTENTLIIMAIRNHSTLHKPMYFFL  
 ANMSFLEIWYVTVTIPKMLAGFVGSQDGHGQLISFEGCMTQLYFFLGLGCTECVLLAVMAYD  
 RYMAICYPLHYPVIVSGRLCVQMAAGSWAGGFGISMVKVFLISGLSYCGPNINHFFCDVSPLL  
 40 NLSCTDMSTAELTDFILAIFILLGPLSVTGASYVAITGAVMHISAAAGRYKAFSTCASHLTVVIF  
 YAASIFTYARPKALSAFDNTKLVSVLVAVIVPLLNPIIYCLRNQEVKRALCCTLHLYQHQPDP  
 KKASRNV (SEQ ID NO: 423).

ATGGAGTGGCGGAACCATAGTGGGAGAGTGAGTGAGTTTGTGTTGCTGGGCTTCCCTGCT  
 45 CCTGCGCCACTACAGGTACTATTGTTTGGCCTTTTGTGCTGGCCTATGTGTTGGTGCTGAC  
 TGAGAACACACTCATCATTATGGCAATTAGGAACCATTTACCCTCCACAAACCCATGTAC  
 TTTTTTCTAGCTAATATGTCCTTTCTGGAGATCTGGTATGTCAGTGTCACTATTCCCAAGAT  
 GCTTGCTGGCTTTGTTGGATCCAAACAGGATCATGGACAGCTAATCTCCTTTGAGGGATGC  
 ATGACACAGCTCTACTTTTTCTTGGCTTGGGCTGCACTGAGTGTGTCCTTCTCGCTGTTAT  
 50 GGCCTATGATCGCTATATGGCCATCTGCTATCCTCTCCACTACCCAGTCATTGTCACTGGCC  
 GGCTGTGTGTGCAGATGGCTGCTGGCTCTTGGGCTGGAGGTTTTGGCATCTCCATGGTCAA  
 AGTTTTTCTTATTTCTGGCCTCTCTTACTGTGGCCCCAACATCATCAACCACTTTTTCTGTG  
 ATGCTCTCTCATTGCTCAACCTCTCATGCACTGATATGTCCACAGCAGAGCTTACAGATTTC  
 ATCCTGGCCATTTTATTCTTCTAGGGCCACTCTCTGCACTGGGGCCTCCTATGTGGCCAT  
 55 TACTGGTGCTGTGATGCACATATCTTCGGCTGCTGGACGCTATAAGGCCTTTTCCACCTGT  
 GCCTCTCATCTCACTGTTGTGATAATCTTCTATGCAGCCAGTATCTTCATCTATGCTCGGCC

AAAGGCACTCTCAGCTTTTGACACCAACAAGTTGGTCTCTGTACTGTATGCTGTCATTGTA  
CCATTGCTCAATCCCATCATTTACTGCCTGCGCAATCAAGAGGTCAAGAGAGCCCTATGCT  
GTACTCTGCACCTGTACCAGCACCAGGATCCTGACCCCAAGAAAGCTAGCAGAAATGTATA  
G (SEQ ID NO: 424).

5

**AOLFR227 sequences:**

MEPQNTSTVTNPFQLLGFQNLLEWQALLFVIFLLIYCLTIIGNVVITVVSQGLRLHSPMYMFLQH  
LSELEVWYTTSTTVPLLLANLLSWGQAI SFSACMAQLYFFVFLGATECFLLAFMAYDRYLAICSP  
LRYPFMLMRGLCARLVVSWCTGVSTGFLHSMMSRLDFCGRNQNHFFCDLPPLMQLSCSR  
10 YITEVTIFILSIAVLCICFFLTLPYVVFVSSILRIPSTSGRRKTFSTCGSHLAVVTLYYGTMISMVY  
CPSPHLLPEINKIISVFYTVVTPLLNPVIYSLRNKDFKEAVRKVMRRKCGILWSTSKRKF  
LY (SEQ ID NO: 425).

ATGGAGCCCCAAAATACCTCCACTGTGACTAACTTTCAGCTGTTAGGATTCCAGAACCTTC  
15 TTGAATGGCAGGCCCTGCTCTTTGTCATTTTCCTGCTCATCTACTGCCTGACCATTATAGGG  
AATGTTGTCTATCATCACCGTGGTGAGCCAGGGCCTGCGACTGCACTCCCCTATGTACATGT  
TCCTCCAGCATCTCTCCTTTCTGGAGGTCTGTGTACACGTCCACCAGTGTGCCCTTCTCCTA  
GCCAACCTGCTGTCTGGGGCCAGGCATCTCCTTCTCTGCTGCATGGCACAGCTCTACT  
TCTTCGTATTCTCGGCGCCACCGAGTGCTTTCTCCTGGCCTTCATGGCCTATGACCGTTAC  
20 CTGGCCATCTGCAGCCCACTCCGCTACCCCTTTCTCATGCATCGTGGGCTATGTGCCAGGTT  
GGTGGTGGTCTCATGGTGCACAGGGGTGAGCACAGGCTTTCTGCATTCCATGATGATTTCC  
AGGTTGGACTTCTGTGGGCGCAATCAGATTAACCATTTCTTCTGCGACCTCCCGCCACTCA  
TGCAGCTCTCCTGTTCCAGAGTTTATATCACCGAGGTGACCATCTTCATCCTGTCAATTGCC  
GTGCTGTGCATTTGTTTTTTCTGACACTGGGGCCCTATGTTTTTCATTGTGTCTCCATATT  
25 GAGAATCCCTTCCACCTCTGGCCGGAGAAAGACCTTTTCCACATGTGGCTCCACCTGGCT  
GTTGTCACTCTCTACTACGGGACCATGTCTCCATGTATGTGTGTCCAGTCCCCACCTGTT  
GCCTGAAATCAACAAGATCATTTCTGTCTTCTACACTGTGGTCACACCAGTCTGAAACCA  
GTTATCTACAGCTTGAGGAACAAAGACTTCAAAGAAGCTGTTAGAAAGGTCATGAGAAGG  
AAATGTGGTATTCTATGGAGTACAAGTAAAAGGAAGTTCCTTTATTAG (SEQ ID NO: 426).

30

**AOLFR229 sequences:**

MFYVNQIPFQLYHISFVYPTELWSRAIIPCMTLSFWVCSATPVSPGFFALILLVFVTSIASNVVK  
IILIHDSRLHTPMYFLLSQLSLRDILYISTIVPKMLVDQVMSQRAISFAGCTAQHFLYLTLGAE  
FFLLGLMSCDRYVAICNPLHYPDLMRSKICWLIVAAA WLGGSIDGFLLPVTMQFPFCASREIN  
35 HFFCEVPALLKLSCTDTSAYETAMYVCCIMMLLIPFSVISGSYTRILITVYRMSEABGRRKAVAT  
CSSHMVVVSLFYGAAMYTYVLPHSYHTPEQDKAVSAFYTLTPMLNPLIYSLRNKDVGTALQK  
VVGRCVSSGKVTIF (SEQ ID NO: 427).

ATGTTTTATGTAAATCAGATACCTTTCCAACCTTATCATATCTCTTTCTGTTACCTACAGA  
40 GCTATGGAGCAGAGCAATTATCCGTGTATGCCGACTTTATCCTTCTGGGTTTGTTCAGCA  
ACGCCCGTTTTCCCTGGCTTCTTTGCCCTCATTCTCCTGGTCTTTGTGACCTCCATAGCCAG  
CAACGTGGTCAAGATCATTCTCATCCACATAGACTCCCGCCTCCACACCCCATGTACTTC  
CTGCTCAGCCAGCTCTCCCTCAGGGACATCCTGTATATTCCACCAATTGTGCCAAAATGTCT  
GGTCGACCAGGTGATGAGCCAGAGGCCATTTCCCTTTGCTGGATGCACTGCCCAACACTTC  
45 CTCTACTTGACCTTAGCAGGGGCTGAGTTCTTCTCCTAGGACTCATGTCTGTGATCGCTA  
CGTAGCCATCTGCAACCCTCTGCACTATCCTGACCTCATGAGCCGCAAGATCTGCTGGTTG  
ATTGTGGCGGCAGCCTGGCTGGGAGGGTCTATCGATGGTTTCTTGCTACCCCCGTCACCA  
TGCAGTTCCCCTTCTGTGCCTCTCGGGAGATCAACCACTTCTTCTGCGAGGTGCCTGCCCTT  
CTGAAGCTCTCCTGCACGGACACATCAGCCTACGAGACAGCCATGTATGTCTGCTGTATTA  
50 TGATGCTCCTCATCCCTTCTCTGTGATCTCGGGCTCTTACACAAGAATTCTCATTACTGTT  
TATAGGATGAGCGAGGCAGAGGGGAGGCGAAAGGCTGTGGCCACCTGCTCCTCACACATG  
GTGGTTGTGACCTCTTCTATGGGGCTGCCATGTACACATACGTGCTGCCTCATTCTTACCA  
CACCCCTGAGCAGGACAAAGCTGTATCTGCCTTCTACACCATCCTCACTCCCATGCTCAAT  
CCACTCATTTACAGCCTTAGGAACAAGGATGTACGCGGGGCCCTACAGAAGGTTGTTGGG  
55 AGGTGTGTGCTCCTCAGGAAAGGTAACCACTTTCTAA (SEQ ID NO: 428).



**AOLFR230 sequences:**

MGMEGLLQNSTNFVLTGLITHPAFPGLLFAIVFSIFVVAITANLVMILLIHMD SRLHTPMYFLLS  
 QLSIMDTIYICTV PKMLQDLLSKDKTISFLGCAVQIFLYLTLIGGEFFLLGLMAYDRYVAVCNP  
 LRYPLLMNRRVCLFMVVGSWVGGSLDGFMLTPVTMSFPFCRSREINHFFCEIPAVLKLSDTDS  
 5 LYETLMYACCVLMLLIPLSVISVSYTHILLTVHRMNSAEGRRKAFATCSSHIMVVSVFYGAIFY  
 TNVLPHSYHTPEKDKVVSAFYTILTPMLNPLIYSLRNKDVAALRKVLGRCGSSQSIRVATVIR  
 KG (SEQ ID NO: 429).

ATGGGCATGGAGGGTCTTCTCCAGAACTCCACTAACTTCGTCCTCACAGGCCTCATCACCC  
 10 ATCCTGCCTTCCCCGGGCTTCTCTTTGCAATAGTCTTCTCCATCTTTGTGGTGGCTATAACA  
 GCCAACTTGGTCATGATTCTGCTCATCCACATGGACTCCCGCTCCACACACCCATGTACTT  
 CTTGCTCAGCCAGCTCTCCATCATGGATACCATCTACATCTGTATCACTGTCCCAAGATGC  
 TCCAGGACCTCCTGTCCAAGGACAAGACCATTTCCTTCCTGGGCTGTGCAGTTCAGATCTT  
 CCTCTACCTGACCCTGATTGGAGGGGAATTCCTCCTGCTGGGTCTCATGGCCTATGACCGC  
 15 TATGTGGCTGTGTGCAACCCCTCTACGGTACCCTCTCCTCATGAACCGCAGGGTTTGCTTATT  
 CATGGTGGTCCGGCTCCTGGGTGGTGGTTCCTTGGATGGGTTCATGCTGACTCCTGTCACT  
 ATGAGTTTCCCTTCTGTAGATCCCGAGAGATCAATCACTTTTTCTGTGAGATCCCAGCCGT  
 GCTGAAGTTGTCTTGCACAGACACGTCATCTATGAGACCCTGATGTATGCCTGCTGCGTG  
 CTGATGCTGCTTATCCCTCTATCTGTCTCTGTCTCCTACACGCACATCCTCCTGACTGT  
 20 CCACAGGATGAACTCTGCTGAGGGCCGCGCAAAGCCTTTGCTACGTGTTCTCCACATT  
 ATGGTGGTGAGCGTTTCTACGGGGCAGCCTTCTACACCAACGTGCTGCCCCACTCCTACC  
 AACTCCAGAGAAAGATAAAGTGGTGTCTGCCTTCTACACCATCCTCACCCCATGCTCAA  
 CCCACTCATCTACAGCTTGAGGAATAAAGATGTGGCTGCAGCTCTGAGGAAAGTACTAGG  
 GAGATGTGGTTCCTCCAGAGCATCAGGGTGGCGACTGTGATCAGGAAGGGCTAG (SEQ ID  
 25 NO: 430).

**AOLFR231 sequences:**

MERANHSVVSEFILLGLSKSQNLQILFGLFVSFVGVGLGNLLILVTVTFDSSLHTPMYFLLSNL  
 SCIDMILASFATPKMIVDFLRERKTISWWGCYSQMFFMHLLGGSEMMLLVAMADRYVAICKP  
 30 LHYMTIMSPRVLTGLLLSSYAVGVFHSSSQMAFMLTLPFCGPNVIDSFFCDLPLVIKLACKDTYI  
 LQLVIADSGLLSLVCFLLLVSYGVIFSVRYRAASRSSKAFSTLSAHITVVTFFAPCVFIYVW  
 PFSRYSVDKILSVFYTIFTPLNPIIYTLRNQEVKAAIKKRLCI (SEQ ID NO: 431).

ATGGAAAGAGCAAACCATTCACTGGTATCGGAATTTATTTTGTGGGACTTTCCAAATCTC  
 35 AAAATCTTCAGATTTTATTCTTCTTGGGATTCTCTGTGGTCTTCGTGGGGATTGTGTTAGGA  
 AACCTGCTCATCTTGGTGACTGTGACCTTTGATTCTGCTCCTTCACACACCAATGTATTTCT  
 GCTTAGCAACCTCCTGCAATTGATATGATCCTGGCTTCTTTGCTACCCCTAAGATGATTG  
 TAGATTTCTCCGAGAACGTAAGACCATCTCATGGTGGGGATGTTATTTCCAGATGTTCTT  
 TATGCACCTCCTGGGTGGGAGTGAGATGATGTTGCTTGTAGCCATGGCAATAGACAGGTAT  
 40 GTTGCCATATGCAAACCCCTCCATTACATGACCATCATGAGCCACGGGTGCTCACTGGGC  
 TACTGTTATCCTCCTATGCAGTTGGATTGTGCACTCATCTAGTCAAATGGCTTTCATGTTG  
 ACTTGCCCTTCTGTGGTCCCAATGTTATAGACAGCTTTTTCTGTGACCTTCCCTTGTGAT  
 TAACTTGCTGCAAGGACACCTACATCCTACAGCTCCTGGTCATTGCTGACAGTGGGCTC  
 CTGTCACCTGGTCTGCTTCTCCTCTTGTCTCCTATGGAGTCATAATATTCTCAGTTAG  
 45 GTACCGTGCTGCTAGTCGATCCTCTAAGGCTTTCTCCACTCTCTCAGCTCACATCACAGTTG  
 TGACTCTGTTCTTTGCTCCGTGTGCTTTATCTACGTCTGGCCCTTCAGCAGATACTCGGTA  
 GATAAAATTCTTTCTGTGTTTTACACAATTTACACACCTCTCTTAAATCCTATTATTTATAC  
 ATTAAGAAATCAAGAGGTAAAAGCAGCCATTAAAAAAGACTCTGCATATAA (SEQ ID NO:  
 432).

50

**AOLFR232 sequences:**

MDNITWMASHTGWSDFILMGLFRQSKHPMANITWMANHTGWSDFILLGLFRQSKHPALLCV  
 VIFVVFLMALSGNAVLILLIHCDHLHTPMYFFISQLSLMDMAYISVTPKMLLDQVMGVNKS  
 APECGMQMFFYVTLAGEFFLLATMAYDRYVAICHPLRYPVLMNHRVCLFLSSGCWFLGSVD  
 55 GFTFTPTMTFPFRGSREIHFFCEVPAVLNLSCDTSLYEIFMYLCCVLMLLPVVVISSSYLLILL

TIHGMNSAEGRRKKAFAATCSSHLTVVILFYGAATYTYMLPSSYHTPEKDDMMVSVFYTILTPVVNP  
LIYSLRNKDVGMGALKKMLTVEPAFQKAME (SEQ ID NO: 433).

5 ATGGACAACATCACCTGGATGGCCAGCCACACTGGATGGTCGGATTTTCATCCTGATGGGAC  
TCTTCAGACAATCCAAACATCCAATGGCCAATATCACCTGGATGGCCAACCACACTGGATG  
GTCGGATTTTCATCCTGTTGGGACTCTTCAGACAATCCAAACATCCAGCACTACTTTGTGTG  
GTCATTTTTGTGGTTTTCTGATGGCGTTGTCTGGAAATGCTGTCCTGATCCTTCTGATACA  
CTGTGACGCCCACCTCCACACCCCCATGTACTTTTTTCATCAGTCAATTGTCTCTCATGGACA  
TGGCGTACATTTCTGTCACTGTGCCCCAAGATGCTCCTGGACCAGGTCATGGGTGTGAATAA  
10 GATCTCAGCCCCCTGAGTGTGGGATGCAGATGTTCTTCTACGTGACACTAGCAGGTTTCAGAA  
TTTTTCTTCTAGCCACCATGGCCTATGACCGCTACGTGGCCATCTGCCATCCTCTCCGTTA  
CCCTGTCTCATGAACCATAGGGTGTGTCTCTTCTGTCATCAGGCTGCTGGTTCTGGGCT  
CAGTGGATGGCTTCACATTCACCTCCCATCACCATGACCTTCCCCCTCCGTGGATCCCGGGA  
GATTCATCATTTCTTCTGTGAAGTTCCTGCTGTATTGAATCTCTCCTGCTCAGACACCTCAC  
15 TCTATGAGATTTTCATGTACTTGTGCTGTGTCTCATGCTCCTCATCCCTGTGGTGATCATT  
TCAAGCTCCTATTTACTCATCTCCTCACCATCCACGGGATGAACTCAGCAGAGGGCCGGA  
AAAAGGCCTTTGCCACCTGCTCCTCCACCTGACTGTGGTCATCCTCTTCTATGGGGCTGCC  
ATCTACACCTACATGCTCCCCAGCTCCTACACACCCCTGAGAAGGACATGATGGTATCTG  
TCTTCTATACCATCCTCACTCCAGTGGTGAACCCCTTAACTCTATAGTCTTAGGAATAAGGAT  
20 TCGATGGGGGCTCTGAAGAAAATGTTAACAGTGGAACCTGCCTTTCAAAAAGCTATGGAG  
TAG (SEQ ID NO: 434).

#### AOLFR233 sequences:

25 MANITRMANHTGKLDFILMGLFRRSKHPALLSVVIFVFLKALSGNAVLILLIHCD AHLHSPMY  
FFISQLSLMDMAYISVTVPKMLLDQVMGVNKVSAPECGMQMFLYLTLAGSEFFLLATMAYDR  
YVAICHPLRYPVLMNHRVCLFLASGCWFLGSVDGFMLTPITMSFPFCRSWEIHHFFCEVPAVTI  
LSCSDTSLYETLMYLCCVLMLLIPVTHISSYLLILLTVHRMNSAEGRRKKAFAATCSSHLTVVILFY  
GAAVYTYMLPSSYHTPEKDDMMVSVFYTILTPVLNPLIYSLRNKDVGMGALKKMLTVRFVL  
(SEQ ID NO: 435).

30 ATGGCCAACATCACCAAGGATGGCCAACCACACTGGAAAGTTGGATTTTCATCCTCATGGGAC  
TCTTCAGACGATCCAAACATCCAGCTCTACTTAGTGTGGTCATCTTTGTGGTTTTCTGAA  
GCGTTGTCTGGAAATGCTGTCTGATCCTTCTGATACACTGTGACGCCCACCTCCACAGCC  
CCATGTACTTTTTTCATCAGTCAATTGTCTCTCATGGACATGGCGTACATTTCTGTCACTGTG  
35 CCCAAGATGCTCCTGGACCAGGTCATGGGTGTGAATAAGGTCTCAGCCCCTGAGTGTGGG  
ATGCAGATGTTCTCTATCTGACACTAGCAGGTTTCGGAATTTTCTTCTAGCCACCATGGC  
CTATGACCGCTACGTGGCCATCTGCCATCCTCTCCGTTACCCTGTCTCATGAACCATAGG  
GTCTGTCTTTTCTGGCATCGGGCTGCTGGTTCTGGGCTCAGTGGATGGCTTCATGCTCAC  
TCCCATCACCATGAGCTTCCCCCTTCTGCAGATCCTGGGAGATTCATCATTTCTTCTGTGAAG  
40 TCCCTGCTGTAACGATCCTGTCTGCTCAGACACCTCACTCTATGAGACCCTCATGTACCTA  
TGCTGTGTCTCATGCTCCTCATCCCTGTGACGATCATTTCAGCTCCTATTTACTCATCCT  
CCTCACCGTCCACAGGATGAACTCAGCAGAGGGCCGGA AAAAAGGCCTTTGCCACCTGCTC  
CTCCACCTGACTGTGGTCATCCTCTTCTATGGGGCTGCCGTCTACACCTACATGCTCCCCA  
GCTCCTACCACACCCCTGAGAAGGACATGATGGTATCTGTCTTCTATACCATCCTCACTCC  
45 GGTGCTGAACCCCTTAACTCTATAGTCTTAGGAATAAGGATGTCATGGGGGCTCTGAAGAAA  
ATGTTAACTGTGAGATTCGTCCTTTAG (SEQ ID NO: 436).

#### AOLFR234 sequences:

50 MPNSTTVMEFLLMRFSVDVWTLQILHSASFFMFLYVTLMGNILIVTVTTCDSSLHMPMYFFLRN  
LSILDACYISVTVPTSCVNSLLDSTTISKAGCVAQVFLVFFVYVELLFLTIMAHDRYVAVCQPL  
HYPVIVNSRICQMTLASLLSGLVYAGMHTGSTFQLPFCRSNVIHQFFCDIPSLKLSCSDTFSNE  
VMIVVSALGVGGGCFIFIRSYIHIFSTVLGFPRGADRTKAFSTCIPHILVVSVFLSSCSSVYLRPP  
AIPAATQDLILSGFYSIMPLFNPIIYSLRNKQIKVAIKKIMKRIFYSENV (SEQ ID NO: 437).

55 ATGCCCAATTCAACCACCGTGATGGAATTTCTCCTCATGAGGTTTTCTGATGTGTGGACAC  
TACAGATTTTACATTCTGCATCCTTCTTATGTTGTATTTGGTAACTCTAATGGGAAACATC

CTCATTGTGACCGTCACCACCTGTGACAGCAGCCTTCACATGCCCATGTACTTCTTCCTCAG  
 GAATCTGTCTATCTTGGATGCCTGCTACATTTCTGTTACAGTCCCTACCTCATGTGTCAATT  
 CCCTACTGGACAGCACCACCATTCTAAGGCGGGATGTGTAGCTCAGGTCCTCCTCGTGGT  
 TTTTTTGTATATGTGGAGCTTCTGTTTCTCACCATTATGGCTCATGACCGCTATGTGGCTG  
 5 TCTGCCAGCCACTTCACTACCCTGTGATCGTGAACCTCTCGAATCTGCATCCAGATGACACT  
 GGCTCCCTACTCAGTGGTCTTGTCTATGCAGGCATGCACACTGGCAGCACATTCCAGCTG  
 CCCTTCTGTGCGGTCCAACGTTATTCATCAATTCTTCTGTGACATCCCCTCTCTGCTGAAGCT  
 CTCTTGCTCTGACACCTTCAGCAATGAGGTCATGATTGTTGTCTCTGCTCTGGGGGTAGGT  
 GCGGGCTGTTTCATCTTTATCATCAGGTCTTACATTCACATCTTTTCGACCGTGTCTGGGTT  
 10 TCCAAGAGGAGCAGACAGAACAAAGGCCTTTCCACCTGCATCCCTCACATCCTGGTGGTG  
 TCAGTCTTCTCAGTTCATGCTCTTCTGTGTACCTCAGGCCACCTGCGATACCTGCAGCCAC  
 CCAGGATCTGATCCTTTCTGGTTTTATTCATAATGCCTCCCCTCTTTAACCTATTATTTA  
 CAGTCTTAGAAATAAGCAAATAAAGGTGGCCATCAAGAAAATCATGAAGAGAATTTTTTA  
 TTCAGAAAATGTGTAA (SEQ ID NO: 438).

15

**AOLFR235 sequences:**

MDGVNDSSLQGFVLMGISDHPQLEMIFFIALLFSYLLTLLGNSTIILSRLEARLHTPMYFFLSNL  
 SSLLDAFATSSVPQMLINLWGPCKTISYGGCITQLYVFLWLGATECILLVVMFAFDYVAVCRPL  
 RYTAIMNPQLCWLLAVIACLGGLGNSVIQSTFTLQLPLCGHRRVEGFLCEVPAMIKLACGDTSL  
 20 NQAVLNGVCTFFTA VPLSIIVISYCLIAQAVLKIRSAEGRRKAFNTCLSHLLVFLFYGSASYGY  
 LLPAKNSKQDQGFISLFYSLVTPMVNPLIYTLRNMVKGALRRLLGKGREVG (SEQ ID NO:  
 439).

ATGGACGGGGTGAATGATAGCTCCTTGCAGGGCTTTGTTCTGATGGGCATATCAGACCATC  
 25 CCCAGCTGGAGATGATCTTTTATAGCCATCCTCTCTCCTATTTGCTGACCCTACTTGGG  
 AACTCAACCATCATCTTGCTTTCCCGCCTGGAGGCCCGGCTCCATACACCCATGTACTTCTT  
 CCTCAGCAACCTCTCCTCCTTGGACCTTGCTTTGCTACTAGTTCAGTCCCCCAAATGCTGA  
 TCAATTTATGGGGACCAGGCAAGACCATCAGCTATGGTGGCTGCATAACCCAGCTCTATGT  
 CTTCCTTTGGCTGGGGGCCACCGAGTGCATCCTGCTGGTGGTGATGGCATTGACCGCTAC  
 30 GTGGCAGTGTGCCGGCCCCCTCCGCTACACCGCCATCATGAACCCCCAGCTCTGCTGGCTGC  
 TGGCTGTGATTGCCTGCCTGGGTGGCTTGGGCAACTCTGTGATCCAGTCAACATTCACTCT  
 GCAGCTCCCATTTGTGTGGGCACCGGAGGGTGGAGGGATTCTCTGCGAGGTGCCTGCCAT  
 GATCAAACTGGCCTGTGGCGACACAAGTCTCAACCAGGCTGTGCTCAATGGTGTCTGCACC  
 TTCTTCACTGCAGTCCCACTAAGCATCATCGTGATCTCCTACTGCCTCAATTGCTCAGGCAGT  
 35 GCTGAAAATCCGCTCTGCAGAGGGGAGGCGAAAGGCGTTCAATACGTGCCTCTCCCATCT  
 GCTGGTGGTGTTCCTCTTCTATGGCTCAGCCAGCTATGGGTATCTGCTTCCGGCCAAGAAC  
 AGCAAACAGGACCAGGGCAAGTTCATTTCCCTGTTCTACTCGTTGGTCACACCCATGGTGA  
 ATCCCCTCATCTACACGCTGCGGAACATGGAAGTGAAGGGCGCACTGAGGAGGTTGCTGG  
 GGAAAGGAAGAGAAGTTGGCTGA (SEQ ID NO: 440).

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**AOLFR236 sequences:**

MTSQERDTAIYSINVSFVAKGMTSRSVCEKMTMTTENPNQTVVSHFFLEGLRYTAKHSSLFFL  
 LFLLIYSITVAGNLLILLTVGSDSHLSLPMYHFLGHSFLDACLSTVTPKVMAGLLTLDGKVIS  
 FBGCAVQLYCFHFLASTEFLYTVMAYDRYLAICQPLHYPVAMNRRMCAEMAGITWAIGATH  
 45 AAHTSLTFRLLYCGPCHIAFFCDIPPVLKLACTDTTINELVMLASIGIVAAGCLILIVISYIFIVA  
 AVLRTAQGRQRAFPCTAQLTGVLVYVPPVCTYLQPRSSEAGAGAPAVFYTTVTPMLNPFY  
 TLRNKEVKHALQRLLCSSFRESTAGSPPP (SEQ ID NO: 441).

ATGACATCTCAGGAAAGGGATACAGCTATTTATTCCATTAATGTCAGTTTTGTTGCAAAGG  
 50 GGATGACTAGCCGCTCTGTGTGTGAGAAGATGACCATGACAACGGAGAACCCCAACCAGA  
 CTGTGGTGAGCCACTTCTTCCTGGAGGGTTTGAGGTACACCGCTAAACATTCTAGCCTCTT  
 CTTCTCCTCTTCTCCTCATCTACAGCATCACTGTGGCTGGGAATCTCCTCATCCTCCTAA  
 CTGTGGGCTCTGACTCTCACCTCAGCTTACCACGTACCACTTCTGGGGCAGCTCTCCTTC  
 CTGGATGCCTGTTTGTCTACAGTGACAGTGCCCAAGGTCATGGCAGGCTGCTGACTCTGG  
 55 ATGGGAAGGTGATCTCCTTTGAGGGCTGTGCCGTACAGCTTTATTGCTTCCACTTTCTGGC  
 CAGCACTGAGTGCTTCTGTACACAGTCATGGCCTATGACCGCTATCTGGCTATCTGTCAA

CCCCTGCACTACCCAGTGGCCATGAACAGAAGGATGTGTGCAGAAATGGCTGGAATCACC  
TGGGCCATAGGTGCCACGCACGCTGCAATCCACACCTCCCTCACCTTCCGCCTGCTCTACT  
GTGGGCCTTGCCACATTGCCTACTTCTTCTGCGACATACCCCCTGTCCTAAAGCTCGCCTGT  
ACAGACACCACCATTAATGAGCTAGTCATGCTTGCCAGCATTGGCATCGTGGCTGCAGGCT  
5 GCCTCATCCTCATCGTTATTTCTACATCTTCATCGTGGCAGCTGTGTTGCGCATCCGCACA  
GCCCAGGGCCGGCAGCGGGCCTTCTCCCCCTGCACTGCCAGCTCACTGGGGTGCTCCTGT  
ACTACGTGCCACCTGTCTGTATCTACCTGCAGCCTCGCTCCAGTGAGGCAGGAGCTGGGGC  
CCCTGCTGTCTTCTACACAATCGTAACTCCAATGCTCAACCCATTCAATTTACACTTTGCGGA  
ACAAGGAGGTGAAGCATGCTCTGCAAAGGCTTTTGTGCAGCAGCTTCCGAGAGTCTACAG  
10 CAGGCAGCCCACCCCATAG (SEQ ID NO: 442).

**AOLFR237 sequences:**

MDQRNYTRVKEFTFLGITQSRBLSQVLFLLFLVYMTTLMGNFLIMVTVTCESHLHTPMYFLL  
RNLSDICFSSITAPKVLIDLLSETKTISFSGCVTQMFFHLLGGADVFSLSVMAFDRIYAISKPL  
15 HYMTIMSRGRCTGLIVGFLGGGLVHSIAQISLLLPLVCGPNVLDTFYCDVPQVLKLACTDTFT  
LELLMISNNGLVSWFVFFLLISYTVILMMLRSHTGEGRRKAISTCTSHITVTVLHFVPCIVVYA  
RPFTALPTDTAISVTFTVISPLNPIITYTLRNQEMKLAMRKLKRRRLGQSERILIQ (SEQ ID NO:  
443).

20 ATGGATCAGAGAAATTACACCAGAGTGAAAGAATTTACCTTCCTGGGAATTACTCAGTCCC  
GAGAACTGAGCCAGGTCTTATTTACCTTCCTGTTTTTGGTGTACATGACAACTCTAATGGG  
AACTTCCTCATCATGGTTACAGTTACCTGTGAATCTCACCTTCATACGCCCATGTACTTCC  
TGCTCCGCAACCTGTCTATTCTTGACATCTGCTTTTCTCCATCACAGCTCCTAAGGTCCTG  
ATAGATCTTCTATCAGAGACAAAAACCATCTCCTTCAGTGGCTGTGTCACTCAAATGTTCT  
25 TCTTCCACCTTCTGGGGGGGAGCAGACGTTTTTCTCTCTCTGTGATGGCGTTTGACCGCTAT  
ATAGCCATCTCCAAGCCCCTGCACTATATGACCATCATGAGTAGGGGGCGATGCACAGGCC  
TCATCGTGGGCTTCCTGGGTGGGGGGCTGTCCACTCCATAGCGCAGATTTCTCTATTGCT  
CCCACTCCCTGTCTGTGGACCCAATGTTCTTGACACTTTCTACTGCGATGTCCCCAGGTCC  
TCAAACCTTGCTGCACTGACACCTTCACTCTGGAGCTCCTGATGATTTCAAATAATGGGTT  
30 AGTCAGTTGGTTTGTATTCTTCTTCTCCTCATATCTTACACGGTCATCTTGATGATGCTGA  
GGTCTCACACTGGGGAAGGCAGGAGGAAAGCCATCTCCACCTGCACCTCCACATCACCG  
TGGTGACCCTGCATTTCTGTGCCCTGCATCTATGTCTATGCCCCGGCCCTTCACTGCCCTCCCC  
ACAGACACTGCCATCTCTGTACCTTCACTGTCTATCTCCCTTTGCTCAATCCTATAATTTA  
CACGCTGAGGAATCAGGAAATGAAGTTGGCCATGAGGAACTGAAGAGACGGCTAGGAC  
35 AATCAGAAAGGATTTTAATTCAATAA (SEQ ID NO: 444).

**AOLFR238 sequences:**

MAPENFTRVTEFILTVSSPELQIPFLVFLVLYVLTLMAGNLGIITLTSVDSRLQTPMYFFLRHL  
AIINLGNSTVIAPKMLMNFVKKKTTSFYECATQLGGFLFFIVSEVMMLAVMAYDRYVAICNP  
40 LLYMVVVSRRRLCLLLVSLTYLYGFSTAIVVSPCIFSVSYCSSNIINHFCDIAPLLALSCSDTYPE  
TIVFISAAATNLFFSMITVLVSYNIVLSILRIRSPEGRKKAFTSCASHMIAVTVFYGTMLFMYLQP  
QTNHSLDTDKMASVFYTLVIPMLNPLIYSLRNNDVNVALKKFMENPCYSFKSM (SEQ ID NO:  
445).

45 ATGGCTCCTGAAAAATTCACCAGGGTCACTGAGTTTATTCTCACAGGTGTCTCTAGCTGTC  
CAGAGCTCCAGATTCCCCTCTTCTGGTCTTCTAGTGCTCTATGTGCTGACCATGGCAGG  
GAACCTGGGCATCATCACCTCACCAGTGTGACTCTCGACTTCAAACCCCATGTACTTTT  
TCCTGAGACATCTAGCTATCATCAATCTTGCCAACTCTACTGTCATTGCCCTAAAATGCTG  
ATGAACTTTTTAGTAAAGAAAGAAACTACCTCATTCTATGAATGTGCCACCCAACTGGGAG  
50 GGTTCTTGTTCTTTATTGTATCGGAGGTAATGATGCTGGCTGTGATGGCCTATGACCGCTA  
TGTGGCAATTTGTAACCTCTGCTCTACATGGTGGTGGTGTCTCGCGGCTCTGCCTCCTGCT  
TGGTGTCCCTCAGTACCTCTATGGCTTTTCTACAGCTATTGTGGTTTCACTTGTATATT  
TCTGTGTCTTATTGCTCTTCTAATATAATCAATCATTTTTACTGTGATATTGCACCTCTGTT  
AGCATTATCTTGCTCTGATACTTACATAACCAGAAACAATAGTCTTTATATCTGCAGCAACA  
55 AATTTGTTTTTTTCCATGATTACAGTTCTAGTATCTTATTTCAATATTGTTTTGTCCATTCTA  
AGGATACGTTACCAGAAGGAAGGAAAAAGCCTTTTCCACCTGCGCTTCGCATATGATA

GCAGTCACGGTTTTCTATGGGACAATGCTATTTATGTATTTGCAGCCCCAAACCAACCACT  
 CACTGGATACTGATAAGATGGCTTCTGTGTTTTACACATTGGTGATTCTATGCTGAATCC  
 CTTGATCTACAGCCTGAGGAATAATGATGTAAATGTTGCCTTAAAGAAATTCATGGAAAAT  
 CCATGTTACTCCTTTAAATCAATGTAA (SEQ ID NO: 446).

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**AOLFR239 sequences:**

MDPQNYSLVSEFVLHGLCTSRHLQNFFFIFFGVYVAIMLGNLLILVTVISDPCLHSSPMYFLLG  
 NLAFLDMWLASFATPKMIRDFLSDQKLISFGGCMQAQIFLHFTGGAEMVLLVSMAYDRYVAIC  
 KPLHYMTLMSWQTCIRLVLASWVVG FVHSISQVAVTVNLPYCGPNEVDSFFCDLPLVIKLACM  
 10 DTYVLGIIMISDSGLLSLSCFLLLISYTVILLAIRQRAAGSTSKALSTCSAHIMVVTLFFGPCIFV  
 YVRPFSRFSVDKLLSVFYTIFTPLNPIIYTLRNEEMKAAMKKLQNRRTVFQ (SEQ ID NO: 447).

ATGGACCCACAGAACTATTCCTTGGTGTGAGAATTTGTGTTGCATGGACTCTGCACTTCAC  
 GACATCTTCAAAATTTTTCTTTATATTTTTCTTTGGGGTCTATGTGGCCATTATGCTGGGT  
 15 AACCTTCTCATTTTGGTCACTGTAATTTCTGATCCCTGCCTGCACTCCTCCCCTATGTACTT  
 CCTGCTGGGGAACCTAGCTTTCTGACATGTGGCTGGCCTCATTTGCCACTCCCAAGATG  
 ATCAGGGATTTCTTAGTGATCAAAAACCTCATCTCCTTTGGAGGATGTATGGCTCAAATCT  
 TCTTCTTGCACTTACTGGTGGGGCTGAGATGGTGTCTCCTGGTTCCATGGCCTATGACAG  
 ATATGTGGCCATATGCAAACCTTGCAATTACATGACTTTGATGAGTTGGCAGACTTGCATC  
 20 AGGCTGGTGTGCTGGCTTCATGGGTGCTTGGATTGTGCACTCCATCAGTCAAGTGGCTTTCA  
 CTGTAAATTTGCCTTACTGTGGCCCCAATGAGGTAGACAGCTTCTTCTGTGACCTCCCTCTG  
 GTGATCAAACCTTGCTGCAATGGACACCTATGTCTTGGGTATAATTATGATCTCAGACAGTG  
 GGTTGCTTTCTTGAGCTGTTTTCTGCTCCTCCTGATCTCCTACACCGTGATCCTCCTCGCT  
 ATCAGACACGCTGCTGCCGGTAGCACATCCAAAGCACTCTCCACTTGCTCTGCACATATCA  
 25 TGGTAGTGACGCTGTTCTTTGGCCCTTGCAATTTTGTATGTGCGGCCCTTCAGTAGGTTT  
 TCTGTGGACAAGCTGCTGTCTGTGTTTTATAACATTTTACTCCACTCCTGAACCCATTAT  
 CTACACATTGAGAAATGAGGAGATGAAAGCAGCTATGAAGAACTGCAAAACCGACGGGT  
 GACTTTTCAATGA (SEQ ID NO: 448).

**AOLFR240 sequences:**

MAGENHTTLPEFLLLGFSDLKALQGPLFWVVLVYLVTLLGNSLIILLTQVSPALHSPMYFFLR  
 QLSVVELFYTTDIVPRTLNLGSPHPQAISFQGCAAQMYVFIVLGISECCLLTAMAYDRYVAIC  
 QPLRYSTLLSPRACLAMVGSSWLTGTTATTHASLIFSLPFRSHPIPHFLCDILPVLRLASAGKHR  
 SEISVMTATIVFIMIPFSLIVTSYIRILGAILAMASTQSRRKVFSTCSSHLLVVSLEFFGTASITYIRPQ  
 35 AGSSVTTDRVLSLFYTVTTPMLNPIIYTLRNKDVRRALRHLVKRQRPS (SEQ ID NO: 449).

ATGGCTGGGGAAAACCATACTACACTGCCTGAATTCCTCCTTCTGGGATTCTCTGACCTCA  
 AGGCCCTGCAGGGCCCCCTGTTCTGGGTGGTGCTTCTGGTCTACCTGGTCACCTTGCTGGG  
 40 TAACTCCCTGATCATCCTCCTCACACAGGTCAGCCCTGCCCTGCACTCCCCCATGTACTTCT  
 TCCTGCGCCAACTCTCAGTGGTGGAGCTCTTCTACACCACTGACATCGTGCCAGGACCCT  
 GGCCAATCTGGGCTCCCCGCATCCCCAGGCCATCTCTTCCAGGGCTGTGACGCCAGATG  
 TACGTCTTCATTGTCTGCGCATCTCGGAGTGCTGCCTGCTCACGGCCATGGCCTATGACC  
 GATATGTTGCCATCTGCCAGCCCCCTACGCTATTCCACCTCTTGAGCCCACGGGCCTGCTT  
 GGCCATGGTGGGGTCTCCTGGCTCACAGGCATCATCACGGCCACCACCCATGCCTCCCTC  
 45 ATCTTCTCTACCTTTTCGACGCCACCCGATCATCCCGCACTTTCTCTGTGACATCCTGCC  
 AGTACTGAGGCTGGCAAGTGCTGGGAAGCACAGGAGCGAGATCTCCGTGATGACAGCCAC  
 CATAGTCTTCATTATGATCCCCTTCTCTGATTGTACCTCTTACATCCGCATCCTGGGTG  
 CCATCCTAGCAATGGCCTCCACCCAGAGCCGCGCAAGGTCTTCTCCACCTGCTCCTCCA  
 TCTGCTCGTGGTCTCTCTCTTCTTGGAAACAGCCAGCATCACCTACATCCGGCCGACAGGCA  
 50 GGCTCCTCTGTTACCACAGACCGGCTCCTCAGTCTCTTCTACACAGTCATCACACCCATGCT  
 CAACCCCATCATCTACACCCTTCGGAACAAGGACGTGAGGAGGGCCCTGCGACACTTGGT  
 GAAGAGGCAGCGCCCCCTCACCTGA (SEQ ID NO: 450).

**AOLFR241 sequences:**

MPQILIFTYLNMFYFFPPLQILAENLTMVTEFLLLGFSLSLGEIQLALFVVFLFLYLVLSGNVTHIS  
 55 VIHLDKSLHTPMYFFLGILSTSETFYTFVLPKMLINLLSVARTISFNCCALQMFFFLGFAITNCLL

LGVMGYDRYAAICHPLHYPTLMSWQVCGKLAAACAIGGFLASLTVVNLVFSLPFCSANKVNH  
YFCDISAVILLACTNTDVNEFVIFICGVLVLVVPFLFICVSYLCILRTLKIPSAEGRRKAFSTCAS  
HLSVVIVHYGCASFYLRPTANYVSNKDRLVTVTYITVPLLNPMVYSLRNKDVQLAIRKVLG  
KKGSLKLYN (SEQ ID NO: 451).

5

ATGCCCCAAATTCTTATATTCACATACCTGAATATGTTTTACTTCTTTCCCCCTTTGCAGAT  
CTTGGCAGAAAACCTCACCATGGTCACCGAATTCCTGTGTGCTGGGTTTTTCAGCCTTGGT  
GAAATTCAGCTGGCCCTCTTTGTAGTTTTCTTTTTCTGTATCTAGTCATTCTTAGTGGCAA  
TGTCACCATTATCAGTGTCACTCCACCTGGATAAAAAGCCTCCACACACCAATGTACTTCTTCC  
10 TTGGCATTCTCTCAACATCTGAGACCTTTCTACACCTTTGTCAATTCTACCCAAGATGCTCATC  
AATCTACTTTCTGTGGCCAGGACAATCTCCTTCAACTGTTGTGCTCTTCAAATGTTCTTCTT  
CCTTGGTTTTTGCCATTACCAACTGCCTGCTATTGGGTGTGATGGGTATGATCGCTATGCTG  
CCATTTGTACCCCTCTGCATTACCCCACTCTTATGAGCTGGCAGGTGTGTGAAAACCTGGC  
AGCTGCCTGTGCAATTGGTGGCTTCTTGGCCTCTCTTACAGTAGTAAATTTAGTTTTTCAGCC  
15 TCCCTTTTGTAGCGCCAACAAAGTCAATCATTACTTCTGTGACATCTCAGCAGTCATTCTT  
CTGGCTTGTACCAACACAGATGTTAACGAATTTGTGATATTCATTTGTGGAGTTCTTGTAC  
TTGTGGTTCCCTTTCTGTTTATCTGTGTTCTTATCTCTGCATTCTGAGGACTATCCTGAAG  
ATTCCTCAGCTGAGGGCAGACGGAAGCGTTTTCCACCTGCGCCTCTCACCTCAGTGTG  
TTATTGTTCAATTATGGCTGTGCTTCTTACCTACCTGAGGCCTACAGCAAACCTATGTGTCC  
20 AACAAAGACAGGCTGGGTGACGGTGACATACAGATTGTCACTCCATTACTAAACCCCATG  
GTTTATAGCCTCAGAAACAAGGATGTCCAACCTGCTATCAGAAAAGTGTGGGCAAGAAA  
GGTCTCTAAACTATATAATTGA (SEQ ID NO: 452).

**AOLFR242 sequences:**

25 MNTTLFHPYSFLLGIPGLESMHLWVGPFPAVFLTAVLGNITILFVIQTDSSLHHPMFYFLAILS  
SIDPGLSTSTIPKMLGTFWFTLREISFEGCLTQMFFIHLCTGMESA VLVAMAYDCYVAICDPLCY  
TLVLTNKVSVSMALAIPLRPLVFVIPFVFLRLPFCGHQIIPHTYGEHMGARLSCASIRVNIYIG  
LCAISILVFDIIAIVISYVQILCAVFLSSHARLKAFSTCGSHVCVMLTFYMPAFFSFMTHFRGR  
NIPHFHILLANFYVIPPALNSVIYGVRTKQIRAQVLKMFENK (SEQ ID NO: 453).

30

ATGAATACCACTCTATTTTCATCCTTACTCTTTCTTCTTCTGGGAATTCCTGGGCTGGAAAG  
TATGCATCTCTGGGTTGGTTTTCTTTCTTGTCTGTGTTCTTGACAGCTGTCCTTGGGAATA  
TCACCATCCTTTTTGTGATTGAGACTGACAGTAGTCTCCATCATCCCATGTTCTACTTCTCTG  
GCCATTCTGTCTATTGACCCGGGCCTGTCTACATCCACCATCCCTAAAATGCTTGGCAC  
35 CTTCTGGTTTACCCTGAGAGAAATCTCCTTTGAAGGATGCCTTACCAGATGTTCTTCATCC  
ACCTGTGCACTGGCATGGAATCAGCTGTGCTTGTGGCCATGGCCTATGATTGCTATGTGGC  
CATCTGTGACCCCTCTTTGCTACACGTTGGTGCTGACAAACAAGGTGGTGTGCAAGTTATGGCA  
CTGGCCATCTTTCTGAGACCCCTTAGTCTTTGTGATACCCCTTTGTTCTATTTATCCTAAGGCT  
TCCATTTTGTGGACACCAAATTATTCCTCATACTTATGGTGAGCACATGGGCATTGCCCGC  
40 CTGTCTTGTGGCAGCATCAGGGTTAACATCATCTATGGCTTATGTGCCATCTCTATCCTGGT  
CTTTGACATCATAGCAATTGTCATTTCTTATGTACAGATCCTTTGTGCTGTATTTCTACTCT  
CTTCACATGATGCACGACTCAAGGCATTGAGCACCTGTGGCTCTCATGTGTGTGTCATGTT  
GACTTTCTATATGCCTGCATTTTCTCATTGATGACCCATAGGTTTGGTCCGAATATACCTC  
ACTTTATCCACATTCTTCTGGCTAATTTCTATGTAGTCATTCCACCTGCTCTCAACTCTGTA  
45 ATTTATGGTGTGAGAACCAACAGATTAGAGCACAAAGTGCTGAAAATGTTTTTCAATAAAT  
AA (SEQ ID NO: 454).

**AOLFR243 sequences:**

MEQVNKTVVREFVVLGFSSLARLQQLLFVIFLLLYLFTLGTNAIISTIVLDRALHTPMYFFLAIL  
50 SCSEICYTFVIVPKMLVDLLSQKKTISFLGCAIQMFSFLFFGSSHSFLAAMGYDRYMAICNPLR  
YSVLMGHGVCMGLMAAACACGFTVSLVTTSLVFHLPFHSSNQLHHFFCDISPVLKLSQHSFG  
SQLVIFMLGVFALVPLLLILVSYRIISAILKIPSSVGRYKTFSTCASHLIVVTVHYSASFYLRPK  
TNYTSSQDTLISVSYTILTPLFNPMIYSLRNKEFKSALRRRTIGQTFYPLS (SEQ ID NO: 455).

55 ATGGAGCAAGTCAATAAGACTGTGGTGAGAGAGTTCGTCGTCCTCGGCTTCTCATCCCTGG  
CCAGGCTGCAGCAGCTGCTCTTTGTTATCTTCTCTCTCTACCTGTTCACTCTGGGCACC

AATGCAATCATCATTTCCACCATTGTGCTGGACAGAGCCCTTCATACTCCCATGTACTTCTT  
 CTTGCCATCCTTTCTTGTCTGAGATTGTCTATACCTTTGTCAATTGTACCCAAGATGCTGG  
 TTGACCTGCTGTCCCAGAAGAAGACCATTCTTTCTGGGCTGTGCCATCCAAATGTTTTCC  
 TTCTCTTCTTTGGCTCCTCTCACTCCTTCTGCTGGCAGCCATGGGGCTATGATCGCTATAT  
 5 GGCCATCTGTAAACCACTGCGCTACTCAGTGCTCATGGGACATGGGGTGTGTATGGGACTA  
 ATGGCTGCTGCCTGTGCCTGTGGCTTCACTGTCTCCCTGGTCACCACCTCCCTAGTATTTCA  
 TCTGCCCTTCCACTCCTCCAACCAGCTCCATCACTTCTTCTGTGACATCTCCCCTGTCCTTA  
 AACTGGCATCTCAGCACTCCGGCTTCACTCAGCTGGTCATATTCATGCTTGGTGTATTTGC  
 CTTGGTCATTCCCTCTGCTACTTATCCTAGTCTCCTACATCCGCATCATCTCTGCCATTCTAA  
 10 AAATCCCTTCCCTCCGTTGGAAGATAACAAGACCTTCTCCACCTGTGCCTCCCATCTCATTGTG  
 GTAAGTGTCACTACAGTTGTGCCTCTTTCATCTACTTAAGGCCCAAGACTAATTACACTTC  
 AAGCCAAGACACCCTAATATCTGTGTCATACACCATCCTTACCCCATTTGTTCAATCCAATG  
 ATTTATATCTGAGAAATAAGGAATTCAAATCAGCCCTACGAAGAACAATCGGCCAAACT  
 TTCTATCCTCTTAGTTAA (SEQ ID NO: 456).

15

**AOLFR244 sequences:**

MWQEYYFLNVFFPLLKVCCLTINSHVILLPWECYHLIWKILPYIGTTVGSMEEYNTSSTDFTF  
 MGLFNKRKETSGLFAHSIHFFALMANGVMFLIQTDLRLHTPMYFLLSHLSLIDMMYISTIVPKM  
 LVNYLLDQRTISFVGCTAQHFLYLTLVGAEFFLLGLMAYDRYVAICNPLRYPVLMSSRRVCWMI  
 20 IAGSWFGGSLDGFLLPITMSFPFCNSREINHFFCEAPVLKACADTALYETVMYVCCVLMML  
 IPFSVVLASYARILTTVQCMSSVEGRKKAFATCSSHMTTVVSLFYGAAMYTYMLPHSYHKPAQ  
 DKVLSVFYITLTPMLNPLIYSLRNKDVGTALKRALGRFKGPQRVSGGVF (SEQ ID NO: 457).

ATGTGGCAAGAATACTATTTTTTAAATGTTTTCTTCCCACTTTTAAAAGTTTGCTGCCTAAC  
 25 AATTAATTCACATGTTGTTATTTTACTGCCCTGGGAATGCTATCATCTTATTTGGAAGATAT  
 TACCTTATATCGGCACAACTGTAGGATCAATGGAAGAGTACAACACATCCTCTACAGACTT  
 CACTTTTCATGGGGCTGTTCAACAGAAAGGAAACCTCAGGTCTTATTTTTGCCATCATCTCT  
 ATCATCTTCTTCAACGCACTGATGGCCAATGGGGTTATGATCTTCTGATCCAAACAGATT  
 TGCGCCTTCATACACCCATGTACTTCTCCTCAGCCACCTTTCCTTAATTGACATGATGTAT  
 30 ATTTCCACTATTGTGCCTAAGATGCTGGTTAATTACCTGCTGGATCAAAGGACCATTTCCTT  
 TGTGGGGTGCACAGCTCAACACTTCTCTACCTTACCCTTGTGGGAGCTGAATTCTTCTCT  
 CTGGGCCTCATGGCCTATGACCGCTATGTGGCCATTGCAACCCCTCTGAGATACCTGTGCC  
 TCATGAGCCGCCGGGTCTGTTGGATGATTATAGCAGGTTCTGGTTTGGGGGCTCTTTGGA  
 TGGCTTCTCTCTAACCCCATCACCATGAGCTTCTCCTTCTGCAATTCCCGGGAGATTAAAC  
 35 ACTTCTTCTGTGAGGCACCAGCAGTCTGAAGTTGGCATGTGCAGACACAGCCCTCTACGA  
 GACAGTGATGTATGTGTGCTGTGTTTTGATGCTGCTGATTCTTTCTCTGTAGTCCTTGCTT  
 CCTATGCCCCGAATCCTGACTACAGTTCAAGTGCATGAGCTCAGTGGAGGGCAGGAAGAAGG  
 CATTTGCCACTTGCTCATCCACATGACTGTGGTGTCTTGTCTACGGGGCTGCCATGTAC  
 ACCTACATGCTGCCACATTCTTACCACAAGCCAGCCAGGACAAAGTCTCTCTGTGTTTT  
 40 ACACCATCTCACACCATGCTGAACCCCTCATCTACAGCCTTAGAAACAAGGATGTGAC  
 TGGAGCTCTGAAGAGGGCCTTGGGGAGGTTCAAGGGTCTCAAAGGGTGTGAGGAGGTGT  
 CTTTTGA (SEQ ID NO: 458).

**AOLFR245 sequences:**

MDLKNGLSVTEFILLGFFGRWELQIFFVTFSLIYGATVMGNILIMVTVTCSRSTLHSPLYFLLGN  
 45 LSFLDMCLSTATTPKMIIDLLTDHKTISVWGCVTQMFFMHFFGGAEMTLLIIMAFDRYVAICKP  
 LHYRTIMSHKLLKGFAILSWIIGFLHSISQIVLTMLNLPFCGHNVINNIFCDLPLVIKLCIETYTLE  
 LFVIADSGLLSFTCFILLVSYIVILVSVPKKSSHGLSKALSTLSAHIIVVTLFFGPCIFYVWPFS  
 ASNKTLAVFYTVITPLNPSIYTLRNKKMQEAIKRLRFQYVSSAQNF (SEQ ID NO: 459).

50

ATGGATCTTAAAAATGGATCTCTAGTGACCGAGTTTATTTTACTAGGATTTTTTGGACGAT  
 GGGAACTTCAAATTTCTTCTTTGTGACATTTCCCTGATCTACGGTGCTACTGTGATGGGA  
 AACATTCTCATTATGGTCACAGTGACATGTAGGTCAACCCCTTATTCTCCCTTGTAATTTCT  
 CCTTGGAAATCTCTCTTTTTTGGACATGTGTCTCTCCACTGCCACAACACCCAAGATGATCA  
 55 TAGATTTGCTCACTGACCACAAGACCATCTCTGTGTGGGGCTGCGTGACCCAGATGTTCTT  
 CATGCACTTCTTTGGGGGTGCTGAGATGACTCTTCTGATAATCATGGCCTTTGACAGGTAT

GTAGCCATATGTAAACCCCTGCACTATAGGACAATCATGAGCCACAAGCTGCTAAAGGGG  
TTTGCGATACTTTTCATGGATAATTGGTTTTTTTACACTCCATAAGCCAGATAGTTTTAAACAAT  
GAACTTGCCCTTTCTGTGGCCACAATGTCATAAACAACATATTTTGTGATCTTCCCCTTGTGA  
TCAAGCTTGCTTGCATTGAAACATACACCCTGGAATTATTTGTGATTGCTGACAGCGGGCT  
5 GCTCTCTTTTACCTGTTTCATCCTCTTGCTTGTCTTACATTGTCATCCTGGTCAGTGTACC  
AAAAAAATCATCACATGGGCTCTCCAAGGCGCTGTCCACATTGTCTGCCCACATCATTTGTG  
GTCACCTCTGTTCTTTGGACCTTGATTTTTATCTATGTTTGGCCATTGAGTAGTTTGGCAAG  
CAATAAAACTCTTGCCGTATTTTATACAGTTATCACACCCTTACTGAATCCGAGTATTTATA  
10 CCCTGAGAAATAAGAAAATGCAAGAGGCCATAAGAAAATTACGGTTCCAATATGTTAGTT  
CTGCACAGAATTTCTAG (SEQ ID NO: 460).

**AOLFR246 sequences:**

MSPENQSSVSEFLLGLPIRPEQQAFFTLFLGMYLTTVLGNLLIMLLIQLDSHLHTPMYFFLSH  
LALTDISFSSVTVPKMLMDMRTKYKSLYEECISQMYFFIFFDLDLSFLITSMAYDRYVAICHPL  
15 HYTVIMREELCVFLVAVSWILSCASSLSHTLLTRLFSFAANTIPHVFCDLAALLKLSCSDIFLNE  
LVMFTVGVVVITLPMCLVSYGYIGATILRVPSTKGHKLSTCGSHLSVSVSLYYSIRGQYLF  
PTVSSSIDKDVIVALMYTVVTPMLNPFYSLRNRDMKEALGKLFSTRATFFSW (SEQ ID NO:  
461).

20 ATGAGCCCTGAGAAACCAGAGCAGCGTGTCCGAGTTCCTCCTTCTGGGCCTCCCCATCCGGC  
CAGAGCAGCAGGCTGTGTTCTTACCCTGTTCTGGGCATGTACCTGACCACGGTGCTGGG  
GAACCTGCTCATCATGCTGCTCATCCAGCTGGACTCTACCTTCACACCCCCATGTACTTCT  
TCCTCAGCCACTTGCTCTCACTGACATCTCCTTTTCATCTGTCACTGTCCCTAAGATGCTG  
ATGGACATGCGGACTAAGTACAAATCGATCCTCTATGAGGAATGCATTCTCAGATGTATT  
25 TTTTATATTTTTACTGACCTGGACAGCTTCCTTATTACATCAATGGCATATGACCGATAT  
GTTGCCATATGTCACCCTCTCCACTACACTGTCATCATGAGGGAAGAGCTCTGTGTCTTCTT  
AGTGGCTGTATCTTGATTCTGTCTTGTGCCAGCTCCCTCTCTCACACCCTTCTCCTGACCC  
GGCTGTCTTTCTGTGCTGCGAACACCATCCCCATGTCTTCTGTGACCTTGCTGCCCTGCTC  
AAGCTGTCTGCTCAGATATCTTCTCAATGAGCTGGTCATGTTTACAGTAGGGGTGGTGG  
30 TCATTACCCTGCCATTCATGTGTATCCTGGTATCATATGGCTACATTGGGGCCACCATCCTG  
AGGGTCCCTTCAACCAAAGGGATCCACAAAGCATTGTCCACATGTGGCTCCCATCTCTCTG  
TGGTGTCTCTCTATTATGGGTCAATATTTGGCCAGTACCTTTTCCGACTGTAAGCAGTTCT  
ATTGACAAGGATGTCAATTGTGGCTCTCATGTACACGGTGGTCACACCCATGTTGAACCCCT  
TTATCTACAGCCTTAGGAACAGGGACATGAAAGARGCCCTTGGGAAACTCTTCAGTAGAG  
35 CAACATTTTTCTCCTTGGTGACATCTGACTTTTTAAAAAATTAG (SEQ ID NO: 462).

**AOLFR247 sequences:**

MGQHNLTVLTFILMELTRRPELQIPLFGVFLVIYLTIVVGNLTMILTKLDSHLHTPMYFSIRHL  
ASVDLGNSTVICPKVLANFVVDNRNTISYYACAAQLAFFLMFIIEFFILSAMAYDRYVAICNPLL  
40 YYVIMSQRLLCHVLVGHQYLYSTFQALMFTIKIFTLFCGSNVISHFYCDDVPLLPMLCSNAQEIE  
LLSILFSVFNLISSFLIVLSYMLILLAICQMHSAGRKKAFTSTCGSHLTVVVVFYGSLLFMYMQ  
PNSTHFFDTDKMASVFYTLVIPMLNPLIYSLRNEEVKNAFYKLFEN (SEQ ID NO: 463).

ATGGGCCAACACAATCTAACAGTGCTAACTGAATTCATTCTGATGGAACCTACAAGGCGGC  
45 CTGAGCTGCAGATTCCCCTTTTTGGAGTCTTCTCGTCATCTACCTAATCACAGTGGTGGGC  
AACCTAACTATGATCATTTTGACCAAACCTGGACTCCCACTTACATACACCTATGTACTTTTC  
TATCAGACATTTGGCTTCTGTTGATCTTGGTAATTCTACTGTCATTTGTCCCAAGGTGCTGG  
CAAATTTTGTGTGGATCGAAATACTATTTTCTATTATGCATGTGCTGCACAGCTGGCATTCT  
TTCTTATGTTTATTATCAGTGAATTTTTCATCCTGTCAGCCATGGCCTATGACCGCTATGT  
50 GGCCATTTGTAACCCCTCTGCTCTATTATGTTATTATGTTCTCAGCGACTGTGTCATGTACTGG  
TGGCATTCAATATCTCTACAGCACATTTGAGGCTCTGATGTTCACTATTAAGATTTTTACA  
TTGACCTTCTGTGGCTCTAATGTCTCATGTCAGTCATTTTACTGTGATGATGTTCTTTGCTACC  
TATGCTTTGCTCAAATGCACAGGAAATAGAATTGTTGAGCATACTATTTTCTGTATTTAATT  
TGATCTCCTCCTTTCTGATAGTCTTAGTGTCTACATGTTGATTTTGTAGCTATATGTCAA  
55 ATGCATTCTGCAGAGGGCAGGAAAAAGGCTTTCTCCACATGTGGTTCCTATTTGACAGTGG  
TGGTTGTGTTCTATGGGTCTCTACTCTTCATGTACATGCAGCCCAATTCCACTCACTTCTTT



GATACTGATAAAATGGCTTCTGTGTTTTACACTTTAGTAATCCCCATGCTTAACCCCTTGAT  
TTACAGCTTAAGAAACGAAGAGGTGAAAAATGCCTTCTATAAGCTCTTTGAGAAATGA  
(SEQ ID NO: 464).

5 **AOLFR248 sequences:**

MPCMPALPTGGLLPHQHTMMEIANVSSPEVFLVLLGFSTRPSLETVLFIVVLSFYMVLSILGNGI  
IILVSHTDVHLHTPMYFFLANLPFLDMSFTTSIVPQLLANLWGPQKTISYGGCVVQFYISHWL  
ATECVLLATMSYDRYAAICRPLHYTVIMHPQLCLGLALASWLGLTSMVGSILTMLPLCG  
NNCIDHFFCEMPLIMQLACVDTSLNEMEMYLASFVFLVPLGLILVSYGHIARAVLKIRSAEGR  
10 RKAFNTCSSHVAVVSLFYGSIFMYLQPAKSTSHEQGFIALFYTVVTPALNPLIYTLRNTTEVKS  
ALRHMVLENC CGSAGKLAQI (SEQ ID NO: 465).

ATGCCCTGTATGCCCTGTGCTCTTCCACAGGTGGCCTTTTGCCCCACCCACAGCATAACAAT  
GATGGAAATAGCCAATGTGAGTCTCCAGAAGTCTTTGTCCTCCTGGGCTTCTCCACACGA  
15 CCCTCACTAGAACTGTCTCTTCATAGTTGTCTTGAGTTTTTACATGGTATCGATCTTGGG  
CAATGGCATCATCATTCTGGTCTCCCATACAGATGTGCACCTCCACACACCTATGTACTTCT  
TTCTTGCCAACTCCCTTCTGGACATGAGCTTACCACGAGCATTGTCCACAGCTCCTG  
GCTAACCTCTGGGGACCACAGAAAACCATAAGCTATGGAGGGTGTGTGGTCCAGTTCTAT  
ATCTCCCATTTGGCTGGGGGCAACCGAGTGTGTCTGCTGGCCACCATGTCTATGACCGCT  
20 ACGCTGCCATCTGCAGGCCACTCCATTACACTGTCATTATGCATCCACAGCTTTGCCTTGG  
GCTAGCTTTGGCCTCCTGGCTGGGGGGTCTGACCACCAGCATGGTGGGCTCCACGCTCACC  
ATGCTCCTACCGCTGTGTGGGAACAATTGCATCGACCACTTCTTTTGGAGATGCCCTCA  
TTATGCAACTGGCTTGTGTGGATACCAGCTCAATGAGATGGAGATGTACCTGGCCAGCTT  
TGTCTTTGTTGTCTGCTCTGGGGCTCATCCTGGTCTCTTACGGCCACATGGCCCGGGCCG  
25 TGTTGAAGATCAGGTCAGCAGAAAGGGCGGAGAAAGGCATTCAACACCTGTTCTTCCACG  
TGGCTGTGGTGTCTCTGTTTTACGGGAGCATCATCTTCATGTATCTCCAGCCAGCCAAGAG  
CACCTCCCATGAGCAGGGCAAGTTCATAGCTCTGTTCTACACCGTAGTCACTCCTGCGCTG  
AACCCACTTATTTACACCCTGAGGAACACGGAGGTGAAGAGCGCCCTCCGGCACATGGTA  
TTAGAGAACTGCTGTGGCTCTGCAGGCAAGCTGGCGCAAATTTAG (SEQ ID NO: 466).

30

**AOLFR249 sequences:**

MKSQIEKSDLKYRAILLQKVTRMFLLFWVLLLVLSRLLVVMGRGNSTEVTEFHLLGFGVQHEF  
QHVLFIVLLLIYVTSIGNIGMILLIKTDSRLQTPMYFFPQHAFVDICYTSAITPKMLQSFTEN  
NLITFRGCVIQFLVYATFATSDCYLLAIMAMDCYVAICKPLRYPMIMSQT VYIQLVAGSYIGSI  
35 NASVHTGFTFSLSFCKSNKINHFFCDGLPILALSCSNIDINILDVVFVGFDFLMTLVIIFSYTYIM  
VTILKMSSTAGRKKSFSSTCASHLTA VTFYGTLSYMYLQPQSNNSQENMKVASIFYGTVIPMLN  
PLIYSLRNKEGK (SEQ ID NO: 467).

ATGAAAAGTCAAATTGAAAAAGTGACTTAAATATAGAGCCATTTTATTGCAAAAAGTC  
40 ACAAGGATGTTCTGCTTTTCTGGGTCCTTCTCTTGGTCCCTTCTAGACTTTTGGTAGTCAT  
GGGTCGAGGAAACAGCACTGAAGTGACTGAATTCATCTTCTGGGATTTGGTGTCCAACAC  
GAATTTCAAGCATGTCCTTTTCACTGTACTTCTTCTATCTATGTGACCTCCCTGATAGGAAA  
TATTGGAATGATCTTACTCATCAAGACCGATTCCAGACTTCAAACACCCATGTACTTTTTTC  
CACAACATTTGGCTTTTGTGATATCTGTTATACTTCTGCTATCACTCCCAAGATGCTCCAA  
45 AGCTTCACAGAAGAAAATAATTTGATAACATTTCCGGGGCTGTGTGATACAATTCTTAGTTT  
ATGCAACATTTGCAACCAGTGACTGTTACCTCCTAGCTATTATGGCAATGGATTGTTATGT  
TGCCATCTGTAAGCCCTTTCGCTATCCCATGATCATGTCCCAAACAGTCTACATCCAACCTCG  
TAGCTGGCTCATATATTATAGGCTCAATAAATGCCTCTGTACATACAGGTTTTACATTTTCA  
CTGTCCTTCTGCAAGTCTAATAAAATCAATCACTTTTCTGTGATGGTCTCCCAATTCTTGC  
50 CCTTTCATGCTCCAACATTGACATCAACATCATTCTAGATGTTGTCTTTGTGGGATTTGACT  
TGATGTTCACTGAGTTGGTCATCATCTTTTCTACATCTACATTATGGTCACCATCCTGAAG  
ATGCTTCTACTGCTGGGAGGAAAAATCCTTCTCCACATGTGCCTCCCACTGACAGCAG  
TAACCATTTTCTATGGGACACTCTTACATGTACTTACAGCCTCAGTCAATAATTCTCAG  
GAGAATATGAAAGTAGCCTCTATATTTTATGGCACTGTTATTCCCATGTTGAATCCTTTAAT  
55 CTATAGCTTGAGAAATAAGGAAGGAAAATAA (SEQ ID NO: 468).

**AOLFR250 sequences:**

MENQSSISEFFLRGISAPPEQQQSLFGIFLCMYLVTLTGNLLIILAIGSDLHLHTPMYFFLANLSFV  
 DMGLTSSTVTKMLVNIQTRHHTISYTGCLTQMYFFLMFGDLDSFFLAAMAYDRYVAICHPLCY  
 STVMRPQVCALMLALCWVLTNIVALHTFILMARLSFCVTGEIAHFFCDITPVLKLSGSDTHINE  
 5 MMVFVLGGTVLIVPFLCIVTSYIHIVPAILRVTRGGVGKAFSTCSSHLCVVCFYGTLFSAAYLC  
 PPSIASEEKDIAAAAMYTTVTPMLNPFYISLRNKDMKGALKRLFSHRIVSS (SEQ ID NO: 469).

ATGGAACCAATCCAGCATTTCTGAATTTTCTCCGAGGAATATCAGCGCCTCCAGAGC  
 AACAGCAGTCCCTCTTCGGAATTTTCTGTGTATGTATCTTGTACCTTGACTGGGAACCTG  
 10 CTCATCATCCTGGCCATTGGCTCTGACCTGCACCTCCACACCCCATGTACTTTTCTTGGC  
 CAACCTGTCTTTTGTGACATGGGTTTAACTGCTCCACAGTTACCAAGATGCTGGTGAAT  
 ATACAGACTCGGCATCACACCATCTCCTATACGGGTGCTCACGCAAAATGTATTTCTTTCT  
 GATGTTTGGTGATCTAGACAGCTTCTTCTGGCTGCCATGGCGTATGACCGCTATGTGGCC  
 ATTTGCCACCCCTCTGCTACTCCACAGTCATGAGGCCCAAGTCTGTGCCCTAATGCTTGC  
 15 ATTTGTGCTGGGTCTCACCAATATCGTTGCCCTGACTCACAGTTCCTCATGGCTCGGTTGT  
 CCTTCTGTGTGACTGGGGAATTGCTCATTCTTCTGTGACATCACTCCTGTCTGAAGCTG  
 TCATGTTCTGACACCCACATCAACGAGATGATGGTTTGTCTTGGGAGGCACCGTACTCA  
 TCGTCCCTTTTATGCATTGTCACCTCCTACATCCACATTGTGCCAGCTATCCTGAGGGTC  
 CGAACCCGTGGTGGGGTGGGCAAGGCCTTTCCACCTGCAGTTCACCTCTGCGTTGTTT  
 20 GTGTGTTCTATGGGACCTCTTCAGTGCCTACCTGTGTCTCCTCCCTCCATTGCCTCTGAAGAG  
 AAGGACATTGCAGCAGCTGCAATGTACACCATAGTGACTCCCATGTTGAACCCCTTTATCT  
 ATAGCCTAAGGAACAAGGACATGAAGGGGGCCCTAAAGAGGCTCTTCAGTCACAGGAGTA  
 TTGTTTCTCTTAG (SEQ ID NO: 470).

**AOLFR251 sequences:**

MEGNKTWITDITLPRFQVGPALAILLCGLFSAFYTLTLGNGVIFGIIICLDCKLHTPMYFFLSHLA  
 IVDISYASNYVPKMLTNLMNQESTISFFPCIMQTFLYLAFAHVECLILVMSYDRYADICHPLRY  
 NILMSWRVCTVLAVASWVFSLLALVPLVLILRLPFCGPHEINHFEILSVLKLACADTWLNQV  
 VIFAACVFILVGPLCLVLVSYLRLAAILRIQSGEGRRKAFSTCSSHLCVVGLFFGSAIVTYMAPK  
 30 SRHPPEEQQKVLISLFLNPNMLNPLIYSLRNAEVKGALRRALRKERLT (SEQ ID NO: 471).

ATGGAAGGCAACAAGACATGGATCACAGACATCACCTTGCCGCGATTCCAGGTTGGTCCA  
 GCACTGGAGATTCTCCTCTGTGGACTTTTCTCTGCCTTCTATACACTCACCTGCTGGGGAA  
 TGGGGTCATCTTTGGGATTATCTGCCTGGACTGTAAGCTTCACACACCCATGTACTTCTTCC  
 35 TCTCACACCTGGCCATTGTTGACATATCCTATGCTTCCAATATGTCCCAAGATGCTGACG  
 AATCTTATGAACCAGGAAAGCACCATCTCCTTTTTTCCATGCATAATGCAGACATTCTTGT  
 ATTTGGCTTTTGCTCACGTAGAGTGTCTGATTTTGGTGGTGATGTCCTATGATCGCTATGCG  
 GACATCTGCCACCCCTTACGTTACAATATCCTCATGAGCTGGAGAGTGTGCACTGTCTGG  
 CTGTGGCTTCTGGGTGTTCACTTCTCCTGGCTCTGGTCCCTTTAGTTCTCATCCTGAGG  
 40 CTGCCCTTCTGCGGGCCTCATGAAATCAACCATTCTGTGAAATCCTGTCTGTCTCAAGTT  
 GGCCTGTGCTGACACCTGGCTCAACCAGTGGTCACTTTGTCAGCCTGCGTGTTCATCCTG  
 GTGGGGCCACTCTGCCTGGTGTCTGCTCCTACTTGCATCCTGGCCGCCATCTTGAGGA  
 TCCAGTCTGGGGAGGGCCGAGAAAGGCCTTCTCCACCTGCTCCTCCACCTTTGCGTGGT  
 GGGACTCTTCTTTGGCAGCGCCATTGTACGTACATGGCCCCCAAGTCCCGCCATCCTGAG  
 45 GAGCAGCAGAAAGTTCTTTCCCTGTTTTACAGCCTTTTCAATCCAATGCTGAACCCCTGA  
 TATATAGCCTAAGGAATGCAGAGGTCAAGGGCGCCCTGAGGAGGGCACTGAGGAAGGAG  
 AGGCTGACGTGA (SEQ ID NO: 472).

**AOLFR252 sequences:**

MRLANQTLGGDFLLGIFSQISHPGRCLLIFSIFLMAVSWNITLILLIHIDSSLHTPMYFFINQLSL  
 IDLTYSIVTVPKMLVNQLAKDKTISVLGCGTQMYFYQLGGAECCLLAAMAYDRYVAICHPLR  
 YSVLMSHRVCLLLASGCWFVGSVDGFMLTPIAMSFFPCRSHBIQHFFCEVPAVLKLSGSDTSLY  
 KIFMYLCCVIMLLIPVTVISVSYYYIILTIHKMNSVEGRKKAFTTCSHITVVSIFYGAAIYNMYL  
 PSSYQTPEKDMSSFFYTILTPVLNPIIYSFRNKDVTRALKKMLSVQKPPY (SEQ ID NO: 473).

55

ATGCGGCTGGCCAACCAGACCCCTGGGTGGTGACTTTTTCCTGTTGGGAATCTTCAGCCAGA  
TCTCACACCCTGGCCGCTCTGCTTGCTTATCTTCAGTATATTTTTGATGGCTGTGTCTTGG  
AATATTACATTGATACTTCTGATCCACATTGACTCCTCTCTGCATACTCCCATGTACTTCTT  
TATAAACCAGCTCTCACTCATAGACTTGACATATATTTCTGTCAGTGTCCCCAAAATGCTG  
5 GTGAACCAGCTGGCCAAAGACAAGACCATCTCGGTCCTTGGGTGTGGCACCCAGATGTAC  
TTCTACCTGCAGTTGGGAGGTGCAGAGTGCTGCCTTCTAGCCGCCATGGCCTATGACCGCT  
ATGTGGCTATCTGCCATCCTCTCCGTTACTCTGTGCTCATGAGCCATAGGGTATGTCTCCTC  
CTGGCATCAGGCTGCTGGTTTGTGGGCTCAGTGGATGGCTTCATGCTCACTCCCATCGCCA  
TGAGCTTCCCCCTTCTGCAGATCCCATGAGATTGAGCACTTCTTCTGTGAGGTCCCTGCTGTT  
10 TTGAAGCTCTCTTGCTCAGACACCTCACTTTACAAGATTTTCATGTACTTGTGCTGTGTCAT  
CATGCTCCTGATACCTGTGACGGTCATTTCAAGTGTCTTACTACTATATCATCTCCACCATCC  
ATAAGATGAACCTCAGTTGAGGGTCGGAAGGCTTCACCACTGCTCCTCCACATTAC  
AGTGGTCAGCCTCTTCTATGGAGCTGCTATTTACAACTACATGCTCCCCAGCTCCTACCAA  
ACTCCTGAGAAAGATATGATGTCATCCTTTTCTACACTATCCTTACACCTGTCTTGAATCC  
15 TATCATTTACAGTTTCAGGAATAAGGATGTCACAAGGGCTTTGAAAAAATGCTGAGCGT  
GCAGAAACCTCCATATTAA (SEQ ID NO: 474).

**AOLFR253 sequences:**

MTFFSSGGNCEPVMCSGNQTSQNQTASTDFLTGLFAESKHAALLYTVTFLLFLMALTGNALL  
20 ILLIHSEPRLHTPMYFFISQLALMDLMLYLCVTPKMLVGQVTGDDTISPSGCGIQMFFHLTLAG  
AEVFLAAMAYDRYAAVCRPLHYPLLMNQVRVQQLVSACWVLGMVDGLLLTPITMSFPFCQS  
RKILSFFCETPALLKLSGSDVSLYKMLTYLCCILMLLTPIMVISSSYTLILHLHRMNSAAGRKA  
LATCSSHMIIIVLLLFASFYTYMLRSSYHTAEQDMMVSAFYTIFTPLNPLIYSLRNKDVTRAL  
RSMQMQRMNQBEK (SEQ ID NO: 475).

25 ATGACTTTTTTTTCTCAGGGGGAAACTGTGAGCCAGTCATGTGCTCAGGGAATCAGACTT  
CTCAGAATCAAACAGCAAGCACTGATTTACCCCTCACGGGACTCTTTGCTGAGAGCAAGCA  
TGCTGCCCTCCTCTACACCGTGACCTTCCTTCTTTTCTTGATGGCCCTCACTGGGAATGCCC  
TCCTCATCCTCCTCATCCACTCAGAGCCCCGCCTCCACACCCCCATGTACTTCTTCATCAGC  
30 CAGCTCGCGCTCATGGATCTCATGTACCTATGCGTGACTGTGCCCAAGATGCTTGTGGGCC  
AGGTCAGTGGAGATGATACCATTTCCCCGTGAGGCTGTGGGATCCAGATGTTCTTCCACCT  
GACCTGGCTGGAGCTGAGGTTTTCTCTGGCTGCCATGGCCTATGACCGATATGCTGCT  
GTTTGCAGACCTCTCCATTACCCACTGCTGATGAACCAGAGGGTGTGCCAGCTCCTGGTGT  
CAGCCTGCTGGGTTTTGGGAATGGTTGATGGTTTGTGCTCACCCCCATTACCATGAGCTT  
35 CCCCTTTTGCCAGTCTAGGAAAATCCTGAGTTTTTCTGTGAGACTCCTGCCCTGCTGAAGC  
TCTCCTGCTCTGACGTCTCCCTCTATAAGATGCTCACGTACCTGTGCTGCATCCTCATGCTT  
CTCACCCCCATCATGGTCATCTCCAGCTCATACACCCCTCATCTGCATCTCATCCACAGGAT  
GAATTCTGCCGCCGCCGCGCAGGAAGGCCTTGGCCACCTGCTCCTCCACATGATCATAGTG  
CTGCTGCTCTTCGGTGCTTCTTCTACACCTACATGCTCCGAGTTCTTACCACACAGCTGA  
40 GCAGGACATGATGGTGTCTGCCTTTTACACCATCTTCACTCCTGTGCTGAACCCCTCATTT  
ACAGTCTCCGCAACAAAGATGTCAACAGGGCTCTGAGGAGCATGATGCAGTCAAGAATGA  
ACCAAGAAAAGTAG (SEQ ID NO: 476).

**AOLFR254 sequences:**

45 MTNTSSSDFTLLGLLVNSEAAGIVFTVILAVFLGAVTANLVMIFLIQVDSRLHTPMYFLLSQLSI  
MDTLFICTTVPKLLADMVSKEKIIISFVACGIQIFLYLTMIGSEFFLLGLMAYDCYVAVCNPLRYP  
VLMNRKKCLLLAAGAWFGGSLDGFLLTPTITMNVPHYCGSRNHHFFCEIPAVLKLACADTSLYET  
LMYICCVLMILLIPISISTSYSLILLTHRMPSAEGRKKAFTTCSHLTVVSIFYGAIFYTYVLPQS  
FHTPEQDKVVSAFYTIVTPMLNPLIYSLRNKDVIGAFKKVFACSSAQKVATSDA (SEQ ID NO:  
50 477).

ATGACGAACACATCATCCTCTGACTTCACCCCTCCTGGGGCTTCTGGTGAACAGTGAGGCTG  
CCGGGATTGTATTTACAGTGATCCTTGCTGTTTTCTTGGGGGCCGTGACTGCAAATTTGGT  
CATGATATTCTTGATTGAGGTGGACTCTCGCTCCACACCCCCATGTACTTCTGCTCAGTC  
55 AGCTGTCCATCATGGACACCCTTTTTCTGTGTACCACTGTCCCAAACTCCTGGCAGACAT  
GGTTTCTAAAGAGAAGATCATTTTCTTTGTGGCCTGTGGCATCCAGATCTTCTCTACCTG

ACCATGATTGGTTCTGAGTTCTTCCTCCTGGGCCTCATGGCCTATGACTGCTACGTGGCTGT  
 CTGTAACCCTCTGAGATACCCAGTCCTGATGAACCGCAAGAAGTGCTTTTGCTGGCTGCT  
 GGTGCCTGGTTTGGGGGCTCCCTCGATGGCTTTCTGCTCACTCCCATCACCATGAATGTCC  
 CTTACTGTGGCTCCCGAAGTATCAACCATTTTTCTGTGAGATCCCAGCAGTTCTGAAACT  
 5 GGCCTGTGCAGACACGTCCTTGTATGAAACTCTGATGTACATCTGCTGTGCTCCTCATGTTG  
 CTCATCCCCATCTCTATCATCTCCACTTCCTACTCCCTCATCTTGTTAACCATCCACCGCAT  
 GCCCTCTGCTGAAGGTCGAAAAAGGCCTTCACCACCTGTTCCCTCCCACTTGACTGTAGTT  
 AGCATCTTCTATGGGGCTGCCTTCTACACATACGTGCTGCCCCAGTCCTTCCACACCCCCG  
 AGCAGGACAAAGTAGTGTGACGCTTCTATACCATTGTGACGCCCATGCTTAATCCTCTCAT  
 10 CTACAGCCTCAGAAACAAGGACGTCATAGGGGCATTAAAAAGGTATTTGCATGTTGCTCA  
 TCTGCTCAGAAAGTAGCAACAAGTGATGCTTAG (SEQ ID NO: 478).

#### AOLFR255 sequences:

MEQSNYSVYADFILLGLFSNARFPWLLFALILLVFLTSIASNVVKIILIHIDSRHTPMYFLLSQLS  
 15 LRDILYISTIVPKMLVDQVMSQRAISFAGCTAQHFLYLTLAGAEFFLLGLMSYDRYVAICNPLH  
 YPVLMSRKICWLIVAAAWLGGSIDGFLTPVTMQFPFCASREINHFFCEVPALLKLSCTDTSAY  
 ETAMYVCCIMMLLPFSVISGSYTRILITVYRMSEABGRGKAVATCSSHMVVVSLFYGAAMYT  
 YVLPHSYHTPEQDKAVSAFYTILTPMLNPLIYSLRNKDVGTALQKVVGRCVSSGKVTTT (SEQ  
 ID NO: 479).

20 ATGGAGCAGAGCAATTATTCCGTGTATGCCGACTTTATCCTTCTGGGTTTGTTTCAGCAACG  
 CCCGTTTCCCCTGGCTTCTCTTTGCCCTCATTCTCCTGGTCTTTTGGACCTCCATAGCCAGC  
 AACGTGGTCAAGATCATTCTCATCCACATAGACTCCCGCTCCACACCCCCATGTACTTCTCT  
 GCTCAGCCAGCTCTCCCTCAGGGACATCCTGTATATTTCACCATTTGTGCCAAAATGCTG  
 25 GTCGACCAGGTGATGAGCCAGAGAGCCATTTCCTTTGCTGGATGCACTGCCCAACACTTCC  
 TCTACTTGACCTTAGCAGGGGCTGAGTTCTTCTCCTCCTAGGACTCATGTCCTATGATCGCTAC  
 GTAGCCATCTGCAACCCTCTGCACTATCCTGTCCTCATGAGCCGCAAGATCTGCTGGTTGA  
 TTGTGGCGGCAGCCTGGCTGGGAGGGTCTATCGATGGTTTCTTGCTCACCCCCGTCACCAT  
 GCAGTTCCCCTTCTGTGCCTCTCGGGAGATCAACCACTTCTTCTGCGAGGTGCCTGCCCTTC  
 30 TGAAGCTCTCCTGCACGGACACATCAGCCTACGAGACAGCCATGTATGTCTGCTGTATTAT  
 GATGCTCCTCATCCCTTTCTCTGTCTATCTCGGGCTCTTACACAAGAATTCTCATTACTGTTT  
 ATAGGATGAGCGAGGCAGAGGGGAGGGGAAAGGCTGTGGCCACCTGCTCCTCACACATGG  
 TGGTTGTGACGCTCTTCTATGGGGCTGCCATGTACACATACGTGCTGCCTCATTCTTACCAC  
 ACCCTGAGCAGGACAAAGCTGTATCTGCCTTCTACACCATCCTTACTCCCATGCTCAATC  
 35 CACTCATTTACAGCCTTAGGAACAAGGATGTACAGGGGCCCTACAGAAGGTTGTGGGA  
 GGTGTGTGCTCCTCAGGAAAGGTAACCACTTTCTAA (SEQ ID NO: 480).

#### AOLFR256 sequences:

MGGKQPWVTEFILVGFQVGPALAILLCGLFSVFYTLTLLGNGVIFGIIICLDSKLHTPMYFFLSHL  
 40 AIIDMSYASNNVPKMLANLMNQKSTISFVPCIMQTFLYLAFVTECLILVMSYDRYVAICHPF  
 QYTVIMSWRVCTILASTCWIISFLMALVHITHILRPPFCGPQKINHFICQIMSVFKLACAGPRLNQ  
 VVLYAGSAFIVEGPLCLELVSNLHILSRHLEDPMGRAADRLTLPAPSHLCMVGLLFGSTMMV  
 YMAPKSRHPPEEQKVLFLFYSLFNPMLNPLIYSLRNAEVKGALKRVLWKQRSK (SEQ ID NO:  
 481).

45 ATGGGAGGCAAGCAGCCCTGGGTACAGAAATTCATCCTGGTGGGATTCCAGGTTGGTCCA  
 GCACTGGCGATTCTCCTCTGTGGACTCTTCTCTGTCTTCTATACACTCACCTGCTGGGGAA  
 TGGGGTCATCTTTGGGATTATCTGCCTGGACTCTAAGCTTCACACACCCATGTACTTCTTCC  
 TCTCACACCTGGCCATCATTGACATGTCTATGCTTCCAACAATGTTCCCAAGATGTTGGC  
 50 AAACCTAATGAACCAGAAAAGCACCATCTCCTTTGTTCCATGCATAATGCAGACTTTTTTG  
 TATTTGGCTTTTGTCTGTTACAGAGTGCCTGATTTTGGTGGTGATGTCCTATGATAGGTATGT  
 GGCCATCTGCCACCTTTCCAGTACACTGTCATCATGAGCTGGAGAGTGTGCACGATCCTG  
 GCCTCAACATGCTGGATAATTAGCTTTCTCATGGCTCTGGTCCATATAACTCATATTCTGAG  
 GCCGCTTTTTGTGGCCCAAAAAGATCAACCACTTTATCTGTCAAATCATGTCCGTATTCA  
 55 AATTGGCCTGTGCTGGCCCTAGGCTCAACAGGTGGTCTTATATGCGGGTCTGCGTTCAT  
 CGTAGAGGGGCCGCTCTGCCTGGAGCTGGTCTCCAACCTGCACATCCTGTGCGGCCATCTT

GAGGATCCAGTAATGGGGAGGGCCGCGAGACCGACTTACTCTTCCTGCTCCTTCCCACCTTT  
 GCATGGTGGGACTCCTTTTTTGGCAGCACCATGGTCATGTACATGGCCCCCAAGTCCCGCCA  
 CCCTGAGGAGCAGCAGAAGGTCCTTTCCCTGTTTTACAGCCTTTTCAACCCGATGCTGAAC  
 CCCTTGATCTACAGCCTGAGGAACGCAGAGGTCAAGGGTGCCCTGAAAAGAGTGTTGTGG  
 5 AAACAGAGATCAAAGTGA (SEQ ID NO: 482).

**AOLFR257 sequences:**

MESNQTWITEVILLGFQVDPALELFLFGFLLFYSLTLMGNGIILGLIYLD SRLHTPMYVFLSHL  
 AIVDMSYASSTVPKMLANLVMHKKVISFAPCILQTFLYLAFATECLILVMMC YDRYVAICHPL  
 10 QYTLIMNWRVCTVLA STCWIFSELLALVHITLILRLPFCGPQKINHFFCQIMSVFKLACADTRLN  
 QVVLFAGS AFILVGPLCLVLVSYLHILVAILRIQSGEGRRKAFSTCSSHL CVVGLFFGSAIVMYM  
 APKSSHSQERRKILSLFYSLFNPI LNPLIYSLRNAEVKGALKRVLWKQRSM (SEQ ID NO: 483).

ATGGAAAGCAATCAGACCTGGATCACAGAAATCATCCTGTTGGGATTCCAGGTGGACCCA  
 15 GCTCTGGAGTTGTTCTCTTTGGGTTTTTCTTGCTATTCTACAGCTTAACCTGATGGGAAA  
 TGGGATTATCCTGGGGCTCATCTACTTGGACTCTAGACTGCACACACCCATGTATGTCTTC  
 CTGTACACCTGGCCATTGTGGACATGTCCTATGCCTCGAGTACTGTCCCTAAGATGCTAG  
 CAAATCTTGTGATGCACAAAAAGTCATCTCCTTTGCTCCTTGCATACTTCAGACTTTTTTG  
 TATTTGGCGTTTGCTATTACAGAGTGTCTGATTTTGGTGATGATGTGCTATGATCGGTATG  
 20 TGGCAATCTGTCAACCTTGCAATACACCTCATTATGAACTGGAGAGTGTGCACTGTCTCT  
 GGCTCAACTTGCTGGATATTTAGCTTTCTCTTGCTCTGGTCCATATTACTCTTATTCTGA  
 GGCTGCCTTTTTGTGGCCACAAAAAGATCAACCACTTTTTCTGTCAAATCATGTCCGTATTC  
 AAATTGGCCTGTGCTGACACTAGGCTCAACCAGGTGGTCTCTATTTGCGGGTTCTGCGTTCA  
 TCTTAGTGGGGCCGCTCTGCCTGGTGCTGGTCTCCTACTTGACATCCTGGTGGCCATCTTG  
 25 AGGATCCAGTCTGGGGAGGGCCGCGAGAAAGGCCTTCTCTACCTGCTCCTCCACCTCTGCG  
 TGGTGGGGCTTTTTCTTTGGCAGCGCCATTGTCATGTACATGGCCCCCAAGTCAAGCCATTC  
 TCAAGAACGGAGGAAGATCCTTTCCCTGTTTTACAGCCTTTTCAACCCGATCCTGAACCCC  
 CTCATCTACAGCCTTAGGAATGCAGAGGTGAAAGGGGCTCTAAAGAGAGTCTTTGGAAA  
 CAGAGATCAATGTGA (SEQ ID NO: 484).

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**AOLFR259 sequences:**

MGDNQSRVTEFILVGFQLSVEMEVLFWIFSLLYLFSLLANGMILGLICLDPRLRTPMYFFLSHL  
 AVIDIYYASSNLLNMLENLVKHKKTISFISCIMQMALYLTFAAAVCMILVMSYDRFVAICHPL  
 HYTVIMNWRVCTVLAITSWACGFSALINLILRLPFCGPQEVNHFFGEILSVLKLACADTWIN  
 35 EIFVFAGGVFVLVGPLSLMLISYMRILLAILKIQSKEGRKKAFTSCSSHL CVVGLYFGMAMVVY  
 LVPDNSQRQKQKILTLFYSLFNPLL NPLIYSLRNAQVKGALYRALQKRTM (SEQ ID NO:  
 485).

ATGGGGGACAACCAATCACGGGTCACAGAATTCATCCTGGTTGGATTCCAGCTCAGTGTG  
 40 GAGATGGAAGTGCTCCTCTTCTGGATCTTCTCCCTGTTATATCTCTTCAGCCTGCTGGCAA  
 TGGCATGATCTTGGGGCTCATCTGTCTGGATCCCAGACTGCGCACCCCATGTACTTCTTCC  
 TGTCACACTTGGCCGTCATTGACATATACTATGCTTCCAGCAATTTGCTCAACATGCTGGA  
 AAACCTAGTGAAACACAAAAAACTATCTCGTTTCACTCTTGCATTATGCAGATGGCCTTG  
 TATTTGACTTTTGCTGCTGCAGTGTGCATGATTTTGGTGGTGATGTCTATGACAGATTTGT  
 45 GCGATCTGCCATCCCCTGCATTACACTGTCAATCATGAACTGGAGAGTGTGCACAGTACTG  
 GCTATTACTTCTTGGGCATGTGGATTTTCCCTGGCCCTCATAAATCTAATTCTCCTTCTAAG  
 GCTGCCCTTCTGTGGGCCCCAGGAGGTGAACCACTTCTTCGGTGAAATTCTGTCTGTCTC  
 AAATGGCCTGTGCAGACACCTGGATTAATGAAATTTTGTCTTTGCTGGTGGTGTGTTTG  
 TCTTAGTCGGGCCCCCTTTCCTTGATGCTGATCTCCTACATGCGCATCCTCTTGGCCATCCTG  
 50 AAGATCCAGTCAAAGGAGGGCCGCAAAAAAGCCTTTTCCACCTGCTCCTCCACCTCTGTG  
 TGGTTGGGCTTTACTTTGGCATGGCCATGGTGGTTTACCTGGTCCCAGACAACAGTCAACG  
 ACAGAAGCAGCAGAAAAATTCTACCCGTGTTTACAGCCTTTTCAACCCATTGCTGAACCCC  
 CTCATCTACAGCCTGCGGAATGCTCAAGTGAAGGGTGCTTATACAGAGCACTGCAGAAA  
 AAGAGGACCATGTGA (SEQ ID NO: 486).

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**AOLFR24B sequences:**

MPSINDTHFYPPFFLLLGIPGLDTLHIWISFPFCIVYLIAIVGNMTILFVIKTEHSLHQPMFYFLAM  
 LSMIDLGLSTSTIPKMLGIFWFNLQEISFGGCLLQMFFIHMFTGMEVLLVVMAYDRFVAICNP  
 LQYTMILTNTKISILASVVVGRNLVLVTPFVFLILRLPFCGHNIVPHTYCEHRGLAGLACAPIKIN  
 5 IYGLMVISYIIVDVILIASYVLLRAVFRLP SQDVRLKAFNTCGSHVCVMLCFYTPAFFSFMTH  
 RFGQNPHYIHILLANLYVVVPPALNPVIYGVRTKQIREQIVKIFVQKE (SEQ ID NO: 487)

ATGCCTTCTATCAATGACACCCACTTCTATCCCCCTTCTTCCTCCTGCTAGGAATACCAGG  
 ACTGGACACTTTACATATCTGGATTTCTTTCCCATTCTGTATTGTGTACCTGATTGCCATTG  
 10 TGGGGAATATGACCATTCTCTTTGTGATCAAACTGAACATAGTCTACACCAGCCCATTGTT  
 CTACTTCCTGGCCATGTTGTCTATGATTGATCTGGGTCTGTCCACATCCACTATCCCCAAAA  
 TGCTAGGAATCTTCTGGTTCAACCTCCAAGAGATCAGCTTTGGGGGATGCCTTCTTCAGAT  
 GTTCTTTATTCACATGTTTACAGGCATGGAGACTGTTCTGTTGGTGGTCATGGCTTATGACC  
 GCTTTGTTGCCATCTGCAACCCCTCTCCAGTACACCATGATCCTCACCAATAAAACCATCAG  
 15 TATCCTAGCTTCTGTGGTTGTTGGAAGAAATTTAGTTCTTGTAACCCCATTTGTGTTTCTCA  
 TTCTGCGTCTGCCATTCTGTGGGCATAACATCGTACCTCACACATACTGTGAGCACAGGGG  
 TCTGGCCGGGTTGGCCTGTGCACCCATTAAAGATCAACATAATCTATGGGCTCATGGTGATT  
 TCTTATATTATTGTGGATGTGATCTTAATTGCCTCTTCCTATGTGCTTATCCTTAGAGCTGT  
 TTTTCGCCCTCCCTCTCAAGATGTCCGACTAAAGGCCTTCAATACCTGTGGTTCTCATGTCT  
 20 GTGTTATGCTGTGCTTTTACACACCAGCATTTTTTTCTTTTATGACACATCGTTTTGGCCAA  
 AACATTCCTCCACTATATCCATATTCTTTTGGCTAACCTGTATGTGGTTGTCCACCTGCCCT  
 TAACCTGTCAATTTATGGAGTCAGGACCAAGCAGATCCGAGAGCAAATTTGTGAAAATATTT  
 GTACAGAAAGAATAA (SEQ ID NO: 488)

**AOLFR33B sequences:**

MLHTNNTQFHPSTFLVVGVPGLVDVHVWIGFPFFAVYLTALLGNIIILFVIQTEQSLHQPMFYFL  
 AMLAGTDLGLSTATIPKMLGIFWFNLGEIAFGACITQMYTHICTGLESVVLTVTGIDRYIAICNP  
 LRYSMILTNTKVIAILGIVHVRTLVFVTPFTFLRLPFCGVRIPHTYCEHMG LAKLACASINVITY  
 GLIAFSVGYIDISVIGFSYVQILRAVFHLPWDARLKALSTCGSHVCVMLAFYLPALFSFMTHRF  
 30 GHNIPHYIHILLANLYVVFPALNSVIYGVKTKQIREQVLRILNPKSFWHFDPKRIFHNNSVRQ  
 (SEQ ID NO: 489)

ATGCTTCATACCAACAATACACAGTTTCACCCTTCCACCTTCCTCGTAGTGGGGGTCCCAG  
 GGCTGGAAGATGTGCATGTATGGATTGGCTTCCCCTTCTTTGCGGTGTATCTAACAGCCCT  
 35 TCTAGGGAACATCATTATCCTGTTTGTGATACAGACTGAACAGAGCCTCCACCAACCCATG  
 TTTTACTTCCTAGCCATGTTGGCCGGCACTGATCTGGGCTTGTCTACAGCAACCATCCCCA  
 AGATGCTGGGAATTTTCTGGTTTAACTTGGAGAGATTGCATTTGGTGCCTGCATCACACA  
 GATGTATACCATTCATATATGCACTGGCCTGGAGTCTGTGGTACTGACAGTCACGGGCATA  
 GATCGCTATATTGCCATCTGCAACCCCTGAGATATAGCATGATCCTTACCAACAAGGTAA  
 40 TAGCCATTCTGGGCATAGTCATCATTGTGAGGACTTTGGTATTTGTGACTCCATTACATTT  
 CTCACCCCTGAGATTGCCTTTCTGTGGTGTCCGATTATCCCTCATACCTATTGTGAACACAT  
 GGGCTTGGCAAAGTTAGCTTGTGCCAGTATTAATGTTATATATGGATTGATTGCCTTCTCA  
 GTGGGATACATTGACATTTCTGTGATTGGATTTTCTATGTCCAGATCCTCCGAGCTGTCTT  
 CCATCTCCCAGCCTGGGATGCCCGGCTTAAGGCACTCAGCACATGTGGCTCTCACGTCTGT  
 45 GTTATGTTGGCTTTCTACCTGCCAGCCCTCTTTTCCTTCATGACACACCGCTTTGGCCACAA  
 CATCCCTCATTACATCCACATTTCTTGGCCAATCTGTATGTGGTTTTTCCCCTGCTCTTA  
 ACTCTGTTATCTATGGGGTCAAAACAAAACAGATACGAGAGCAGGTACTTAGGATACTCA  
 ACCCTAAAAGCTTTTGGCATTGTGACCCCAAGAGGATCTTCCACAACAATTCAGTTAGACA  
 ATAA (SEQ ID NO: 490)

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**AOLFR112B sequences:**

MKNKTVLTEFILLGLTDVPELQVAVFTFLFLAYLLSILGNLTILLTLLDLSHLQTPMYFFLRNFSF  
 LEISFTNIFPRLISITTNKNSISFAGCFTQYFFAMFLGATEFYLLAAMS YDRYVAICKPLHYTTI  
 MSSRICQLIFCSWLGLMAIPTITLMSQQDFCASNRLNHYFCDYEP LLELSCSDTSLIEKVFL  
 55 VASVTLVTVTLVLVLSYAFIHKTLKLPSAQQRKAFSTCSSHMIVISLSYGSCMFMYINPSAKEG  
 DTFNKGVALITSVAPLLNPFYITLRNQVQKQPFKDMVKLLNL (SEQ ID NO: 491)

ATGAAAAATAAAACCGTGTTAACTGAGTTTATCCTTCTGGGTCTAACAGATGTCCCTGAAC  
TCCAGGTGGCAGTTTTCACCTTTCTTTTCTTGCGTATTTACTCAGCATCCTTGGAAATCTG  
ACTATCCTCATCCTCACCTTGCTGGACTCCACCTTCAGACTCCCATGTATTTCTTTCTCCG  
5 GAACTTCTCCTTCTTGAAATTTCTTTCACAAACATCTTCATTCCAAGGGTCTGATTAGCA  
TCACAACAGGGAACAAGAGTATCAGCTTTGCTGGCTGCTTCACTCAGTATTTCTTTGCCAT  
GTTCTTGGGGCTACAGAGTTTTACCTTCTGGCTGCCATGTCCTATGACCGCTATGTGGCC  
ATCTGCAAACCTCTGCATTACACCACCATCATGAGCAGCAGAATCTGCATCCAGCTGATTT  
TCTGCTCTTGGCTGGGTGGGCTAATGGCTATTATACCAACAATCACCTGATGAGTCAGCA  
10 GGACTTTTGTGCATCCAACAGACTGAATCATTACTTCTGTGACTATGAGCCTCTTCTGGAA  
CTCTCATGTTTCAGACACAAGCCTCATAGAGAAGGTTGTCCTTCTTGTGGCATCTGTGACCC  
TGGTGGTCACTCTGGTGTAGTGATTCTCTCCTATGCATTCAATTATCAAGACTATTCTGAAG  
CTCCCTCTGCCCAACAAGGACAAAAGCCTTTTCCACATGTTCTTCCACATGTTCTGTGAT  
CTCCCTCTCTTACGGAAGCTGCATGTTTATGTACATTAATCCCTCTGCAAAAGAAGGGGAT  
15 ACATTCAACAAGGGAGTAGCTCTACTCATTACTTCAGTTGCTCCTTTGTTGAACCCCTTTAT  
TTACACCTAAGGAACCAACAGGTAACAACCCCTTCAAGGATATGGTCAAAAAGCTTCT  
GAATCTTTAA (SEQ ID NO: 492)

**AOLFR130B sequences:**

20 MEGKNQTAPEFHLGFDHLNELQYLLFTIFFLTYICTLGGNVFIIVVTIADSHLHTPMYYFLGNL  
ALIDICYTTTNPQMMVHLLSEKKIISYGGCVTQLFAFIFFVGSECLLLAAMAYDRYIAICKPLR  
YSFIMNKALCSWLAASCWTCGFLNSVLHTVLTFHLPFCGNNQINYYFCDIPLLILSCGDTSLNE  
LALLSIGILISWTPFLCHLSYLYIISTILRIRSSEGRHKAFSTCASHLLIVLYYSAIFTYVRPISSYS  
LEKDRLISVLYSVVTPMLNPVIYTLRNKDIKEAVKAIGRKWQPPVFSSDI (SEQ ID NO: 493)

25 ATGGAAGGAAAGAATCAAACAGCTCCATCTGAATTCATCATCTTGGGGTTCGACCACCTGA  
ATGAATTGCAGTATTTACTCTTCACCATCTTCTTTCTGACCTACATATGCATTTAGGAGGC  
AATGTTTTTATCATGTGTTGGTGACCATAGCTGATTCCCACCTACACACACCCATGTATTATTT  
CCTAGGAAATCTTGCCCTTATTGACATCTGCTACACTACTACTAATGTCCCCCAGATGATG  
30 GTGCATCTTCTGTCAGAGAAGAAATCATTTCCCTATGGAGGCTGTGTGACCCAGCTCTTTG  
CATTCAATTTCTTTGTTGGCTCAGAGTGCTCCTCCTGGCAGCAATGGCATATGATCGATAT  
ATTGCTATCTGTAAGCCGTTAAGGTACTCATTTATTATGAACAAGGCCCTGTGCAGCTGGT  
TAGCAGCCTCATGCTGGACATGTGGGTTTCTCAACTCAGTGTTGCACACCGTTCTGACCTT  
CCACCTGCCCTTCTGTGGTAACAATCAGATCAATTATTTCTTCTGTGACATACCTCCCTTGC  
35 TCATCTTGTCTTGTGGTGATACTTCCCTCAATGAACTGGCTTTGCTGTCCATTGGGATCCTC  
ATAAGCTGGACTCCTTTCTGTGCATCATCCTTTCTACCTTTACATCATCTCCACCATCCT  
GAGGATCCGTTCCCTCTGAGGGGAGGCACAAAGCCTTTTCCACCTGTGCCTCCCACCTGCTC  
ATTGTTATTCTCTATTATGGCAGTGCTATCTTCACGTATGTGAGGCCCATCTCATCTTACTC  
TCTAGAGAAAGATAGATTGATCTCAGTGCTGTATAGTGTTGTCACACCCATGCTGAATCCT  
40 GTAATTTATACGCTAAGGAATAAGGACATCAAAGAGGCTGTGAAGGCCATAGGGAGAAAG  
TGGCAGCCACCAGTTTTCTCTTCTGATATATAA (SEQ ID NO: 494)

**AOLFR142B sequences:**

45 MARKDMAHINCTQATEFILVGLTDHQBELKMPLFVLFLSYLFTVVGNLGLILLIRADTSLNTPM  
YFFLSNLAFFVDFCYSSVTPKMLGNFLYKQNVISFDACATQLGCFLTFMISESLLASMAFYDRY  
VAICNPLLYMVVMTPGICQLVAVPYSYFLMALFHTILTFRLSYCHSNIVNHFYCDDMPLRL  
TCSDRFKQLWIFACAGIMFISSLLIVFVSYMFIIISAILRMHSAEGRQKAFSTCGSHMLAVTIFYG  
TLIFMYLQPSSSHALDTDKMASVFYTVIIPMLNPLIYSLQNKEVKEALKKIIINKN (SEQ ID NO:  
495)

50 ATGGCCAGAAAAGATATGGCTCACATCAATTGCACCCAGGCGACAGAGTTTATTCTTGTGG  
GCCTCACAGACCATCAGGAGTTGAAGATGCCCTCTTTGTGCTATTCTTATCCATCTACCTC  
TTCACAGTGGTAGGCAACTTGGGTTTGATCCTACTCATTAGAGCGGATACAAGTCTCAACA  
CACCAATGTACTTCTTTCTTAGCAACCTAGCTTTTGTGGATTCTGTTACTCTTCTGTCAAT  
55 ACACCCAAAATGCTTGGGAATTTCTTGTACAAACAAAATGTTATATCCTTTGATGCATGTG  
CTACTCAACTGGGCTGCTTTCTCACCTTCATGATATCAGAATCCTTGCTACTGGCTTCCATG

GCCTATGACCGATATGTGGCCATTTGTAAACCCTCTATTGTATATGGTTGTAATGACTCCAG  
 GAATCTGCATTCAACTTGTAGCAGTTCCTTATAGCTATAGCTTCCTAATGGCACTATTTTAC  
 ACCATCCTCACCTTCCGCCTCTCCTATTGCCACTCCAACATTGTCAACCATTCTATTGTGA  
 TGACATGCCTCTCCTCAGGCTAACTTGCTCAGACACTCGCTTCAAACAGCTCTGGATCTTT  
 5 GCCTGTGCTGGTATCATGTTCAATTTCTCCCTTCTGATTGTCTTTGTCTCCTACATGTTTCATC  
 ATTTCTGCCATCCTGAGGATGCATTAGCTGAGGGAAGACAGAAGGCTTTCTCGACGTGTG  
 GCTCTCACATGCTGGCAGTCACCATATTCTATGGGACCCTCATTTTTATGTACTTACAGCCT  
 AGCTCTAGCCATGCCCTGGACACAGACAAGATGGCCTCTGTCTTCTACACAGTGATCATTC  
 CCATGTTGAATCCCTTAATCTATAGCCTCCAGAATAAGGAGGTGAAAGAAGCTCTGAAGA  
 10 AAATCATTATCAATAAAAACTAG (SEQ ID NO: 496)

**AOLFR171C sequences:**

MAEVNIIYVTVFILKGITNRPELQAPCFGVFLVIYLVTVLGNLGLITLIKIDTRLHTPMYYFLSHL  
 AFVDLCYSSAITPKMMVNFVVERNTIPFHACATQLGCFLTFMITECFLLASMAYDCYVAICSP  
 15 HYSTLMSRRVCIQLVAVPYTYSFLVALFHTVITFRLTYCGPNLINHFYCDLPLALSCSDTHMK  
 EILIFAFAGFDMISSSSIVLTSYIFIAAILRIRSTQGQHKAISTCGSHMVTVTIFYGTLIFMYLPKS  
 NHSLDTDKMASVFYTVVIPMLNPLIYSLRNKEVKDASKKALDKGCENLQILFLKIRKLY (SEQ  
 ID NO: 497)

20 ATGGCTGAAGTTAATATCATTTATGTCACTGTATTCACTCTGAAAGGAATTACCAACCGGC  
 CAGAGCTTCAGGCCCGTGCTTTGGGGTGTTTTAGTTATCTATCTGGTCACAGTGCTGGG  
 CAATCTTGGGTTGATTACTTTAATCAAGATTGATACTCGACTCCACACACCTATGTACTATT  
 TCCTCAGCCACCTGGCCTTTGTTGACCTTTGTTACTCCTCTGCTATTACACCGAAGATGATG  
 GTGAATTTTGTGTTGGAACGCAACACCATTCCCTTTCCATGCTTGTGCAACCCAACTGGGTT  
 25 GTTTTCTCACCTTCATGATCACTGAGTGTTTCTTCTAGCCTCCATGGCCTACGATTGCTAT  
 GTCGCCATCTGTAGTCCCCTGCATTATTCAACACTGATGTCAAGAAGAGTCTGCATTCAAC  
 TGGTGCCAGTTCCATATATATACAGCTTCCTGGTTGCCCTCTTCCACACCGTTATCACTTC  
 CGTCTGACTTACTGTGGCCCAAACCTTAATTAACCATTCTATTGTGATGACCTCCCCCTTCTT  
 AGCTCTGTCTGCTCAGACACACACATGAAGGAAATTCTGATATTTGCCTTTGCTGGCTTT  
 30 GATATGATCTCTTCTTCCATTGTCTCCTCACCTCCTACATCTTTATTATTGCCGCTATCCTA  
 AGGATCCGCTCTACTCAGGGGCAACACAAAGCCATTTCACCTGTGGCTCCCATATGGTGA  
 CTGTCACTATTTTCTATGGCACACTGATCTTTATGTACCTACAGCCCAAATCAAATCACTCC  
 TTGGACACAGACAAGATGGCTTCTGTATTTTACACAGTGGTGATCCCCATGTTAAACCCCC  
 TAATCTATAGTCTAAGGAACAAAGAAGTGAAAGATGCCTCAAAGAAAGCCTTGGATAAAG  
 35 GTTGTGAAAACCTACAGATATTAACATTTTAAAAATAAGAAAACCTTTATTAA (SEQ ID NO:  
 498)

**AOLFR225B sequences:**

MKNRTMFGFILLGLTNQPELQVMIFIFLTYMLSILGNLTITLTLDPHLQTPMYFFLRNFSF  
 40 LEISFTSIFIPRLTSMITTGNKVISFAGCLTQYFFAIFLGATEFYLLASMSYDRYVAJCKPLHYLTI  
 MSSRVCIQLVFCSWLGGFLAILPPIILMTQVDFCVSNILNHYYCDYGPLVELACSDTSLLELMVI  
 LLAVVTLMVTLVLVLTLSYTYIIRTLRIPSAQQRKAFSTCSSHMIVISLSYGSCMFMYINPSAKE  
 GGAFNKGIAVLITSVTPLLPFIYTLRNQVQKQAFKDSVKKIVKL (SEQ ID NO: 499)

45 ATGAAAAACAGAACCATGTTTGGTGAGTTTATTCTACTGGGCCTTACAAATCAACCTGAAC  
 TCCAAGTGATGATATTCATCTTTCTGTTCCTCACCTACATGCTAAGTATCCTAGGAAATCTG  
 ACTATTATCACCTCACCTTACTAGACCCCCACCTCCAGACCCCCATGTATTTCTTCCCTCCG  
 GAATTTCTCCTTCTTAGAAAATTTCTCTTACATCCATTTTATTCCCAGATTTCTGACCAGCA  
 TGACAAACAGGAAATAAAGTTATCAGCTTTGTCTGGCTGCTTGACTCAGTATTTTGTGCTAT  
 50 ATTTCTTGGAGCTACCGAGTTTACCTCCTGGCCTCCATGTCTTATGATCGTTATGTGGCCA  
 TCTGCAAACCTTGCATTACCTGACTATTATGAGCAGCAGAGTCTGCATACAACTAGTGTT  
 CTGCTCCTGGTTGGGGGATTCTTAGCAATCTTACCACCAATCATCCTGATGACCCAGGTA  
 GATTTCTGTGTCTCCAACATTCTGAATCACTATTACTGTGACTATGGGCCTCTCGTGGAGCT  
 TGCCTGCTCAGACACAAGCCTCTTAGAACTGATGGTCATCCTCTTGGCCGTTGTGACTCTC  
 55 ATGGTTACTCTGGTGCTGGTGACACTTTCTTACACATACATTATCAGGACTATTCTGAGGA  
 TCCCTTCTGCCAGCAAAGGACAAAGGCCTTTTCCACTTGTTCCTCCCACATGATTGTCATC



TCCCTCTCTTATGGCAGCTGCATGTTTATGTACATTAATCCTTCTGCAAAAGAAGGAGGTG  
 CTTTCAACAAAGGAATAGCTGTACTCATTACTTCGGTTACTCCCTTACTGAATCCCTTCATA  
 TATACTTTAAGAAATCAGCAAGTGAAACAAGCTTTCAAGGACTCAGTCAAAAAGATTGTG  
 AAACTTTAA (SEQ ID NO: 500)

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**AOLFR274B sequences:**

MEFVFLA YPSCPELHLSFLGVSLVYGLIITGNILIVVSIHTETCLCTSMYYFLGSLSGIEICYTAV  
 VVPHILANTLQSEKTITLLGCATQMAFFIALGSADCFLLAAMA YDRYVAICHPLQYPLLMTLTL  
 CVHLVVASVISGLFSLQLVAFIFSLPFCQAQGIEHFFCDVPPVMHVCAQSHIEQSVLVAAIL  
 10 AIAVPFFLITTSYTFIVAALLKIHSAAGRHRAFSTCSSHLTVVLLQYGCCAFMYLCPSSSYNPKQ  
 DRFISLVYTLGTPLLNPLIYALRNSEMKGAVGRVLTRNCLSQNS (SEQ ID NO: 501)

ATGGAATTTGTGTTTCTGGCCTATCCCTCCTGCCAGAACTGCATATTCTGTCTTCTTCTGG  
 GGTGAGCCTGGTTTATGGTTTGATCATCACTGGGAACATTCTCATTGTGGTGTCCATTAC  
 15 ACAGAAACCTGTCTATGCACATCCATGTACTATTTCTGGGCAGCCTTTCTGGGATTGAAA  
 TATGCTACACTGCAGTGGTGGTGCCCATATCCTGGCCAACACCCTACAGTCAGAGAAGAC  
 CATCACTCTCCTGGGCTGTGCCACCCAGATGGCTTTCTTCATTGCACTGGGCAGTGCTGAT  
 TGCTTCCTCTTGGCTGCCATGGCCTATGACCGCTATGTGGCCATTGCCACCCGTTGCAGTA  
 CCCTCTCCTCATGACATTGACTCTTTGTGTCCACTTGGTGTGGCATCAGTCATCAGTGGTC  
 20 TGTTCTGTCTTACAACCTGGTGGCCTTCATCTTCTCTGCTGCACTTCTGCCAGGCTCAGGGC  
 ATTGAGCACTTCTTTTGTGATGTGCCACCAGTCATGCATGTTGTTTGTGCTCAGAGTCACAT  
 TCATGAGCAGTCAGTGCTGGTGGCAGCCATACTAGCCATTGCTGTGCCTTTCTTCCTCATC  
 ACCACCTCCTACACCTTCATAGTGGCTGCTCTGCTCAAGATCCACTCGGCTGCTGGCCGCC  
 ACCGGGCCTTCTCCACCTGCTCTTCCACCTCACTGTGGTGTGCTGCTGCAGTATGGCTGCTGT  
 25 GCCTTCATGTACCTGTGCCAGCTCCAGCTACAACCCCAAGCAAGATCGGTTTCATCTCAC  
 TGGTGTACACATTGGGAACCCCACTGCTCAACCCCACTTATCTATGCCCTGAGGAACAGTGA  
 GATGAAAGGGGCGTAGGGAGAGTTCTTACCAGGAAGTGCCTTCTCCAGAACAGCTAG  
 (SEQ ID NO: 502)

30 **AOLFR276B sequences:**

MGGFGTNISSSTTSFTLTGFPEMKGLEHWLAALLLLLYAISFLGNILILFIKEEQSLHQPMYYFLS  
 LFSVNDLGVSFSTLPTVLAAVCFHAPETTFDACLAQMFFIHFSSWTEFGILLAMSFDHYVAICNP  
 LRYATVLT DVRVAHNGISIVIRSF CMVFPLPFLKRLPFCASVLAHSYCLHADLIRLPWGD  
 TINSMYGLFVISA FGVDSL LLLSYVL LHSVLA IASRGERL KTLN TCVSHIYAVLIFYVPMVSVS  
 35 MVHFRGRHAPEYVHKFMSLCTSNALPNYLFHQD (SEQ ID NO: 503)

ATGGGGGGCTTTGGGACTAACATCTCAAGTACTACCAGCTTCACTCTAACAGGCTTCCCTG  
 AGATGAAGGGTCTGGAGCACTGGCTGGCTGCCCTTCTGCTGCTGCTTTATGCTATTTCCCT  
 40 CCTGGGCAACATCCTCATCCTCTTTATCATAAAGGAAGAGCAGAGCTTGCACCAGCCAATG  
 TACTACTTCTGTCTCTTTTTTCTGTAAATGACCTGGGTGTGTCCTTTCTACATTGCCCACT  
 GTACTGGCTGCTGTGTGTTTTCATGCCCCAGAGACAACCTTTGATGCCTGCCTGGCCCA  
 TGTCTTTCATCCACTTTTCTCCTCGGACAGAGTTTGGCATCCTACTGGCCATGAGTTTTGAC  
 CACTATGTGGCCATCTGTAACCCGCTGCGCTATGCCACAGTGCTCACTGATGTCCGTGTGG  
 CCCACAATGGCATATCCATTGTCATCCGCAGCTTCTGCATGGTATTCCCACTTCCCTTCTC  
 45 CTGAAGAGACTGCCTTTCTGTAAGGCCAGTGTGGTACTGGCCATTCCCTACTGTCTGCATG  
 CAGACCTGATTGCGCTGCCCTGGGGAGACACTACCATCAACAGCATGTATGGCCTGTTTCT  
 TGTATCTCTGCTTGTGTGATTCATGCTCATCCTCCTCTCCTATGTGCTCATTCTAC  
 ATTCTGTGCTGGCCATTGCCTCCAGGGGTGAGAGGCTTAAGACACTCAACACATGTGTGTC  
 ACATATCTATGCAGTGCTGATCTTCTATGTGCCTATGGTTAGTGTGTCCATGGTTCATCGAT  
 50 TTGGGAGGCATGCTCCTGAATATGTGCACAAGTTCATGTCTCTTTGTACCTCCAATGCTCT  
 ACCCAATTATCTATTCCATCAAGACTAA (SEQ ID NO: 504)

**AOLFR311B sequences:**

MDWENCSSLTDFLLGITNPNEMKVTLFAVFLAVYIINF SANLGMIVLIRMDYQLHTPMYFFLS  
 55 HLSFCDLCYSTATGPKMLVDLLAKNKSIPFYGCALQFLVFCIFADSECLLSVMAFDRYKAIINP  
 LLYTVNMSSRVCYLLLTGVYLVGIADALIHMTLAFRLCFCGSNEINHFFCDIPLLLLSRSDTQV

NELVLFTVFGFIELSTISGVFISYCYIILSVLEIHSAGEGRFKALSTCTSHLSAVAIQGTLLFMYFRP  
SSSYSLDQDKMTSLFYTLVVPMLNPLIYSLRNKDVKEALKKLKNKILF (SEQ ID NO: 505)

5 ATGGACTGGGAAAATTGCTCCTCATTAAGTGAATTTTTCTCTTGGGAATTACCAATAACCC  
AGAGATGAAAGTGACCTATTTGCTGTATTCTTGGCTGTTTATATCATTAAATTTCTCAGCAA  
ATCTTGGAATGATAGTTTAAATCAGAATGGATTACCAACTTCACACACCAATGTATTTCTT  
CCTCAGTCATCTGTCTTTCTGTGATCTCTGCTATTCTACTGCAACTGGGCCCAAGATGCTGG  
TAGATCTACTTGCCAAGAACAAGTCAATACCCTTCTATGGCTGTGCTCTGCAATTCTTGGT  
CTTCTGTATCTTTGCAGATTCTGAGTGTCTACTGCTGTCAGTGATGGCCTTTGATCGGTACA  
10 AGGCCATCATCAACCCCTGCTCTATAAGTCAACATGTCTAGCAGAGTGTGCTATCTACT  
CTTGACTGGGGTTTATCTGGTGGGAATAGCAGATGCTTTGATACATATGACACTGGCCTTC  
CGCCTATGCTTCTGTGGGTCTAATGAGATTAATCATTTCTTCTGTGATATCCCTCCTCTCTT  
ATTACTCTCTCGCTCAGATACACAGGTCAATGAGTTAGTGTTATTCACCGTCTTTGGTTTTA  
TTGAACTGAGTACCATTTTCAAGAGTTTTCATTTCTTATTGTTATATCATCCTATCAGTCTTG  
15 GAGATACACTCTGCTGAGGGGAGGTTCAAAGCTCTCTCTACATGCACTTCCCACTTATCTG  
CGGTTGCAATTTTCCAGGGAAGTCTGCTCTTTATGTATTTCCGGCCAAGTTCTTCCTATTCT  
CTAGATCAAGATAAAATGACCTCATTTGTTTACACCTTGTGGTTCCCATGTTGAACCCCT  
GATTTATAGCCTGAGGAACAAGGATGTGAAAGAGGCCCTGAAAAAAGTAAAAATAAAAT  
TTTATTTTAA (SEQ ID NO: 506)

20

**AOLFR314 sequences:**

MEVKNCMVTEFILLGIPHTGLEMTLFLVFLPFYACTLLGNVSILVAVMSSARLHTPMYFFLG  
NLSVDFDMGFSSVTCPKMLLYLMGLSRLISYKDCVCQLFFHFLGSIIEFLFTVMAYDRFTAICY  
PLRYTVIMNPRICVALAVGTWLLGCIHSSILSLTFTLPYCGPNEVDHFFCDIPALLPLACADTSL  
25 AQRVSFTNVGLISLVCFLLILLSYTRITISLSIRTTGRRRAFSTCSAHLIAILCAYGPHTVYLQPT  
PNPMLGTVVQILMNLVGPMLNPLIYTLRNKEVKALKILHRTGHVPES (SEQ ID NO: 507)

30 ATGGAGGTGAAGAACTGCTGCATGGTGACAGAGTTCATCCTTTTGGGAATCCACACACA  
GAGGGGCTGGAGATGACACTTTTTGTCTTATTCTTGCCCTTCTATGCCTGCACTCTACTGGG  
AAATGTGTCTATCCTTGTGCTGTTATGTCTTCTGCTCGCCTTCACACACCTATGTATTTCT  
TCCTGGGAAACTGTCTGTGTTTGACATGGGTTTCTCCTCAGTGACTTGTCCTCAAAATGCT  
GCTCTACCTTATGGGGCTGAGCCGACTCATCTCCTACAAAGACTGTGTCTGCCAGCTTTTCT  
TCTTCCATTTCTCGGGAGCATTGAGTGCTTCTTGTTTACGGTGATGGCCTATGACCGCTTC  
ACTGCCATCTGTTATCCTCTGCGATACACAGTCATCATGAACCCAAGGATCTGTGTGGCCC  
35 TGGCTGTGGGCACATGGCTGTTAGGGTGCAATTCATTCCAGTATCTTGACCTCCCTCACCTTC  
ACCTTGCCATACTGTGGTCCCAATGAAGTGGATCACTTCTTCTGTGACATTCAGCACTGTT  
GCCCTTGGCCTGTGCTGACACATCCTTAGCCAGAGGGTGAGCTTCACCAACGTTGGCCTC  
ATATCTCTTGTCTGCTTTCTGCTAATTCCTTTATCCTACACTAGAATCACAATATCTATCTT  
AAGCATTTCGTACAACTGAGGGCCGTCGCCGTGCTTCTCCACCTGCAGTGCTCACCTCATT  
40 GCCATCCTCTGTGCTATGGGGCCATCATCACTGTCTACCTGCAGCCACACCCAACCCCA  
TGCTGGGAACCGTGGTACAAATTCTCATGAATCTGGTAGGACCAATGCTGAACCCCTTGAT  
CTATACCTTGAGGAATAAGGAAGTAAAAACAGCCCTGAAAACAATATTGCACAGGACAGG  
CCATGTTCTGAGAGTTAG (SEQ ID NO: 508)

**AOLFR324B sequences:**

45 MPIANDTQFHTSSFLLLGIPGLEDVHIWIGFPFFSVYLIALLGNAAIFFVVIQTEQSLHEPMMYYCLA  
MLDSIDLSTATIPKMLGIFWFNIKEISFGGYLSQMFFIHFVTVMESIVLVAMAFDRYIAICKPL  
WYTMILTSKIISLIAGIAVLRSLYMVPLVFLLLRLPFCGHRIPHTYCEHMGIARLACASIKVNM  
FGLGISLILLDVLILSHIRILYAVFCLPSWEARLKALNTCGSHIGVILAFSTPAFFSFFTHCFGH  
50 DIPQYIHIFLANLYVVPPTLNPVIYGVRTKHIRETVLRIFFKTDH (SEQ ID NO: 509)

ATGCCTATAGCTAACGACACCCAGTTCCATACCTTCTTCATTCCCTACTGCTGGGTATCCCAGG  
GCTAGAAGATGTGCACATCTGGATTGGATTCCTTTTTTCTCTGTGTATCTTATTGCACTCC  
TGGGAAATGCTGCTATCTTCTTTGTGATCCAACTGAGCAGAGTCTCCATGAGCCCATGTA  
55 CTACTGCCTGGCCATGTTGGATTCCATTGACCTGAGCTTGTCTACGGCCACCATTCCCAAA  
ATGCTGGGCATCTTCTGGTTCAATATCAAGGAAATATCTTTTGGAGGCTACCTTCTCAGA

TGTTCCTTCATCCATTTCTTCACTGTCATGGAGAGCATCGTATTGGTGGCCATGGCCTTTGAC  
 CGCTACATTGCCATTTGCAAACCTCTTTGGTACACCATGATCCTCACCAGCAAAATCATCA  
 GCCTCATTGCAGGCATTGCTGTCTGAGGAGCTTGTACATGGTCATTCCACTGGTGTTTCT  
 CCTCTTAAGGTTGCCCTTCTGTGGACATCGTATCATCCCTCATACTTACTGTGAGCACATGG  
 5 GCATTGCCCGTCTGGCCTGTGCCAGCATCAAAGTCAACATTATGTTTGGTCTTGGCAGTAT  
 TTCTCTCTTGTATTGGATGTGCTCCTTATTATTCTCTCCCATATCAGGATCCTCTATGCTGT  
 CTTCTGCCTGCCCTCCTGGGAAGCTCGACTCAAAGCTCTCAACACCTGTGGCTCTCACATT  
 GGTGTTATCTTAGCCTTTTCTACACCAGCATTTTCTCTTTCTTTACACACTGCTTTGGCCAT  
 GATATTCCCAATATATCCACATTTTCTTGGCTAATCTATATGTGGTGTTCCTCCACCCT  
 10 CAATCCTGTAATCTATGGGGTCAGAACCAACATATTAGGGAGACAGTGCTGAGGATTTTC  
 TTCAAGACAGATCACTAA (SEQ ID NO: 510)

**AOLFR328 sequences:**

15 MALGNHSTITEFLLGLSADPNIRALLFVFLGLIYLLTIMENLMLLLVRADSLHKPMYFFLSH  
 LSFVDLCFSSVIVPKMLENLLSQRKTISVEGCLAQVFFVFTAGTEACLLSGMAYDRHAARRP  
 LLYGQIMGKQLYMHLVWGSWGLGFLDALINVLLAVNMVFCEAKIIHHYSYEMPSLLPLSCSDI  
 SRSLIVLLCSTLLHGLGNFLLVFLSYTRIISTLSISSTSGRSKAFSTCSAHLTAVTLYYGSGLLRHL  
 MPNSGSPIELFSVQYTVVTPMLNSLIYSLKNKEVKVALKRTLEKYLQYTRR (SEQ ID NO: 511)

20 ATGGCCTTGGGGAATCACAGCACCATCACCGAGTTCCTCCTCCTTGGGCTGTCTGCCGACC  
 CCAACATCCGGGCTCTGCTCTTTGTGCTGTTTCTGGGGATTTACCTCCTGACCATAATGGA  
 AAACCTGATGCTGCTGCTCGTGATCAGGGCTGATTCTTGTCTCCATAAGCCCATGTATTTCT  
 TCCTGAGTCACCTCTCTTTTGTGATCTCTGCTTCTCTTCAAGTCATTGTGCCCAAGATGCTG  
 GAGAACCTCCTGTCACAGAGGAAAACCATTTTCAGTAGAGGGCTGCCTGGCTCAGGTCTTCT  
 25 TTGTGTTTGTCACTGCAGGGACTGAAGCCTGCCTTCTCTCAGGGATGGCCTATGACCGCCA  
 TGCTGCCATCCGCCGCCACTACTTTATGGACAGATCATGGGTAAACAGCTGTATATGCAC  
 CTTGTGTGGGGCTCATGGGGACTGGGCTTTCTGGACGCACTCATCAATGTCTCCTAGCTG  
 TAAACATGGTCTTTTGTGAAGCCAAAATCATTCACCACTACAGCTATGAGATGCCATCCCT  
 CCTCCCTCTGTCTGCTCTGATATCTCCAGAAGCCTCATCGTTTTGTCTGCTCCACTCTCC  
 30 TACATGGGCTGGGAAACTTCCTTTTGGTCTTCTTATCCTACACCCGTATAATCTCTACCATC  
 CTAAGCATCAGCTCTACCTCGGGCAGAAGCAAGGCCTTCTCCACCTGCTCTGCCACCTCA  
 CTGCAGTGACACTTTACTATGGCTCAGGTTTGTCTCCGCCATCTCATGCCAAACTCAGGTTT  
 CCCCATAGAGTTGATCTTCTCTGTGCAGTATACTGTAGTCACTCCCATGCTGAATTCCTCA  
 TCTATAGCCTGAAAAATAAGGAAGTGAAGGTAGCTCTGAAAAGAACTTTGGAAAAATATT  
 35 TGCAATATACCAGACGTTGA (SEQ ID NO: 512)

CLAIMS

What is Claimed:

1. An isolated nucleic acid sequence selected from the group consisting of:
  - 5 (i) an isolated nucleotide sequence selected from the group consisting of: SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID NO: 60, SEQ ID NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID NO: 70, SEQ ID NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 80, SEQ ID NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 90, SEQ ID NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID NO: 100, SEQ ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 108, SEQ ID NO: 110, SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 116, SEQ ID NO: 118, SEQ ID NO: 120, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID NO: 128, SEQ ID NO: 130, SEQ ID NO: 132, SEQ ID NO: 134, SEQ ID NO: 136, SEQ ID NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, SEQ ID NO: 144, SEQ ID NO: 146, SEQ ID NO: 148, SEQ ID NO: 150, SEQ ID NO: 152, SEQ ID NO: 154, SEQ ID NO: 156, SEQ ID NO: 158, SEQ ID NO: 160, SEQ ID NO: 162, SEQ ID NO: 164, SEQ ID NO: 166, SEQ ID NO: 168, SEQ ID NO: 170, SEQ ID NO: 172, SEQ ID NO: 174, SEQ ID NO: 176, SEQ ID NO: 178, SEQ ID NO: 180, SEQ ID NO: 182, SEQ ID NO: 184, SEQ ID NO: 186, SEQ ID NO: 188, SEQ ID NO: 190, SEQ ID NO: 192, SEQ ID NO: 194, SEQ ID NO: 196, SEQ ID NO: 198, SEQ ID NO: 200, SEQ ID NO: 202, SEQ ID NO: 204, SEQ ID NO: 206, SEQ ID NO: 208, SEQ ID NO: 210, SEQ ID NO: 212, SEQ ID NO: 214, SEQ ID NO: 216, SEQ ID NO: 218, SEQ ID NO: 220, SEQ ID NO: 222, SEQ ID NO: 224, SEQ ID NO: 226, SEQ ID NO: 228, SEQ ID NO: 230, SEQ ID NO: 232, SEQ ID NO: 234, SEQ ID NO: 236, SEQ ID NO: 238, SEQ ID NO: 240, SEQ ID NO: 242, SEQ ID NO: 244, SEQ ID NO: 246, SEQ ID NO: 248, SEQ ID NO: 250, SEQ ID NO: 252, SEQ ID NO: 254, SEQ ID NO: 256, SEQ ID NO: 258, SEQ ID NO: 260, SEQ ID NO: 262, SEQ ID

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 25 NO: 480, SEQ ID NO: 482, SEQ ID NO: 484, SEQ ID NO: 486, SEQ ID NO: 488,  
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 NO: 498, SEQ ID NO: 500, SEQ ID NO: 502, SEQ ID NO: 504, SEQ ID NO: 506,  
 SEQ ID NO: 508, SEQ ID NO: 510; and SEQ ID NO: 512, or a fragment thereof

which comprises at least 75 nucleotides;

- 30 (ii) an isolated cDNA or an insoluble RNA transcribed therefrom that encodes a  
 polypeptide having an amino acid sequence selected from the group consisting of:  
 SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ  
 ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ

ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ  
ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ  
ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ  
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which encodes at least 25 contiguous amino acids of said polypeptide;

- (iii) a nucleic acid sequence that comprises at least 30% sequence identity with an isolated nucleic acid sequence selected from the group consisting of: SEQ ID NO: 2, 25 SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID NO: 52, 30 SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID NO: 60, SEQ ID NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID NO: 70, SEQ ID NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 80, SEQ ID NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 90, SEQ ID NO: 92,

SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID NO: 100, SEQ ID  
NO: 102, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 108, SEQ ID NO: 110,  
SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 116, SEQ ID NO: 118, SEQ ID  
NO: 120, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID NO: 128,  
5 SEQ ID NO: 130, SEQ ID NO: 132, SEQ ID NO: 134, SEQ ID NO: 136, SEQ ID  
NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, SEQ ID NO: 144, SEQ ID NO: 146,  
SEQ ID NO: 148, SEQ ID NO: 150, SEQ ID NO: 152, SEQ ID NO: 154, SEQ ID  
NO: 156, SEQ ID NO: 158, SEQ ID NO: 160, SEQ ID NO: 162, SEQ ID NO: 164,  
SEQ ID NO: 166, SEQ ID NO: 168, SEQ ID NO: 170, SEQ ID NO: 172, SEQ ID  
10 NO: 174, SEQ ID NO: 176, SEQ ID NO: 178, SEQ ID NO: 180, SEQ ID NO: 182,  
SEQ ID NO: 184, SEQ ID NO: 186, SEQ ID NO: 188, SEQ ID NO: 190, SEQ ID  
NO: 192, SEQ ID NO: 194, SEQ ID NO: 196, SEQ ID NO: 198, SEQ ID NO: 200,  
SEQ ID NO: 202, SEQ ID NO: 204, SEQ ID NO: 206, SEQ ID NO: 208, SEQ ID  
NO: 210, SEQ ID NO: 212, SEQ ID NO: 214, SEQ ID NO: 216, SEQ ID NO: 218,  
15 SEQ ID NO: 220, SEQ ID NO: 222, SEQ ID NO: 224, SEQ ID NO: 226, SEQ ID  
NO: 228, SEQ ID NO: 230, SEQ ID NO: 232, SEQ ID NO: 234, SEQ ID NO: 236,  
SEQ ID NO: 238, SEQ ID NO: 240, SEQ ID NO: 242, SEQ ID NO: 244, SEQ ID  
NO: 246, SEQ ID NO: 248, SEQ ID NO: 250, SEQ ID NO: 252, SEQ ID NO: 254,  
SEQ ID NO: 256, SEQ ID NO: 258, SEQ ID NO: 260, SEQ ID NO: 262, SEQ ID  
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SEQ ID NO: 274, SEQ ID NO: 276, SEQ ID NO: 278, SEQ ID NO: 280, SEQ ID  
NO: 282, SEQ ID NO: 284, SEQ ID NO: 286, SEQ ID NO: 288, SEQ ID NO: 290,  
SEQ ID NO: 292, SEQ ID NO: 294, SEQ ID NO: 296, SEQ ID NO: 298, SEQ ID  
NO: 300, SEQ ID NO: 302, SEQ ID NO: 304, SEQ ID NO: 306, SEQ ID NO: 308,  
25 SEQ ID NO: 310, SEQ ID NO: 312, SEQ ID NO: 314, SEQ ID NO: 316, SEQ ID  
NO: 318, SEQ ID NO: 320, SEQ ID NO: 322, SEQ ID NO: 324, SEQ ID NO: 326,  
SEQ ID NO: 328, SEQ ID NO: 330, SEQ ID NO: 332, SEQ ID NO: 334, SEQ ID  
NO: 336, SEQ ID NO: 338, SEQ ID NO: 340, SEQ ID NO: 342, SEQ ID NO: 344,  
SEQ ID NO: 346, SEQ ID NO: 348, SEQ ID NO: 350, SEQ ID NO: 352, SEQ ID  
30 NO: 354, SEQ ID NO: 356, SEQ ID NO: 358, SEQ ID NO: 360, SEQ ID NO: 362,  
SEQ ID NO: 364, SEQ ID NO: 366, SEQ ID NO: 368, SEQ ID NO: 370, SEQ ID  
NO: 372, SEQ ID NO: 374, SEQ ID NO: 376, SEQ ID NO: 378, SEQ ID NO: 380,  
SEQ ID NO: 382, SEQ ID NO: 384, SEQ ID NO: 386, SEQ ID NO: 388, SEQ ID



NO: 390, SEQ ID NO: 392, SEQ ID NO: 394, SEQ ID NO: 396, SEQ ID NO: 398,  
 SEQ ID NO: 400, SEQ ID NO: 402, SEQ ID NO: 404, SEQ ID NO: 406, SEQ ID  
 NO: 408, SEQ ID NO: 410, SEQ ID NO: 412, SEQ ID NO: 414, SEQ ID NO: 416,  
 SEQ ID NO: 418, SEQ ID NO: 420, SEQ ID NO: 422, SEQ ID NO: 424, SEQ ID  
 5 NO: 426, SEQ ID NO: 428, SEQ ID NO: 430, SEQ ID NO: 432, SEQ ID NO: 434,  
 SEQ ID NO: 436, SEQ ID NO: 438, SEQ ID NO: 440, SEQ ID NO: 442, SEQ ID  
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 NO: 462, SEQ ID NO: 464, SEQ ID NO: 466, SEQ ID NO: 468, SEQ ID NO: 470,  
 10 SEQ ID NO: 472, SEQ ID NO: 474, SEQ ID NO: 476, SEQ ID NO: 478, SEQ ID  
 NO: 480, SEQ ID NO: 482, SEQ ID NO: 484, SEQ ID NO: 486, SEQ ID NO: 488,  
 SEQ ID NO: 490, SEQ ID NO: 492, SEQ ID NO: 494, SEQ ID NO: 496, SEQ ID  
 NO: 498, SEQ ID NO: 500, SEQ ID NO: 502, SEQ ID NO: 504, SEQ ID NO: 506,  
 SEQ ID NO: 508, SEQ ID NO: 510 and SEQ ID NO: 512, or to a fragment thereof

15 which comprises at least 100 contiguous nucleotides thereof;

(iv) a nucleic acid sequence that encodes a polypeptide having at least 40%  
 sequence identity at the amino acid level with a polypeptide having an amino acid  
 sequence selected from the group consisting of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ  
 ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID  
 20 NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID  
 NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID  
 NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID  
 NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID  
 NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID  
 25 NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID  
 NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID  
 NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID  
 NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ  
 ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113,  
 30 SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID  
 NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131,  
 SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID  
 NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149,

SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID  
NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167,  
SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID  
NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185,  
5 SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID NO: 191, SEQ ID NO: 193, SEQ ID  
NO: 195, SEQ ID NO: 197, SEQ ID NO: 199, SEQ ID NO: 201, SEQ ID NO: 203,  
SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID  
NO: 213, SEQ ID NO: 215, SEQ ID NO: 217, SEQ ID NO: 219, SEQ ID NO: 221,  
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SEQ ID NO: 241, SEQ ID NO: 243, SEQ ID NO: 245, SEQ ID NO: 247, SEQ ID  
NO: 249, SEQ ID NO: 251, SEQ ID NO: 253, SEQ ID NO: 255, SEQ ID NO: 257,  
SEQ ID NO: 259, SEQ ID NO: 261, SEQ ID NO: 263, SEQ ID NO: 265, SEQ ID  
NO: 267, SEQ ID NO: 269, SEQ ID NO: 271, SEQ ID NO: 273, SEQ ID NO: 275,  
15 SEQ ID NO: 277, SEQ ID NO: 279, SEQ ID NO: 281, SEQ ID NO: 283, SEQ ID  
NO: 285, SEQ ID NO: 287, SEQ ID NO: 289, SEQ ID NO: 291, SEQ ID NO: 293,  
SEQ ID NO: 295, SEQ ID NO: 297, SEQ ID NO: 299, SEQ ID NO: 301, SEQ ID  
NO: 303, SEQ ID NO: 305, SEQ ID NO: 307, SEQ ID NO: 309, SEQ ID NO: 311,  
SEQ ID NO: 313, SEQ ID NO: 315, SEQ ID NO: 317, SEQ ID NO: 319, SEQ ID  
20 NO: 321, SEQ ID NO: 323, SEQ ID NO: 325, SEQ ID NO: 327, SEQ ID NO: 329,  
SEQ ID NO: 331, SEQ ID NO: 333, SEQ ID NO: 335, SEQ ID NO: 337, SEQ ID  
NO: 339, SEQ ID NO: 341, SEQ ID NO: 343, SEQ ID NO: 345, SEQ ID NO: 347,  
SEQ ID NO: 349, SEQ ID NO: 351, SEQ ID NO: 353, SEQ ID NO: 355, SEQ ID  
NO: 357, SEQ ID NO: 359, SEQ ID NO: 361, SEQ ID NO: 363, SEQ ID NO: 365,  
25 SEQ ID NO: 367, SEQ ID NO: 369, SEQ ID NO: 371, SEQ ID NO: 373, SEQ ID  
NO: 375, SEQ ID NO: 377, SEQ ID NO: 379, SEQ ID NO: 381, SEQ ID NO: 383,  
SEQ ID NO: 385, SEQ ID NO: 387, SEQ ID NO: 389, SEQ ID NO: 391, SEQ ID  
NO: 393, SEQ ID NO: 395, SEQ ID NO: 397, SEQ ID NO: 399, SEQ ID NO: 401,  
SEQ ID NO: 403, SEQ ID NO: 405, SEQ ID NO: 407, SEQ ID NO: 409, SEQ ID  
30 NO: 411, SEQ ID NO: 413, SEQ ID NO: 415, SEQ ID NO: 417, SEQ ID NO: 419,  
SEQ ID NO: 421, SEQ ID NO: 423, SEQ ID NO: 425, SEQ ID NO: 427, SEQ ID  
NO: 429, SEQ ID NO: 431, SEQ ID NO: 433, SEQ ID NO: 435, SEQ ID NO: 437,  
SEQ ID NO: 439, SEQ ID NO: 441, SEQ ID NO: 443, SEQ ID NO: 445, SEQ ID

- NO: 447, SEQ ID NO: 449, SEQ ID NO: 451, SEQ ID NO: 453, SEQ ID NO: 455, SEQ ID NO: 457, SEQ ID NO: 459, SEQ ID NO: 461, SEQ ID NO: 463, SEQ ID NO: 465, SEQ ID NO: 467, SEQ ID NO: 469, SEQ ID NO: 471, SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID NO: 477, SEQ ID NO: 479, SEQ ID NO: 481, SEQ ID NO: 483, SEQ ID NO: 485, SEQ ID NO: 487, SEQ ID NO: 489, SEQ ID NO: 491, SEQ ID NO: 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511 or a nucleic acid sequence encoding at least 50 contiguous amino acid residues thereof;
- (v) an isolated nucleic acid sequence which encodes an olfactory receptor or a fragment thereof that specifically hybridizes and exhibits at least 30% sequence identity under stringent conditions to a nucleic acid sequence selected from the group consisting of: SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID NO: 60, SEQ ID NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID NO: 70, SEQ ID NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 80, SEQ ID NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 90, SEQ ID NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID NO: 100, SEQ ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 108, SEQ ID NO: 110, SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 116, SEQ ID NO: 118, SEQ ID NO: 120, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID NO: 128, SEQ ID NO: 130, SEQ ID NO: 132, SEQ ID NO: 134, SEQ ID NO: 136, SEQ ID NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, SEQ ID NO: 144, SEQ ID NO: 146, SEQ ID NO: 148, SEQ ID NO: 150, SEQ ID NO: 152, SEQ ID NO: 154, SEQ ID NO: 156, SEQ ID NO: 158, SEQ ID NO: 160, SEQ ID NO: 162, SEQ ID NO: 164, SEQ ID NO: 166, SEQ ID NO: 168, SEQ ID NO: 170, SEQ ID NO: 172, SEQ ID NO: 174, SEQ ID NO: 176, SEQ ID NO: 178, SEQ ID NO: 180, SEQ ID NO: 182, SEQ ID NO: 184, SEQ ID NO: 186, SEQ ID NO: 188, SEQ ID NO: 190, SEQ ID NO: 192, SEQ ID NO: 194, SEQ ID NO: 196, SEQ ID NO: 198,

SEQ ID NO: 200, SEQ ID NO: 202, SEQ ID NO: 204. SEQ ID NO: 206, SEQ ID  
NO: 208, SEQ ID NO: 210, SEQ ID NO: 212, SEQ ID NO: 214, SEQ ID NO: 216,  
SEQ ID NO: 218, SEQ ID NO: 220, SEQ ID NO: 222, SEQ ID NO: 224, SEQ ID  
NO: 226, SEQ ID NO: 228, SEQ ID NO: 230, SEQ ID NO: 232, SEQ ID NO: 234,  
5 SEQ ID NO: 236, SEQ ID NO: 238, SEQ. ID NO. 240, SEQ ID NO: 242, SEQ ID  
NO: 244, SEQ ID NO: 246, SEQ ID NO: 248, SEQ ID NO: 250, SEQ ID NO: 252,  
SEQ ID NO: 254, SEQ ID NO: 256, SEQ ID NO: 258, SEQ ID NO: 260, SEQ ID  
NO: 262, SEQ ID NO: 264, SEQ ID NO: 266, SEQ ID NO: 268, SEQ ID NO: 270,  
SEQ ID NO: 272, SEQ ID NO: 274, SEQ ID NO: 276, SEQ ID NO: 278, SEQ ID  
10 NO: 280, SEQ ID NO: 282, SEQ ID NO: 284, SEQ ID NO: 286, SEQ ID NO: 288,  
SEQ ID NO: 290, SEQ ID NO: 292, SEQ ID NO: 294, SEQ ID NO: 296, SEQ ID  
NO: 298, SEQ ID NO: 300, SEQ ID NO: 302, SEQ ID NO: 304, SEQ ID NO: 306,  
SEQ ID NO: 308, SEQ ID NO: 310, SEQ ID NO: 312, SEQ ID NO: 314, SEQ ID  
NO: 316, SEQ ID NO: 318, SEQ ID NO: 320, SEQ ID NO: 322, SEQ ID NO: 324,  
15 SEQ ID NO: 326, SEQ ID NO: 328, SEQ ID NO: 330, SEQ ID NO: 332, SEQ ID  
NO: 334, SEQ ID NO: 336, SEQ ID NO: 338, SEQ ID NO: 340, SEQ ID NO: 342,  
SEQ ID NO: 344, SEQ ID NO: 346, SEQ ID NO: 348, SEQ ID NO: 350, SEQ ID  
NO: 352, SEQ ID NO: 354, SEQ ID NO: 356, SEQ ID NO: 358, SEQ ID NO: 360,  
SEQ ID NO: 362, SEQ ID NO: 364, SEQ ID NO: 366, SEQ ID NO: 368, SEQ ID  
20 NO: 370, SEQ ID NO: 372, SEQ ID NO: 374, SEQ ID NO: 376, SEQ ID NO: 378,  
SEQ ID NO: 380, SEQ ID NO: 382, SEQ ID NO: 384, SEQ ID NO: 386, SEQ ID  
NO: 388, SEQ ID NO: 390, SEQ ID NO: 392, SEQ ID NO: 394, SEQ ID NO: 396,  
SEQ ID NO: 398, SEQ ID NO: 400, SEQ ID NO: 402, SEQ ID NO: 404, SEQ ID  
NO: 406, SEQ ID NO: 408, SEQ ID NO: 410, SEQ ID NO: 412, SEQ ID NO: 414,  
25 SEQ ID NO: 416, SEQ ID NO: 418, SEQ ID NO: 420, SEQ ID NO: 422, SEQ ID  
NO: 424, SEQ ID NO: 426, SEQ ID NO: 428, SEQ ID NO: 430, SEQ ID NO: 432,  
SEQ ID NO: 434, SEQ ID NO: 436, SEQ ID NO: 438, SEQ ID NO: 440, SEQ ID  
NO: 442, SEQ ID NO: 444, SEQ ID NO: 446, SEQ ID NO: 448, SEQ ID NO: 450,  
SEQ ID NO: 452, SEQ ID NO: 454, SEQ ID NO: 456, SEQ ID NO: 458, SEQ ID  
30 NO: 460, SEQ ID NO: 462, SEQ ID NO: 464, SEQ ID NO: 466, SEQ ID NO: 468,  
SEQ ID NO: 470, SEQ ID NO: 472, SEQ ID NO: 474, SEQ ID NO: 476, SEQ ID  
NO: 478, SEQ ID NO: 480, SEQ ID NO: 482, SEQ ID NO: 484, SEQ ID NO: 486,  
SEQ ID NO: 488, SEQ ID NO: 490, SEQ ID NO: 492, SEQ ID NO: 494, SEQ ID

NO: 496, SEQ ID NO: 498, SEQ ID NO: 500, SEQ ID NO: 502, SEQ ID NO: 504,  
SEQ ID NO: 506, SEQ ID NO: 508, SEQ ID NO: 510 and SEQ ID NO: 512;

(vi) an isolated nucleic acid sequence that specifically hybridizes to (i) or a portion  
thereof under stringent hybridization conditions that is at least 20-30 nucleotides in

5 length; and

(vii) a naturally occurring allelic or synthetic variant of a nucleic acid sequence  
according to (i) or (ii), containing at least one substitution, deletion or addition  
mutation in the coding region.

10 2. The isolated nucleic acid sequence of Claim 1 which is selected from  
the group consisting of: SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID  
NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID  
NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID  
NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID  
15 NO: 38, SEQ ID NO: 40, SEQ ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID  
NO: 48, SEQ ID NO: 50, SEQ ID NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID  
NO: 58, SEQ ID NO: 60, SEQ ID NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID  
NO: 68, SEQ ID NO: 70, SEQ ID NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID  
NO: 78, SEQ ID NO: 80, SEQ ID NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID  
20 NO: 88, SEQ ID NO: 90, SEQ ID NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID  
NO: 98, SEQ ID NO: 100, SEQ ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 106,  
SEQ ID NO: 108, SEQ ID NO: 110, SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID  
NO: 116, SEQ ID NO: 118, SEQ ID NO: 120, SEQ ID NO: 122, SEQ ID NO: 124,  
SEQ ID NO: 126, SEQ ID NO: 128, SEQ ID NO: 130, SEQ ID NO: 132, SEQ ID  
25 NO: 134, SEQ ID NO: 136, SEQ ID NO: 138, SEQ ID NO: 140, SEQ ID NO: 142,  
SEQ ID NO: 144, SEQ ID NO: 146, SEQ ID NO: 148, SEQ ID NO: 150, SEQ ID  
NO: 152, SEQ ID NO: 154, SEQ ID NO: 156, SEQ ID NO: 158, SEQ ID NO: 160,  
SEQ ID NO: 162, SEQ ID NO: 164, SEQ ID NO: 166, SEQ ID NO: 168, SEQ ID  
NO: 170, SEQ ID NO: 172, SEQ ID NO: 174, SEQ ID NO: 176, SEQ ID NO: 178,  
30 SEQ ID NO: 180, SEQ ID NO: 182, SEQ ID NO: 184, SEQ ID NO: 186, SEQ ID  
NO: 188, SEQ ID NO: 190, SEQ ID NO: 192, SEQ ID NO: 194, SEQ ID NO: 196,  
SEQ ID NO: 198, SEQ ID NO: 200, SEQ ID NO: 202, SEQ ID NO: 204, SEQ ID  
NO: 206, SEQ ID NO: 208, SEQ ID NO: 210, SEQ ID NO: 212, SEQ ID NO: 214,

SEQ ID NO: 216, SEQ ID NO: 218, SEQ ID NO: 220, SEQ ID NO: 222, SEQ ID  
NO: 224, SEQ ID NO: 226, SEQ ID NO: 228, SEQ ID NO: 230, SEQ ID NO: 232,  
SEQ ID NO: 234, SEQ ID NO: 236, SEQ ID NO: 238, SEQ. ID NO. 240, SEQ ID  
NO: 242, SEQ ID NO: 244, SEQ ID NO: 246, SEQ ID NO: 248, SEQ ID NO: 250,  
5 SEQ ID NO: 252, SEQ ID NO: 254, SEQ ID NO: 256, SEQ ID NO: 258, SEQ ID  
NO: 260, SEQ ID NO: 262, SEQ ID NO: 264, SEQ ID NO: 266, SEQ ID NO: 268,  
SEQ ID NO: 270, SEQ ID NO: 272, SEQ ID NO: 274, SEQ ID NO: 276, SEQ ID  
NO: 278, SEQ ID NO: 280, SEQ ID NO: 282, SEQ ID NO: 284, SEQ ID NO: 286,  
SEQ ID NO: 288, SEQ ID NO: 290, SEQ ID NO: 292, SEQ ID NO: 294, SEQ ID  
10 NO: 296, SEQ ID NO: 298, SEQ ID NO: 300, SEQ ID NO: 302, SEQ ID NO: 304,  
SEQ ID NO: 306, SEQ ID NO: 308, SEQ ID NO: 310, SEQ ID NO: 312, SEQ ID  
NO: 314, SEQ ID NO: 316, SEQ ID NO: 318, SEQ ID NO: 320, SEQ ID NO: 322,  
SEQ ID NO: 324, SEQ ID NO: 326, SEQ ID NO: 328, SEQ ID NO: 330, SEQ ID  
NO: 332, SEQ ID NO: 334, SEQ ID NO: 336, SEQ ID NO: 338, SEQ ID NO: 340,  
15 SEQ ID NO: 342, SEQ ID NO: 344, SEQ ID NO: 346, SEQ ID NO: 348, SEQ ID  
NO: 350, SEQ ID NO: 352, SEQ ID NO: 354, SEQ ID NO: 356, SEQ ID NO: 358,  
SEQ ID NO: 360, SEQ ID NO: 362, SEQ ID NO: 364, SEQ ID NO: 366, SEQ ID  
NO: 368, SEQ ID NO: 370, SEQ ID NO: 372, SEQ ID NO: 374, SEQ ID NO: 376,  
SEQ ID NO: 378, SEQ ID NO: 380, SEQ ID NO: 382, SEQ ID NO: 384, SEQ ID  
20 NO: 386, SEQ ID NO: 388, SEQ ID NO: 390, SEQ ID NO: 392, SEQ ID NO: 394,  
SEQ ID NO: 396, SEQ ID NO: 398, SEQ ID NO: 400, SEQ ID NO: 402, SEQ ID  
NO: 404, SEQ ID NO: 406, SEQ ID NO: 408, SEQ ID NO: 410, SEQ ID NO: 412,  
SEQ ID NO: 414, SEQ ID NO: 416, SEQ ID NO: 418, SEQ ID NO: 420, SEQ ID  
NO: 422, SEQ ID NO: 424, SEQ ID NO: 426, SEQ ID NO: 428, SEQ ID NO: 430,  
25 SEQ ID NO: 432, SEQ ID NO: 434, SEQ ID NO: 436, SEQ ID NO: 438, SEQ ID  
NO: 440, SEQ ID NO: 442, SEQ ID NO: 444, SEQ ID NO: 446, SEQ ID NO: 448,  
SEQ ID NO: 450, SEQ ID NO: 452, SEQ ID NO: 454, SEQ ID NO: 456, SEQ ID  
NO: 458, SEQ ID NO: 460, SEQ ID NO: 462, SEQ ID NO: 464, SEQ ID NO: 466,  
SEQ ID NO: 468, SEQ ID NO: 470, SEQ ID NO: 472, SEQ ID NO: 474, SEQ ID  
30 NO: 476, SEQ ID NO: 478, SEQ ID NO: 480, SEQ ID NO: 482, SEQ ID NO: 484,  
SEQ ID NO: 486, SEQ ID NO: 488, SEQ ID NO: 490, SEQ ID NO: 492, SEQ ID  
NO: 494, SEQ ID NO: 496, SEQ ID NO: 498, SEQ ID NO: 500, SEQ ID NO: 502,  
SEQ ID NO: 504, SEQ ID NO: 506, SEQ ID NO: 508, SEQ ID NO: 510 and SEQ ID

NO: 512 or a fragment thereof which comprises at least 75 contiguous nucleotides thereof.

3. The isolated nucleic acid sequence of Claim 1 which encodes a  
5 polypeptide having an amino acid sequence selected from the group consisting of:  
SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ  
ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ  
ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ  
ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ  
10 ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ  
ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ  
ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ  
ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ  
ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ  
15 ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ  
ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109,  
SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID  
NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127,  
SEQ ID NO: 129, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID  
20 NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145,  
SEQ ID NO: 147, SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID  
NO: 155, SEQ ID NO: 157, SEQ ID NO: 159, SEQ ID NO: 161, SEQ ID NO: 163,  
SEQ ID NO: 165, SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID  
NO: 173, SEQ ID NO: 175, SEQ ID NO: 177, SEQ ID NO: 179, SEQ ID NO: 181,  
25 SEQ ID NO: 183, SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID  
NO: 191, SEQ ID NO: 193, SEQ ID NO: 195, SEQ ID NO: 197, SEQ ID NO: 199,  
SEQ ID NO: 201, SEQ ID NO: 203, SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID  
NO: 209, SEQ ID NO: 211, SEQ ID NO: 213, SEQ ID NO: 215, SEQ ID NO: 217,  
SEQ ID NO: 219, SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID NO: 225, SEQ ID  
30 NO: 227, SEQ ID NO: 229, SEQ ID NO: 231, SEQ ID NO: 233, SEQ ID NO: 235,  
SEQ ID NO: 237, SEQ ID NO: 239, SEQ ID NO: 241, SEQ ID NO: 243, SEQ ID  
NO: 245, SEQ ID NO: 247, SEQ ID NO: 249, SEQ ID NO: 251, SEQ ID NO: 253,  
SEQ ID NO: 255, SEQ ID NO: 257, SEQ ID NO: 259, SEQ ID NO: 261, SEQ ID

NO.: 263, SEQ ID NO.: 265, SEQ ID NO: 267, SEQ ID NO: 269, SEQ ID NO: 271,  
 SEQ ID NO: 273, SEQ ID NO: 275, SEQ ID NO: 277, SEQ ID NO: 279, SEQ ID  
 NO: 281, SEQ ID NO: 283, SEQ ID NO: 285, SEQ ID NO: 287, SEQ ID NO: 289,  
 SEQ ID NO: 291, SEQ ID NO: 293, SEQ ID NO: 295, SEQ ID NO: 297, SEQ ID  
 5 NO: 299, SEQ ID NO: 301, SEQ ID NO: 303, SEQ ID NO: 305, SEQ ID NO: 307,  
 SEQ ID NO: 309, SEQ ID NO: 311, SEQ ID NO: 313, SEQ ID NO: 315, SEQ ID  
 NO: 317, SEQ ID NO: 319, SEQ ID NO: 321, SEQ ID NO: 323, SEQ ID NO: 325,  
 SEQ ID NO: 327, SEQ ID NO: 329, SEQ ID NO: 331, SEQ ID NO: 333, SEQ ID  
 NO: 335, SEQ ID NO: 337, SEQ ID NO: 339, SEQ ID NO: 341, SEQ ID NO: 343,  
 10 SEQ ID NO: 345, SEQ ID NO: 347, SEQ ID NO: 349, SEQ ID NO: 351, SEQ ID  
 NO: 353, SEQ ID NO: 355, SEQ ID NO: 357, SEQ ID NO: 359, SEQ ID NO: 361,  
 SEQ ID NO: 363, SEQ ID NO: 365, SEQ ID NO: 367, SEQ ID NO: 369, SEQ ID  
 NO: 371, SEQ ID NO: 373, SEQ ID NO: 375, SEQ ID NO: 377, SEQ ID NO: 379,  
 SEQ ID NO: 381, SEQ ID NO: 383, SEQ ID NO: 385, SEQ ID NO: 387, SEQ ID  
 15 NO: 389, SEQ ID NO: 391, SEQ ID NO: 393, SEQ ID NO: 395, SEQ ID NO: 397,  
 SEQ ID NO: 399, SEQ ID NO: 401, SEQ ID NO: 403, SEQ ID NO: 405, SEQ ID  
 NO: 407, SEQ ID NO: 409, SEQ ID NO: 411, SEQ ID NO: 413, SEQ ID NO: 415,  
 SEQ ID NO: 417, SEQ ID NO: 419, SEQ ID NO: 421, SEQ ID NO: 423, SEQ ID  
 NO: 425, SEQ ID NO: 427, SEQ ID NO: 429, SEQ ID NO: 431, SEQ ID NO: 433,  
 20 SEQ ID NO: 435, SEQ ID NO: 437, SEQ ID NO: 439, SEQ ID NO: 441, SEQ ID  
 NO: 443, SEQ ID NO: 445, SEQ ID NO: 447, SEQ ID NO: 449, SEQ ID NO: 451,  
 SEQ ID NO: 453, SEQ ID NO: 455, SEQ ID NO: 457, SEQ ID NO: 459, SEQ ID  
 NO: 461, SEQ ID NO: 463, SEQ ID NO: 465, SEQ ID NO: 467, SEQ ID NO: 469,  
 SEQ ID NO: 471, SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID NO: 477, SEQ ID  
 25 NO: 479, SEQ ID NO: 481, SEQ ID NO: 483, SEQ ID NO: 485, SEQ ID NO: 487,  
 SEQ ID NO: 489, SEQ ID NO: 491, SEQ ID NO: 493, SEQ ID NO: 495, SEQ ID  
 NO: 497, SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505,  
 SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511 or a fragment thereof  
 encoding at least 25 contiguous amino acid residues of said polypeptide.

30

4. An isolated nucleic acid sequence having at least 30-60% sequence  
 identity with a nucleic acid sequence selected from the group consisting of: SEQ ID  
 NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID



NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID  
NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID  
NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID  
NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID  
5 NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID NO: 60, SEQ ID  
NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID NO: 70, SEQ ID  
NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 80, SEQ ID  
NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 90, SEQ ID  
NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID NO: 100, SEQ  
10 ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 108, SEQ ID NO: 110,  
SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 116, SEQ ID NO: 118, SEQ ID  
NO: 120, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID NO: 128,  
SEQ ID NO: 130, SEQ ID NO: 132, SEQ ID NO: 134, SEQ ID NO: 136, SEQ ID  
NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, SEQ ID NO: 144, SEQ ID NO: 146,  
15 SEQ ID NO: 148, SEQ ID NO: 150, SEQ ID NO: 152, SEQ ID NO: 154, SEQ ID  
NO: 156, SEQ ID NO: 158, SEQ ID NO: 160, SEQ ID NO: 162, SEQ ID NO: 164,  
SEQ ID NO: 166, SEQ ID NO: 168, SEQ ID NO: 170, SEQ ID NO: 172, SEQ ID  
NO: 174, SEQ ID NO: 176, SEQ ID NO: 178, SEQ ID NO: 180, SEQ ID NO: 182,  
SEQ ID NO: 184, SEQ ID NO: 186, SEQ ID NO: 188, SEQ ID NO: 190, SEQ ID  
20 NO: 192, SEQ ID NO: 194, SEQ ID NO: 196, SEQ ID NO: 198, SEQ ID NO: 200,  
SEQ ID NO: 202, SEQ ID NO: 204, SEQ ID NO: 206, SEQ ID NO: 208, SEQ ID  
NO: 210, SEQ ID NO: 212, SEQ ID NO: 214, SEQ ID NO: 216, SEQ ID NO: 218,  
SEQ ID NO: 220, SEQ ID NO: 222, SEQ ID NO: 224, SEQ ID NO: 226, SEQ ID  
NO: 228, SEQ ID NO: 230, SEQ ID NO: 232, SEQ ID NO: 234, SEQ ID NO: 236,  
25 SEQ ID NO: 238, SEQ ID NO: 240, SEQ ID NO: 242, SEQ ID NO: 244, SEQ ID  
NO: 246, SEQ ID NO: 248, SEQ ID NO: 250, SEQ ID NO: 252, SEQ ID NO: 254,  
SEQ ID NO: 256, SEQ ID NO: 258, SEQ ID NO: 260, SEQ ID NO: 262, SEQ ID  
NO: 264, SEQ ID NO: 266, SEQ ID NO: 268, SEQ ID NO: 270, SEQ ID NO: 272,  
SEQ ID NO: 274, SEQ ID NO: 276, SEQ ID NO: 278, SEQ ID NO: 280, SEQ ID  
30 NO: 282, SEQ ID NO: 284, SEQ ID NO: 286, SEQ ID NO: 288, SEQ ID NO: 290,  
SEQ ID NO: 292, SEQ ID NO: 294, SEQ ID NO: 296, SEQ ID NO: 298, SEQ ID  
NO: 300, SEQ ID NO: 302, SEQ ID NO: 304, SEQ ID NO: 306, SEQ ID NO: 308,  
SEQ ID NO: 310, SEQ ID NO: 312, SEQ ID NO: 314, SEQ ID NO: 316, SEQ ID

NO: 318, SEQ ID NO: 320, SEQ ID NO: 322, SEQ ID NO: 324, SEQ ID NO: 326,  
 SEQ ID NO: 328, SEQ ID NO: 330, SEQ ID NO: 332, SEQ ID NO: 334, SEQ ID  
 NO: 336, SEQ ID NO: 338, SEQ ID NO: 340, SEQ ID NO: 342, SEQ ID NO: 344,  
 SEQ ID NO: 346, SEQ ID NO: 348, SEQ ID NO: 350, SEQ ID NO: 352, SEQ ID  
 5 NO: 354, SEQ ID NO: 356, SEQ ID NO: 358, SEQ ID NO: 360, SEQ ID NO: 362,  
 SEQ ID NO: 364, SEQ ID NO: 366, SEQ ID NO: 368, SEQ ID NO: 370, SEQ ID  
 NO: 372, SEQ ID NO: 374, SEQ ID NO: 376, SEQ ID NO: 378, SEQ ID NO: 380,  
 SEQ ID NO: 382, SEQ ID NO: 384, SEQ ID NO: 386, SEQ ID NO: 388, SEQ ID  
 NO: 390, SEQ ID NO: 392, SEQ ID NO: 394, SEQ ID NO: 396, SEQ ID NO: 398,  
 10 SEQ ID NO: 400, SEQ ID NO: 402, SEQ ID NO: 404, SEQ ID NO: 406, SEQ ID  
 NO: 408, SEQ ID NO: 410, SEQ ID NO: 412, SEQ ID NO: 414, SEQ ID NO: 416,  
 SEQ ID NO: 418, SEQ ID NO: 420, SEQ ID NO: 422, SEQ ID NO: 424, SEQ ID  
 NO: 426, SEQ ID NO: 428, SEQ ID NO: 430, SEQ ID NO: 432, SEQ ID NO: 434,  
 SEQ ID NO: 436, SEQ ID NO: 438, SEQ ID NO: 440, SEQ ID NO: 442, SEQ ID  
 15 NO: 444, SEQ ID NO: 446, SEQ ID NO: 448, SEQ ID NO: 450, SEQ ID NO: 452,  
 SEQ ID NO: 454, SEQ ID NO: 456, SEQ ID NO: 458, SEQ ID NO: 460, SEQ ID  
 NO: 462, SEQ ID NO: 464, SEQ ID NO: 466, SEQ ID NO: 468, SEQ ID NO: 470,  
 SEQ ID NO: 472, SEQ ID NO: 474, SEQ ID NO: 476, SEQ ID NO: 478, SEQ ID  
 NO: 480, SEQ ID NO: 482, SEQ ID NO: 484, SEQ ID NO: 486, SEQ ID NO: 488,  
 20 SEQ ID NO: 490, SEQ ID NO: 492, SEQ ID NO: 494, SEQ ID NO: 496, SEQ ID  
 NO: 498, SEQ ID NO: 500, SEQ ID NO: 502, SEQ ID NO: 504, SEQ ID NO: 506,  
 SEQ ID NO: 508, SEQ ID NO: 510 and SEQ ID NO: 512; or a fragment thereof  
 comprising at least 100 contiguous nucleotides of any of said sequences.

25           5.       An isolated nucleic acid sequence having at least 60-80% sequence  
 identity with a nucleic acid sequence selected from the group consisting of: SEQ ID  
 NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID  
 NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID  
 NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID  
 30 NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID  
 NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID  
 NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID NO: 60, SEQ ID  
 NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID NO: 70, SEQ ID

NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 80, SEQ ID  
NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 90, SEQ ID  
NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID NO: 100, SEQ  
ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 108, SEQ ID NO: 110,  
5 SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 116, SEQ ID NO: 118, SEQ ID  
NO: 120, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID NO: 128,  
SEQ ID NO: 130, SEQ ID NO: 132, SEQ ID NO: 134, SEQ ID NO: 136, SEQ ID  
NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, SEQ ID NO: 144, SEQ ID NO: 146,  
SEQ ID NO: 148, SEQ ID NO: 150, SEQ ID NO: 152, SEQ ID NO: 154, SEQ ID  
10 NO: 156, SEQ ID NO: 158, SEQ ID NO: 160, SEQ ID NO: 162, SEQ ID NO: 164,  
SEQ ID NO: 166, SEQ ID NO: 168, SEQ ID NO: 170, SEQ ID NO: 172, SEQ ID  
NO: 174, SEQ ID NO: 176, SEQ ID NO: 178, SEQ ID NO: 180, SEQ ID NO: 182,  
SEQ ID NO: 184, SEQ ID NO: 186, SEQ ID NO: 188, SEQ ID NO: 190, SEQ ID  
NO: 192, SEQ ID NO: 194, SEQ ID NO: 196, SEQ ID NO: 198, SEQ ID NO: 200,  
15 SEQ ID NO: 202, SEQ ID NO: 204, SEQ ID NO: 206, SEQ ID NO: 208, SEQ ID  
NO: 210, SEQ ID NO: 212, SEQ ID NO: 214, SEQ ID NO: 216, SEQ ID NO: 218,  
SEQ ID NO: 220, SEQ ID NO: 222, SEQ ID NO: 224, SEQ ID NO: 226, SEQ ID  
NO: 228, SEQ ID NO: 230, SEQ ID NO: 232, SEQ ID NO: 234, SEQ ID NO: 236,  
SEQ ID NO: 238, SEQ ID NO: 240, SEQ ID NO: 242, SEQ ID NO: 244, SEQ ID  
20 NO: 246, SEQ ID NO: 248, SEQ ID NO: 250, SEQ ID NO: 252, SEQ ID NO: 254,  
SEQ ID NO: 256, SEQ ID NO: 258, SEQ ID NO: 260, SEQ ID NO: 262, SEQ ID  
NO: 264, SEQ ID NO: 266, SEQ ID NO: 268, SEQ ID NO: 270, SEQ ID NO: 272,  
SEQ ID NO: 274, SEQ ID NO: 276, SEQ ID NO: 278, SEQ ID NO: 280, SEQ ID  
NO: 282, SEQ ID NO: 284, SEQ ID NO: 286, SEQ ID NO: 288, SEQ ID NO: 290,  
25 SEQ ID NO: 292, SEQ ID NO: 294, SEQ ID NO: 296, SEQ ID NO: 298, SEQ ID  
NO: 300, SEQ ID NO: 302, SEQ ID NO: 304, SEQ ID NO: 306, SEQ ID NO: 308,  
SEQ ID NO: 310, SEQ ID NO: 312, SEQ ID NO: 314, SEQ ID NO: 316, SEQ ID  
NO: 318, SEQ ID NO: 320, SEQ ID NO: 322, SEQ ID NO: 324, SEQ ID NO: 326,  
SEQ ID NO: 328, SEQ ID NO: 330, SEQ ID NO: 332, SEQ ID NO: 334, SEQ ID  
30 NO: 336, SEQ ID NO: 338, SEQ ID NO: 340, SEQ ID NO: 342, SEQ ID NO: 344,  
SEQ ID NO: 346, SEQ ID NO: 348, SEQ ID NO: 350, SEQ ID NO: 352, SEQ ID  
NO: 354, SEQ ID NO: 356, SEQ ID NO: 358, SEQ ID NO: 360, SEQ ID NO: 362,  
SEQ ID NO: 364, SEQ ID NO: 366, SEQ ID NO: 368, SEQ ID NO: 370, SEQ ID

NO: 372, SEQ ID NO: 374, SEQ ID NO: 376, SEQ ID NO: 378, SEQ ID NO: 380,  
SEQ ID NO: 382, SEQ ID NO: 384, SEQ ID NO: 386, SEQ ID NO: 388, SEQ ID  
NO: 390, SEQ ID NO: 392, SEQ ID NO: 394, SEQ ID NO: 396, SEQ ID NO: 398,  
SEQ ID NO: 400, SEQ ID NO: 402, SEQ ID NO: 404, SEQ ID NO: 406, SEQ ID  
5 NO: 408, SEQ ID NO: 410, SEQ ID NO: 412, SEQ ID NO: 414, SEQ ID NO: 416,  
SEQ ID NO: 418, SEQ ID NO: 420, SEQ ID NO: 422, SEQ ID NO: 424, SEQ ID  
NO: 426, SEQ ID NO: 428, SEQ ID NO: 430, SEQ ID NO: 432, SEQ ID NO: 434,  
SEQ ID NO: 436, SEQ ID NO: 438, SEQ ID NO: 440, SEQ ID NO: 442, SEQ ID  
NO: 444, SEQ ID NO: 446, SEQ ID NO: 448, SEQ ID NO: 450, SEQ ID NO: 452,  
10 SEQ ID NO: 454, SEQ ID NO: 456, SEQ ID NO: 458, SEQ ID NO: 460, SEQ ID  
NO: 462, SEQ ID NO: 464, SEQ ID NO: 466, SEQ ID NO: 468, SEQ ID NO: 470,  
SEQ ID NO: 472, SEQ ID NO: 474, SEQ ID NO: 476, SEQ ID NO: 478, SEQ ID  
NO: 480, SEQ ID NO: 482, SEQ ID NO: 484, SEQ ID NO: 486, SEQ ID NO: 488,  
SEQ ID NO: 490, SEQ ID NO: 492, SEQ ID NO: 494, SEQ ID NO: 496, SEQ ID  
15 NO: 498, SEQ ID NO: 500, SEQ ID NO: 502, SEQ ID NO: 504, SEQ ID NO: 506,  
SEQ ID NO: 508, SEQ ID NO: 510 and SEQ ID NO: 512 or a fragment thereof  
comprising at least 100 contiguous nucleotides of any of said sequences.

6. An isolated nucleic acid sequence having at least 80-90% sequence  
20 identity with a nucleic acid sequence selected from the group consisting of: SEQ ID  
NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID  
NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID  
NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID  
NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID  
25 NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID  
NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID NO: 60, SEQ ID  
NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID NO: 70, SEQ ID  
NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 80, SEQ ID  
NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 90, SEQ ID  
30 NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID NO: 100, SEQ  
ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 108, SEQ ID NO: 110,  
SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 116, SEQ ID NO: 118, SEQ ID  
NO: 120, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID NO: 128,

SEQ ID NO: 130, SEQ ID NO: 132, SEQ ID NO: 134, SEQ ID NO: 136, SEQ ID  
NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, SEQ ID NO: 144, SEQ ID NO: 146,  
SEQ ID NO: 148, SEQ ID NO: 150, SEQ ID NO: 152, SEQ ID NO: 154, SEQ ID  
NO: 156, SEQ ID NO: 158, SEQ ID NO: 160, SEQ ID NO: 162, SEQ ID NO: 164,  
5 SEQ ID NO: 166, SEQ ID NO: 168, SEQ ID NO: 170, SEQ ID NO: 172, SEQ ID  
NO: 174, SEQ ID NO: 176, SEQ ID NO: 178, SEQ ID NO: 180, SEQ ID NO: 182,  
SEQ ID NO: 184, SEQ ID NO: 186, SEQ ID NO: 188, SEQ ID NO: 190, SEQ ID  
NO: 192, SEQ ID NO: 194, SEQ ID NO: 196, SEQ ID NO: 198, SEQ ID NO: 200,  
SEQ ID NO: 202, SEQ ID NO: 204. SEQ ID NO: 206, SEQ ID NO: 208, SEQ ID  
10 NO: 210, SEQ ID NO: 212, SEQ ID NO: 214, SEQ ID NO: 216, SEQ ID NO: 218,  
SEQ ID NO: 220, SEQ ID NO: 222, SEQ ID NO: 224, SEQ ID NO: 226, SEQ ID  
NO: 228, SEQ ID NO: 230, SEQ ID NO: 232, SEQ ID NO: 234, SEQ ID NO: 236,  
SEQ ID NO: 238, SEQ ID NO: 240, SEQ ID NO: 242, SEQ ID NO: 244, SEQ ID  
NO: 246, SEQ ID NO: 248, SEQ ID NO: 250, SEQ ID NO: 252, SEQ ID NO: 254,  
15 SEQ ID NO: 256, SEQ ID NO: 258, SEQ ID NO: 260, SEQ ID NO: 262, SEQ ID  
NO: 264, SEQ ID NO: 266, SEQ ID NO: 268, SEQ ID NO: 270, SEQ ID NO: 272,  
SEQ ID NO: 274, SEQ ID NO: 276, SEQ ID NO: 278, SEQ ID NO: 280, SEQ ID  
NO: 282, SEQ ID NO: 284, SEQ ID NO: 286, SEQ ID NO: 288, SEQ ID NO: 290,  
SEQ ID NO: 292, SEQ ID NO: 294, SEQ ID NO: 296, SEQ ID NO: 298, SEQ ID  
20 NO: 300, SEQ ID NO: 302, SEQ ID NO: 304, SEQ ID NO: 306, SEQ ID NO: 308,  
SEQ ID NO: 310, SEQ ID NO: 312, SEQ ID NO: 314, SEQ ID NO: 316, SEQ ID  
NO: 318, SEQ ID NO: 320, SEQ ID NO: 322, SEQ ID NO: 324, SEQ ID NO: 326,  
SEQ ID NO: 328, SEQ ID NO: 330, SEQ ID NO: 332, SEQ ID NO: 334, SEQ ID  
NO: 336, SEQ ID NO: 338, SEQ ID NO: 340, SEQ ID NO: 342, SEQ ID NO: 344,  
25 SEQ ID NO: 346, SEQ ID NO: 348, SEQ ID NO: 350, SEQ ID NO: 352, SEQ ID  
NO: 354, SEQ ID NO: 356, SEQ ID NO: 358, SEQ ID NO: 360, SEQ ID NO: 362,  
SEQ ID NO: 364, SEQ ID NO: 366, SEQ ID NO: 368, SEQ ID NO: 370, SEQ ID  
NO: 372, SEQ ID NO: 374, SEQ ID NO: 376, SEQ ID NO: 378, SEQ ID NO: 380,  
SEQ ID NO: 382, SEQ ID NO: 384, SEQ ID NO: 386, SEQ ID NO: 388, SEQ ID  
30 NO: 390, SEQ ID NO: 392, SEQ ID NO: 394, SEQ ID NO: 396, SEQ ID NO: 398,  
SEQ ID NO: 400, SEQ ID NO: 402, SEQ ID NO: 404, SEQ ID NO: 406, SEQ ID  
NO: 408, SEQ ID NO: 410, SEQ ID NO: 412, SEQ ID NO: 414, SEQ ID NO: 416,  
SEQ ID NO: 418, SEQ ID NO: 420, SEQ ID NO: 422, SEQ ID NO: 424, SEQ ID

NO: 426, SEQ ID NO: 428, SEQ ID NO: 430, SEQ ID NO: 432, SEQ ID NO: 434,  
 SEQ ID NO: 436, SEQ ID NO: 438, SEQ ID NO: 440, SEQ ID NO: 442, SEQ ID  
 NO: 444, SEQ ID NO: 446, SEQ ID NO: 448, SEQ ID NO: 450, SEQ ID NO: 452,  
 SEQ ID NO: 454, SEQ ID NO: 456, SEQ ID NO: 458, SEQ ID NO: 460, SEQ ID  
 5 NO: 462, SEQ ID NO: 464, SEQ ID NO: 466, SEQ ID NO: 468, SEQ ID NO: 470,  
 SEQ ID NO: 472, SEQ ID NO: 474, SEQ ID NO: 476, SEQ ID NO: 478, SEQ ID  
 NO: 480, SEQ ID NO: 482, SEQ ID NO: 484, SEQ ID NO: 486, SEQ ID NO: 488,  
 SEQ ID NO: 490, SEQ ID NO: 492, SEQ ID NO: 494, SEQ ID NO: 496, SEQ ID  
 NO: 498, SEQ ID NO: 500, SEQ ID NO: 502, SEQ ID NO: 504, SEQ ID NO: 506,  
 10 SEQ ID NO: 508, SEQ ID NO: 510 and SEQ ID NO: 512 or a fragment thereof  
 comprising at least 100 contiguous nucleotides of any of said sequences.

7. An isolated nucleic acid sequence having at least 85% sequence  
 identity with a nucleic acid sequence selected from the group consisting of: SEQ ID  
 15 NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID  
 NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID  
 NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID  
 NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID  
 NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID  
 20 NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID NO: 60, SEQ ID  
 NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID NO: 70, SEQ ID  
 NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 80, SEQ ID  
 NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 90, SEQ ID  
 NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID NO: 100, SEQ  
 25 ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 108, SEQ ID NO: 110,  
 SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 116, SEQ ID NO: 118, SEQ ID  
 NO: 120, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID NO: 128,  
 SEQ ID NO: 130, SEQ ID NO: 132, SEQ ID NO: 134, SEQ ID NO: 136, SEQ ID  
 NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, SEQ ID NO: 144, SEQ ID NO: 146,  
 30 SEQ ID NO: 148, SEQ ID NO: 150, SEQ ID NO: 152, SEQ ID NO: 154, SEQ ID  
 NO: 156, SEQ ID NO: 158, SEQ ID NO: 160, SEQ ID NO: 162, SEQ ID NO: 164,  
 SEQ ID NO: 166, SEQ ID NO: 168, SEQ ID NO: 170, SEQ ID NO: 172, SEQ ID  
 NO: 174, SEQ ID NO: 176, SEQ ID NO: 178, SEQ ID NO: 180, SEQ ID NO: 182,

SEQ ID NO: 184, SEQ ID NO: 186, SEQ ID NO: 188, SEQ ID NO: 190, SEQ ID  
NO: 192, SEQ ID NO: 194, SEQ ID NO: 196, SEQ ID NO: 198, SEQ ID NO: 200,  
SEQ ID NO: 202, SEQ ID NO: 204. SEQ ID NO: 206, SEQ ID NO: 208, SEQ ID  
NO: 210, SEQ ID NO: 212, SEQ ID NO: 214, SEQ ID NO: 216, SEQ ID NO: 218,  
5 SEQ ID NO: 220, SEQ ID NO: 222, SEQ ID NO: 224, SEQ ID NO: 226, SEQ ID  
NO: 228, SEQ ID NO: 230, SEQ ID NO: 232, SEQ ID NO: 234, SEQ ID NO: 236,  
SEQ ID NO: 238, SEQ ID NO: 240, SEQ ID NO: 242, SEQ ID NO: 244, SEQ ID  
NO: 246, SEQ ID NO: 248, SEQ ID NO: 250, SEQ ID NO: 252, SEQ ID NO: 254,  
SEQ ID NO: 256, SEQ ID NO: 258, SEQ ID NO: 260, SEQ ID NO: 262, SEQ ID  
10 NO: 264, SEQ ID NO: 266, SEQ ID NO: 268, SEQ ID NO: 270, SEQ ID NO: 272,  
SEQ ID NO: 274, SEQ ID NO: 276, SEQ ID NO: 278, SEQ ID NO: 280, SEQ ID  
NO: 282, SEQ ID NO: 284, SEQ ID NO: 286, SEQ ID NO: 288, SEQ ID NO: 290,  
SEQ ID NO: 292, SEQ ID NO: 294, SEQ ID NO: 296, SEQ ID NO: 298, SEQ ID  
NO: 300, SEQ ID NO: 302, SEQ ID NO: 304, SEQ ID NO: 306, SEQ ID NO: 308,  
15 SEQ ID NO: 310, SEQ ID NO: 312, SEQ ID NO: 314, SEQ ID NO: 316, SEQ ID  
NO: 318, SEQ ID NO: 320, SEQ ID NO: 322, SEQ ID NO: 324, SEQ ID NO: 326,  
SEQ ID NO: 328, SEQ ID NO: 330, SEQ ID NO: 332, SEQ ID NO: 334, SEQ ID  
NO: 336, SEQ ID NO: 338, SEQ ID NO: 340, SEQ ID NO: 342, SEQ ID NO: 344,  
SEQ ID NO: 346, SEQ ID NO: 348, SEQ ID NO: 350, SEQ ID NO: 352, SEQ ID  
20 NO: 354, SEQ ID NO: 356, SEQ ID NO: 358, SEQ ID NO: 360, SEQ ID NO: 362,  
SEQ ID NO: 364, SEQ ID NO: 366, SEQ ID NO: 368, SEQ ID NO: 370, SEQ ID  
NO: 372, SEQ ID NO: 374, SEQ ID NO: 376, SEQ ID NO: 378, SEQ ID NO: 380,  
SEQ ID NO: 382, SEQ ID NO: 384, SEQ ID NO: 386, SEQ ID NO: 388, SEQ ID  
NO: 390, SEQ ID NO: 392, SEQ ID NO: 394, SEQ ID NO: 396, SEQ ID NO: 398,  
25 SEQ ID NO: 400, SEQ ID NO: 402, SEQ ID NO: 404, SEQ ID NO: 406, SEQ ID  
NO: 408, SEQ ID NO: 410, SEQ ID NO: 412, SEQ ID NO: 414, SEQ ID NO: 416,  
SEQ ID NO: 418, SEQ ID NO: 420, SEQ ID NO: 422, SEQ ID NO: 424, SEQ ID  
NO: 426, SEQ ID NO: 428, SEQ ID NO: 430, SEQ ID NO: 432, SEQ ID NO: 434,  
SEQ ID NO: 436, SEQ ID NO: 438, SEQ ID NO: 440, SEQ ID NO: 442, SEQ ID  
30 NO: 444, SEQ ID NO: 446, SEQ ID NO: 448, SEQ ID NO: 450, SEQ ID NO: 452,  
SEQ ID NO: 454, SEQ ID NO: 456, SEQ ID NO: 458, SEQ ID NO: 460, SEQ ID  
NO: 462, SEQ ID NO: 464, SEQ ID NO: 466, SEQ ID NO: 468, SEQ ID NO: 470,  
SEQ ID NO: 472, SEQ ID NO: 474, SEQ ID NO: 476, SEQ ID NO: 478, SEQ ID

NO: 480, SEQ ID NO: 482, SEQ ID NO: 484, SEQ ID NO: 486, SEQ ID NO: 488, SEQ ID NO: 490, SEQ ID NO: 492, SEQ ID NO: 494, SEQ ID NO: 496, SEQ ID NO: 498, SEQ ID NO: 500, SEQ ID NO: 502, SEQ ID NO: 504, SEQ ID NO: 506, SEQ ID NO: 508, SEQ ID NO: 510 and SEQ ID NO: 512, or a fragment thereof  
5 comprising at least 100 contiguous nucleotides of any of said sequences.

8. An isolated nucleic acid sequence having at least 90% sequence identity with a nucleic acid sequence selected from the group consisting of: SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID NO: 60, SEQ ID NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID NO: 70, SEQ ID NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 80, SEQ ID NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 90, SEQ ID NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID NO: 100, SEQ ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 108, SEQ ID NO: 110, SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 116, SEQ ID NO: 118, SEQ ID NO: 120, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID NO: 128, SEQ ID NO: 130, SEQ ID NO: 132, SEQ ID NO: 134, SEQ ID NO: 136, SEQ ID NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, SEQ ID NO: 144, SEQ ID NO: 146, SEQ ID NO: 148, SEQ ID NO: 150, SEQ ID NO: 152, SEQ ID NO: 154, SEQ ID NO: 156, SEQ ID NO: 158, SEQ ID NO: 160, SEQ ID NO: 162, SEQ ID NO: 164, SEQ ID NO: 166, SEQ ID NO: 168, SEQ ID NO: 170, SEQ ID NO: 172, SEQ ID NO: 174, SEQ ID NO: 176, SEQ ID NO: 178, SEQ ID NO: 180, SEQ ID NO: 182, SEQ ID NO: 184, SEQ ID NO: 186, SEQ ID NO: 188, SEQ ID NO: 190, SEQ ID NO: 192, SEQ ID NO: 194, SEQ ID NO: 196, SEQ ID NO: 198, SEQ ID NO: 200, SEQ ID NO: 202, SEQ ID NO: 204, SEQ ID NO: 206, SEQ ID NO: 208, SEQ ID NO: 210, SEQ ID NO: 212, SEQ ID NO: 214, SEQ ID NO: 216, SEQ ID NO: 218, SEQ ID NO: 220, SEQ ID NO: 222, SEQ ID NO: 224, SEQ ID NO: 226, SEQ ID NO: 228, SEQ ID NO: 230, SEQ ID NO: 232, SEQ ID NO: 234, SEQ ID NO: 236,



SEQ ID NO: 238, SEQ. ID NO. 240, SEQ ID NO: 242, SEQ ID NO: 244, SEQ ID  
NO: 246, SEQ ID NO: 248, SEQ ID NO: 250, SEQ ID NO: 252, SEQ ID NO: 254,  
SEQ ID NO: 256, SEQ ID NO: 258, SEQ ID NO: 260, SEQ ID NO: 262, SEQ ID  
NO: 264, SEQ ID NO: 266, SEQ ID NO: 268, SEQ ID NO: 270, SEQ ID NO: 272,  
5 SEQ ID NO: 274, SEQ ID NO: 276, SEQ ID NO: 278, SEQ ID NO: 280, SEQ ID  
NO: 282, SEQ ID NO: 284, SEQ ID NO: 286, SEQ ID NO: 288, SEQ ID NO: 290,  
SEQ ID NO: 292, SEQ ID NO: 294, SEQ ID NO: 296, SEQ ID NO: 298, SEQ ID  
NO: 300, SEQ ID NO: 302, SEQ ID NO: 304, SEQ ID NO: 306, SEQ ID NO: 308,  
SEQ ID NO: 310, SEQ ID NO: 312, SEQ ID NO: 314, SEQ ID NO: 316, SEQ ID  
10 NO: 318, SEQ ID NO: 320, SEQ ID NO: 322, SEQ ID NO: 324, SEQ ID NO: 326,  
SEQ ID NO: 328, SEQ ID NO: 330, SEQ ID NO: 332, SEQ ID NO: 334, SEQ ID  
NO: 336, SEQ ID NO: 338, SEQ ID NO: 340, SEQ ID NO: 342, SEQ ID NO: 344,  
SEQ ID NO: 346, SEQ ID NO: 348, SEQ ID NO: 350, SEQ ID NO: 352, SEQ ID  
NO: 354, SEQ ID NO: 356, SEQ ID NO: 358, SEQ ID NO: 360, SEQ ID NO: 362,  
15 SEQ ID NO: 364, SEQ ID NO: 366, SEQ ID NO: 368, SEQ ID NO: 370, SEQ ID  
NO: 372, SEQ ID NO: 374, SEQ ID NO: 376, SEQ ID NO: 378, SEQ ID NO: 380,  
SEQ ID NO: 382, SEQ ID NO: 384, SEQ ID NO: 386, SEQ ID NO: 388, SEQ ID  
NO: 390, SEQ ID NO: 392, SEQ ID NO: 394, SEQ ID NO: 396, SEQ ID NO: 398,  
SEQ ID NO: 400, SEQ ID NO: 402, SEQ ID NO: 404, SEQ ID NO: 406, SEQ ID  
20 NO: 408, SEQ ID NO: 410, SEQ ID NO: 412, SEQ ID NO: 414, SEQ ID NO: 416,  
SEQ ID NO: 418, SEQ ID NO: 420, SEQ ID NO: 422, SEQ ID NO: 424, SEQ ID  
NO: 426, SEQ ID NO: 428, SEQ ID NO: 430, SEQ ID NO: 432, SEQ ID NO: 434,  
SEQ ID NO: 436, SEQ ID NO: 438, SEQ ID NO: 440, SEQ ID NO: 442, SEQ ID  
NO: 444, SEQ ID NO: 446, SEQ ID NO: 448, SEQ ID NO: 450, SEQ ID NO: 452,  
25 SEQ ID NO: 454, SEQ ID NO: 456, SEQ ID NO: 458, SEQ ID NO: 460, SEQ ID  
NO: 462, SEQ ID NO: 464, SEQ ID NO: 466, SEQ ID NO: 468, SEQ ID NO: 470,  
SEQ ID NO: 472, SEQ ID NO: 474, SEQ ID NO: 476, SEQ ID NO: 478, SEQ ID  
NO: 480, SEQ ID NO: 482, SEQ ID NO: 484, SEQ ID NO: 486, SEQ ID NO: 488,  
SEQ ID NO: 490, SEQ ID NO: 492, SEQ ID NO: 494, SEQ ID NO: 496, SEQ ID  
30 NO: 498, SEQ ID NO: 500, SEQ ID NO: 502, SEQ ID NO: 504, SEQ ID NO: 506,  
SEQ ID NO: 508, SEQ ID NO: 510 and SEQ ID NO: 512 or a fragment thereof  
comprising at least 100 contiguous nucleotides of any of said sequences.

9. An isolated nucleic acid sequence according to Claim 1 which encodes a polypeptide having at least 40-60% sequence identity with a polypeptide having an amino acid sequence selected from the group consisting of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID NO: 191, SEQ ID NO: 193, SEQ ID NO: 195, SEQ ID NO: 197, SEQ ID NO: 199, SEQ ID NO: 201, SEQ ID NO: 203, SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID NO: 213, SEQ ID NO: 215, SEQ ID NO: 217, SEQ ID NO: 219, SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID NO: 225, SEQ ID NO: 227, SEQ ID NO: 229, SEQ ID NO: 231, SEQ ID NO: 233, SEQ ID NO: 235, SEQ ID NO: 237, SEQ ID NO: 239, SEQ ID NO: 241, SEQ ID NO: 243, SEQ ID NO: 245, SEQ ID NO: 247, SEQ ID NO: 249, SEQ ID NO: 251, SEQ ID NO: 253, SEQ ID NO: 255, SEQ ID NO: 257, SEQ ID NO: 259, SEQ ID NO: 261, SEQ ID NO: 263, SEQ ID NO: 265, SEQ ID NO: 267, SEQ ID NO: 269, SEQ ID NO: 271, SEQ ID NO: 273, SEQ ID NO: 275, SEQ ID NO: 277, SEQ ID NO: 279, SEQ ID NO: 281, SEQ ID

NO: 283, SEQ ID NO: 285, SEQ ID NO: 287, SEQ ID NO: 289, SEQ ID NO: 291,  
 SEQ ID NO: 293, SEQ ID NO: 295, SEQ ID NO: 297, SEQ ID NO: 299, SEQ ID  
 NO: 301, SEQ ID NO: 303, SEQ ID NO: 305, SEQ ID NO: 307, SEQ ID NO: 309,  
 SEQ ID NO: 311, SEQ ID NO: 313, SEQ ID NO: 315, SEQ ID NO: 317, SEQ ID  
 5 NO: 319, SEQ ID NO: 321, SEQ ID NO: 323, SEQ ID NO: 325, SEQ ID NO: 327,  
 SEQ ID NO: 329, SEQ ID NO: 331, SEQ ID NO: 333, SEQ ID NO: 335, SEQ ID  
 NO: 337, SEQ ID NO: 339, SEQ ID NO: 341, SEQ ID NO: 343, SEQ ID NO: 345,  
 SEQ ID NO: 347, SEQ ID NO: 349, SEQ ID NO: 351, SEQ ID NO: 353, SEQ ID  
 NO: 355, SEQ ID NO: 357, SEQ ID NO: 359, SEQ ID NO: 361, SEQ ID NO: 363,  
 10 SEQ ID NO: 365, SEQ ID NO: 367, SEQ ID NO: 369, SEQ ID NO: 371, SEQ ID  
 NO: 373, SEQ ID NO: 375, SEQ ID NO: 377, SEQ ID NO: 379, SEQ ID NO: 381,  
 SEQ ID NO: 383, SEQ ID NO: 385, SEQ ID NO: 387, SEQ ID NO: 389, SEQ ID  
 NO: 391, SEQ ID NO: 393, SEQ ID NO: 395, SEQ ID NO: 397, SEQ ID NO: 399,  
 SEQ ID NO: 401, SEQ ID NO: 403, SEQ ID NO: 405, SEQ ID NO: 407, SEQ ID  
 15 NO: 409, SEQ ID NO: 411, SEQ ID NO: 413, SEQ ID NO: 415, SEQ ID NO: 417,  
 SEQ ID NO: 419, SEQ ID NO: 421, SEQ ID NO: 423, SEQ ID NO: 425, SEQ ID  
 NO: 427, SEQ ID NO: 429, SEQ ID NO: 431, SEQ ID NO: 433, SEQ ID NO: 435,  
 SEQ ID NO: 437, SEQ ID NO: 439, SEQ ID NO: 441, SEQ ID NO: 443, SEQ ID  
 NO: 445, SEQ ID NO: 447, SEQ ID NO: 449, SEQ ID NO: 451, SEQ ID NO: 453,  
 20 SEQ ID NO: 455, SEQ ID NO: 457, SEQ ID NO: 459, SEQ ID NO: 461, SEQ ID  
 NO: 463, SEQ ID NO: 465, SEQ ID NO: 467, SEQ ID NO: 469, SEQ ID NO: 471,  
 SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID NO: 477, SEQ ID NO: 479, SEQ ID  
 NO: 481, SEQ ID NO: 483, SEQ ID NO: 485, SEQ ID NO: 487, SEQ ID NO: 489,  
 SEQ ID NO: 491, SEQ ID NO: 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID  
 25 NO: 499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507,  
 SEQ ID NO: 509 and SEQ ID NO: 511 or a fragment thereof that comprises at least  
 40 contiguous amino acids thereof.

10. An isolated nucleic acid sequence according to Claim 1 which encodes  
 30 a polypeptide having at least 60-70% sequence identity with a polypeptide having an  
 amino acid sequence selected from the group consisting of: SEQ ID NO: 1, SEQ ID  
 NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID  
 NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID

NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID  
NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID  
NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID  
NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID  
5 NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID  
NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID  
NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID  
NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ  
ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111,  
10 SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID  
NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129,  
SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID  
NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147,  
SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID NO: 155, SEQ ID  
15 NO: 157, SEQ ID NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165,  
SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID  
NO: 175, SEQ ID NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID NO: 183,  
SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID NO: 191, SEQ ID  
NO: 193, SEQ ID NO: 195, SEQ ID NO: 197, SEQ ID NO: 199, SEQ ID NO: 201,  
20 SEQ ID NO: 203, SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID NO: 209, SEQ ID  
NO: 211, SEQ ID NO: 213, SEQ ID NO: 215, SEQ ID NO: 217, SEQ ID NO: 219,  
SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID NO: 225, SEQ ID NO: 227, SEQ ID  
NO: 229, SEQ ID NO: 231, SEQ ID NO: 233, SEQ ID NO: 235, SEQ ID NO: 237,  
SEQ ID NO: 239, SEQ ID NO: 241, SEQ ID NO: 243, SEQ ID NO: 245, SEQ ID  
25 NO: 247, SEQ ID NO: 249, SEQ ID NO: 251, SEQ ID NO: 253, SEQ ID NO: 255,  
SEQ ID NO: 257, SEQ ID NO: 259, SEQ ID NO: 261, SEQ ID NO: 263, SEQ ID  
NO: 265, SEQ ID NO: 267, SEQ ID NO: 269, SEQ ID NO: 271, SEQ ID NO: 273,  
SEQ ID NO: 275, SEQ ID NO: 277, SEQ ID NO: 279, SEQ ID NO: 281, SEQ ID  
NO: 283, SEQ ID NO: 285, SEQ ID NO: 287, SEQ ID NO: 289, SEQ ID NO: 291,  
30 SEQ ID NO: 293, SEQ ID NO: 295, SEQ ID NO: 297, SEQ ID NO: 299, SEQ ID  
NO: 301, SEQ ID NO: 303, SEQ ID NO: 305, SEQ ID NO: 307, SEQ ID NO: 309,  
SEQ ID NO: 311, SEQ ID NO: 313, SEQ ID NO: 315, SEQ ID NO: 317, SEQ ID  
NO: 319, SEQ ID NO: 321, SEQ ID NO: 323, SEQ ID NO: 325, SEQ ID NO: 327,

SEQ ID NO: 329, SEQ ID NO: 331, SEQ ID NO: 333, SEQ ID NO: 335, SEQ ID  
 NO: 337, SEQ ID NO: 339, SEQ ID NO: 341, SEQ ID NO: 343, SEQ ID NO: 345,  
 SEQ ID NO: 347, SEQ ID NO: 349, SEQ ID NO: 351, SEQ ID NO: 353, SEQ ID  
 NO: 355, SEQ ID NO: 357, SEQ ID NO: 359, SEQ ID NO: 361, SEQ ID NO: 363,  
 5 SEQ ID NO: 365, SEQ ID NO: 367, SEQ ID NO: 369, SEQ ID NO: 371, SEQ ID  
 NO: 373, SEQ ID NO: 375, SEQ ID NO: 377, SEQ ID NO: 379, SEQ ID NO: 381,  
 SEQ ID NO: 383, SEQ ID NO: 385, SEQ ID NO: 387, SEQ ID NO: 389, SEQ ID  
 NO: 391, SEQ ID NO: 393, SEQ ID NO: 395, SEQ ID NO: 397, SEQ ID NO: 399,  
 SEQ ID NO: 401, SEQ ID NO: 403, SEQ ID NO: 405, SEQ ID NO: 407, SEQ ID  
 10 NO: 409, SEQ ID NO: 411, SEQ ID NO: 413, SEQ ID NO: 415, SEQ ID NO: 417,  
 SEQ ID NO: 419, SEQ ID NO: 421, SEQ ID NO: 423, SEQ ID NO: 425, SEQ ID  
 NO: 427, SEQ ID NO: 429, SEQ ID NO: 431, SEQ ID NO: 433, SEQ ID NO: 435,  
 SEQ ID NO: 437, SEQ ID NO: 439, SEQ ID NO: 441, SEQ ID NO: 443, SEQ ID  
 NO: 445, SEQ ID NO: 447, SEQ ID NO: 449, SEQ ID NO: 451, SEQ ID NO: 453,  
 15 SEQ ID NO: 455, SEQ ID NO: 457, SEQ ID NO: 459, SEQ ID NO: 461, SEQ ID  
 NO: 463, SEQ ID NO: 465, SEQ ID NO: 467, SEQ ID NO: 469, SEQ ID NO: 471,  
 SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID NO: 477, SEQ ID NO: 479, SEQ ID  
 NO: 481, SEQ ID NO: 483, SEQ ID NO: 485, SEQ ID NO: 487, SEQ ID NO: 489,  
 SEQ ID NO: 491, SEQ ID NO: 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID  
 20 NO: 499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507,  
 SEQ ID NO: 509 and SEQ ID NO: 511 or a fragment thereof that comprises at least  
 40 contiguous amino acids thereof.

11. An isolated nucleic acid sequence according to Claim 1 which encodes  
 25 a polypeptide having at least 70-80% sequence identity with a polypeptide having an  
 amino acid sequence selected from the group consisting of: SEQ ID NO: 1, SEQ ID  
 NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID  
 NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID  
 NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID  
 30 NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID  
 NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID  
 NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID  
 NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID

NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID  
NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID  
NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ  
ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111,  
5 SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID  
NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129,  
SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID  
NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147,  
SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID NO: 155, SEQ ID  
10 NO: 157, SEQ ID NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165,  
SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID  
NO: 175, SEQ ID NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID NO: 183,  
SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID NO: 191, SEQ ID  
NO: 193, SEQ ID NO: 195, SEQ ID NO: 197, SEQ ID NO: 199, SEQ ID NO: 201,  
15 SEQ ID NO: 203, SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID NO: 209, SEQ ID  
NO: 211, SEQ ID NO: 213, SEQ ID NO: 215, SEQ ID NO: 217, SEQ ID NO: 219,  
SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID NO: 225, SEQ ID NO: 227, SEQ ID  
NO: 229, SEQ ID NO: 231, SEQ ID NO: 233, SEQ ID NO: 235, SEQ ID NO: 237,  
SEQ ID NO: 239, SEQ ID NO: 241, SEQ ID NO: 243, SEQ ID NO: 245, SEQ ID  
20 NO: 247, SEQ ID NO: 249, SEQ ID NO: 251, SEQ ID NO: 253, SEQ ID NO: 255,  
SEQ ID NO: 257, SEQ ID NO: 259, SEQ ID NO: 261, SEQ ID NO: 263, SEQ ID  
NO: 265, SEQ ID NO: 267, SEQ ID NO: 269, SEQ ID NO: 271, SEQ ID NO: 273,  
SEQ ID NO: 275, SEQ ID NO: 277, SEQ ID NO: 279, SEQ ID NO: 281, SEQ ID  
NO: 283, SEQ ID NO: 285, SEQ ID NO: 287, SEQ ID NO: 289, SEQ ID NO: 291,  
25 SEQ ID NO: 293, SEQ ID NO: 295, SEQ ID NO: 297, SEQ ID NO: 299, SEQ ID  
NO: 301, SEQ ID NO: 303, SEQ ID NO: 305, SEQ ID NO: 307, SEQ ID NO: 309,  
SEQ ID NO: 311, SEQ ID NO: 313, SEQ ID NO: 315, SEQ ID NO: 317, SEQ ID  
NO: 319, SEQ ID NO: 321, SEQ ID NO: 323, SEQ ID NO: 325, SEQ ID NO: 327,  
SEQ ID NO: 329, SEQ ID NO: 331, SEQ ID NO: 333, SEQ ID NO: 335, SEQ ID  
30 NO: 337, SEQ ID NO: 339, SEQ ID NO: 341, SEQ ID NO: 343, SEQ ID NO: 345,  
SEQ ID NO: 347, SEQ ID NO: 349, SEQ ID NO: 351, SEQ ID NO: 353, SEQ ID  
NO: 355, SEQ ID NO: 357, SEQ ID NO: 359, SEQ ID NO: 361, SEQ ID NO: 363,  
SEQ ID NO: 365, SEQ ID NO: 367, SEQ ID NO: 369, SEQ ID NO: 371, SEQ ID

NO: 373, SEQ ID NO: 375, SEQ ID NO: 377, SEQ ID NO: 379, SEQ ID NO: 381,  
SEQ ID NO: 383, SEQ ID NO: 385, SEQ ID NO: 387, SEQ ID NO: 389, SEQ ID  
NO: 391, SEQ ID NO: 393, SEQ ID NO: 395, SEQ ID NO: 397, SEQ ID NO: 399,  
SEQ ID NO: 401, SEQ ID NO: 403, SEQ ID NO: 405, SEQ ID NO: 407, SEQ ID  
5 NO: 409, SEQ ID NO: 411, SEQ ID NO: 413, SEQ ID NO: 415, SEQ ID NO: 417,  
SEQ ID NO: 419, SEQ ID NO: 421, SEQ ID NO: 423, SEQ ID NO: 425, SEQ ID  
NO: 427, SEQ ID NO: 429, SEQ ID NO: 431, SEQ ID NO: 433, SEQ ID NO: 435,  
SEQ ID NO: 437, SEQ ID NO: 439, SEQ ID NO: 441, SEQ ID NO: 443, SEQ ID  
NO: 445, SEQ ID NO: 447, SEQ ID NO: 449, SEQ ID NO: 451, SEQ ID NO: 453,  
10 SEQ ID NO: 455, SEQ ID NO: 457, SEQ ID NO: 459, SEQ ID NO: 461, SEQ ID  
NO: 463, SEQ ID NO: 465, SEQ ID NO: 467, SEQ ID NO: 469, SEQ ID NO: 471,  
SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID NO: 477, SEQ ID NO: 479, SEQ ID  
NO: 481, SEQ ID NO: 483, SEQ ID NO: 485, SEQ ID NO: 487, SEQ ID NO: 489,  
SEQ ID NO: 491, SEQ ID NO: 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID  
15 NO: 499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507,  
SEQ ID NO: 509 and SEQ ID NO: 511 or a fragment thereof that comprises at least  
40 contiguous amino acids thereof.

12. An isolated nucleic acid sequence according to Claim 1 which encodes  
20 a polypeptide having at least 80-90% sequence identity with a polypeptide having an  
amino acid sequence selected from the group consisting of: SEQ ID NO: 1, SEQ ID  
NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID  
NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID  
NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID  
25 NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID  
NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID  
NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID  
NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID  
NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID  
30 NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID  
NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ  
ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111,  
SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID

NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129,  
SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID  
NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147,  
SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID NO: 155, SEQ ID  
5 NO: 157, SEQ ID NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165,  
SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID  
NO: 175, SEQ ID NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID NO: 183,  
SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID NO: 191, SEQ ID  
NO: 193, SEQ ID NO: 195, SEQ ID NO: 197, SEQ ID NO: 199, SEQ ID NO: 201,  
10 SEQ ID NO: 203, SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID NO: 209, SEQ ID  
NO: 211, SEQ ID NO: 213, SEQ ID NO: 215, SEQ ID NO: 217, SEQ ID NO: 219,  
SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID NO: 225, SEQ ID NO: 227, SEQ ID  
NO: 229, SEQ ID NO: 231, SEQ ID NO: 233, SEQ ID NO: 235, SEQ ID NO: 237,  
SEQ ID NO: 239, SEQ ID NO: 241, SEQ ID NO: 243, SEQ ID NO: 245, SEQ ID  
15 NO: 247, SEQ ID NO: 249, SEQ ID NO: 251, SEQ ID NO: 253, SEQ ID NO: 255,  
SEQ ID NO: 257, SEQ ID NO: 259, SEQ ID NO: 261, SEQ ID NO: 263, SEQ ID  
NO: 265, SEQ ID NO: 267, SEQ ID NO: 269, SEQ ID NO: 271, SEQ ID NO: 273,  
SEQ ID NO: 275, SEQ ID NO: 277, SEQ ID NO: 279, SEQ ID NO: 281, SEQ ID  
NO: 283, SEQ ID NO: 285, SEQ ID NO: 287, SEQ ID NO: 289, SEQ ID NO: 291,  
20 SEQ ID NO: 293, SEQ ID NO: 295, SEQ ID NO: 297, SEQ ID NO: 299, SEQ ID  
NO: 301, SEQ ID NO: 303, SEQ ID NO: 305, SEQ ID NO: 307, SEQ ID NO: 309,  
SEQ ID NO: 311, SEQ ID NO: 313, SEQ ID NO: 315, SEQ ID NO: 317, SEQ ID  
NO: 319, SEQ ID NO: 321, SEQ ID NO: 323, SEQ ID NO: 325, SEQ ID NO: 327,  
SEQ ID NO: 329, SEQ ID NO: 331, SEQ ID NO: 333, SEQ ID NO: 335, SEQ ID  
25 NO: 337, SEQ ID NO: 339, SEQ ID NO: 341, SEQ ID NO: 343, SEQ ID NO: 345,  
SEQ ID NO: 347, SEQ ID NO: 349, SEQ ID NO: 351, SEQ ID NO: 353, SEQ ID  
NO: 355, SEQ ID NO: 357, SEQ ID NO: 359, SEQ ID NO: 361, SEQ ID NO: 363,  
SEQ ID NO: 365, SEQ ID NO: 367, SEQ ID NO: 369, SEQ ID NO: 371, SEQ ID  
NO: 373, SEQ ID NO: 375, SEQ ID NO: 377, SEQ ID NO: 379, SEQ ID NO: 381,  
30 SEQ ID NO: 383, SEQ ID NO: 385, SEQ ID NO: 387, SEQ ID NO: 389, SEQ ID  
NO: 391, SEQ ID NO: 393, SEQ ID NO: 395, SEQ ID NO: 397, SEQ ID NO: 399,  
SEQ ID NO: 401, SEQ ID NO: 403, SEQ ID NO: 405, SEQ ID NO: 407, SEQ ID  
NO: 409, SEQ ID NO: 411, SEQ ID NO: 413, SEQ ID NO: 415, SEQ ID NO: 417,



SEQ ID NO: 419, SEQ ID NO: 421, SEQ ID NO: 423, SEQ ID NO: 425, SEQ ID  
 NO: 427, SEQ ID NO: 429, SEQ ID NO: 431, SEQ ID NO: 433, SEQ ID NO: 435,  
 SEQ ID NO: 437, SEQ ID NO: 439, SEQ ID NO: 441, SEQ ID NO: 443, SEQ ID  
 NO: 445, SEQ ID NO: 447, SEQ ID NO: 449, SEQ ID NO: 451, SEQ ID NO: 453,  
 5 SEQ ID NO: 455, SEQ ID NO: 457, SEQ ID NO: 459, SEQ ID NO: 461, SEQ ID  
 NO: 463, SEQ ID NO: 465, SEQ ID NO: 467, SEQ ID NO: 469, SEQ ID NO: 471,  
 SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID NO: 477, SEQ ID NO: 479, SEQ ID  
 NO: 481, SEQ ID NO: 483, SEQ ID NO: 485, SEQ ID NO: 487, SEQ ID NO: 489,  
 SEQ ID NO: 491, SEQ ID NO: 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID  
 10 NO: 499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507,  
 SEQ ID NO: 509 and SEQ ID NO: 511 or a fragment thereof that comprises at least  
 40 contiguous amino acids thereof.

13. An isolated nucleic acid sequence according to Claim 1 which encodes  
 15 a polypeptide having about 90-99% sequence identity with a polypeptide having an  
 amino acid sequence selected from the group consisting of: SEQ ID NO: 1, SEQ ID  
 NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID  
 NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID  
 NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID  
 20 NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID  
 NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID  
 NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID  
 NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID  
 NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID  
 25 NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID  
 NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ  
 ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111,  
 SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID  
 NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129,  
 30 SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID  
 NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147,  
 SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID NO: 155, SEQ ID  
 NO: 157, SEQ ID NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165,

SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID  
NO: 175, SEQ ID NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID NO: 183,  
SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID NO: 191, SEQ ID  
NO: 193, SEQ ID NO: 195, SEQ ID NO: 197, SEQ ID NO: 199, SEQ ID NO: 201,  
5 SEQ ID NO: 203, SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID NO: 209, SEQ ID  
NO: 211, SEQ ID NO: 213, SEQ ID NO: 215, SEQ ID NO: 217, SEQ ID NO: 219,  
SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID NO: 225, SEQ ID NO: 227, SEQ ID  
NO: 229, SEQ ID NO: 231, SEQ ID NO: 233, SEQ ID NO: 235, SEQ ID NO: 237,  
SEQ ID NO: 239, SEQ ID NO: 241, SEQ ID NO: 243, SEQ ID NO: 245, SEQ ID  
10 NO: 247, SEQ ID NO: 249, SEQ ID NO: 251, SEQ ID NO: 253, SEQ ID NO: 255,  
SEQ ID NO: 257, SEQ ID NO: 259, SEQ ID NO: 261, SEQ ID NO: 263, SEQ ID  
NO: 265, SEQ ID NO: 267, SEQ ID NO: 269, SEQ ID NO: 271, SEQ ID NO: 273,  
SEQ ID NO: 275, SEQ ID NO: 277, SEQ ID NO: 279, SEQ ID NO: 281, SEQ ID  
NO: 283, SEQ ID NO: 285, SEQ ID NO: 287, SEQ ID NO: 289, SEQ ID NO: 291,  
15 SEQ ID NO: 293, SEQ ID NO: 295, SEQ ID NO: 297, SEQ ID NO: 299, SEQ ID  
NO: 301, SEQ ID NO: 303, SEQ ID NO: 305, SEQ ID NO: 307, SEQ ID NO: 309,  
SEQ ID NO: 311, SEQ ID NO: 313, SEQ ID NO: 315, SEQ ID NO: 317, SEQ ID  
NO: 319, SEQ ID NO: 321, SEQ ID NO: 323, SEQ ID NO: 325, SEQ ID NO: 327,  
SEQ ID NO: 329, SEQ ID NO: 331, SEQ ID NO: 333, SEQ ID NO: 335, SEQ ID  
20 NO: 337, SEQ ID NO: 339, SEQ ID NO: 341, SEQ ID NO: 343, SEQ ID NO: 345,  
SEQ ID NO: 347, SEQ ID NO: 349, SEQ ID NO: 351, SEQ ID NO: 353, SEQ ID  
NO: 355, SEQ ID NO: 357, SEQ ID NO: 359, SEQ ID NO: 361, SEQ ID NO: 363,  
SEQ ID NO: 365, SEQ ID NO: 367, SEQ ID NO: 369, SEQ ID NO: 371, SEQ ID  
NO: 373, SEQ ID NO: 375, SEQ ID NO: 377, SEQ ID NO: 379, SEQ ID NO: 381,  
25 SEQ ID NO: 383, SEQ ID NO: 385, SEQ ID NO: 387, SEQ ID NO: 389, SEQ ID  
NO: 391, SEQ ID NO: 393, SEQ ID NO: 395, SEQ ID NO: 397, SEQ ID NO: 399,  
SEQ ID NO: 401, SEQ ID NO: 403, SEQ ID NO: 405, SEQ ID NO: 407, SEQ ID  
NO: 409, SEQ ID NO: 411, SEQ ID NO: 413, SEQ ID NO: 415, SEQ ID NO: 417,  
SEQ ID NO: 419, SEQ ID NO: 421, SEQ ID NO: 423, SEQ ID NO: 425, SEQ ID  
30 NO: 427, SEQ ID NO: 429, SEQ ID NO: 431, SEQ ID NO: 433, SEQ ID NO: 435,  
SEQ ID NO: 437, SEQ ID NO: 439, SEQ ID NO: 441, SEQ ID NO: 443, SEQ ID  
NO: 445, SEQ ID NO: 447, SEQ ID NO: 449, SEQ ID NO: 451, SEQ ID NO: 453,  
SEQ ID NO: 455, SEQ ID NO: 457, SEQ ID NO: 459, SEQ ID NO: 461, SEQ ID

NO: 463, SEQ ID NO: 465, SEQ ID NO: 467, SEQ ID NO: 469, SEQ ID NO: 471, SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID NO: 477, SEQ ID NO: 479, SEQ ID NO: 481, SEQ ID NO: 483, SEQ ID NO: 485, SEQ ID NO: 487, SEQ ID NO: 489, SEQ ID NO: 491, SEQ ID NO: 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511 or a fragment thereof that comprises at least 40 contiguous amino acids thereof.

14. An isolated nucleic acid sequence which exhibits at least 50% sequence identity with a nucleic acid sequence selected from the group consisting of: SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID NO: 60, SEQ ID NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID NO: 70, SEQ ID NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 80, SEQ ID NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 90, SEQ ID NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID NO: 100, SEQ ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 108, SEQ ID NO: 110, SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 116, SEQ ID NO: 118, SEQ ID NO: 120, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID NO: 128, SEQ ID NO: 130, SEQ ID NO: 132, SEQ ID NO: 134, SEQ ID NO: 136, SEQ ID NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, SEQ ID NO: 144, SEQ ID NO: 146, SEQ ID NO: 148, SEQ ID NO: 150, SEQ ID NO: 152, SEQ ID NO: 154, SEQ ID NO: 156, SEQ ID NO: 158, SEQ ID NO: 160, SEQ ID NO: 162, SEQ ID NO: 164, SEQ ID NO: 166, SEQ ID NO: 168, SEQ ID NO: 170, SEQ ID NO: 172, SEQ ID NO: 174, SEQ ID NO: 176, SEQ ID NO: 178, SEQ ID NO: 180, SEQ ID NO: 182, SEQ ID NO: 184, SEQ ID NO: 186, SEQ ID NO: 188, SEQ ID NO: 190, SEQ ID NO: 192, SEQ ID NO: 194, SEQ ID NO: 196, SEQ ID NO: 198, SEQ ID NO: 200, SEQ ID NO: 202, SEQ ID NO: 204, SEQ ID NO: 206, SEQ ID NO: 208, SEQ ID NO: 210, SEQ ID NO: 212, SEQ ID NO: 214, SEQ ID NO: 216, SEQ ID

NO: 218, SEQ ID NO: 220, SEQ ID NO: 222, SEQ ID NO: 224, SEQ ID NO: 226,  
SEQ ID NO: 228, SEQ ID NO: 230, SEQ ID NO: 232, SEQ ID NO: 234, SEQ ID  
NO: 236, SEQ ID NO: 238, SEQ. ID NO. 240, SEQ ID NO: 242, SEQ ID NO: 244,  
SEQ ID NO: 246, SEQ ID NO: 248, SEQ ID NO: 250, SEQ ID NO: 252, SEQ ID  
5 NO: 254, SEQ ID NO: 256, SEQ ID NO: 258, SEQ ID NO: 260, SEQ ID NO: 262,  
SEQ ID NO: 264, SEQ ID NO: 266, SEQ ID NO: 268, SEQ ID NO: 270, SEQ ID  
NO: 272, SEQ ID NO: 274, SEQ ID NO: 276, SEQ ID NO: 278, SEQ ID NO: 280,  
SEQ ID NO: 282, SEQ ID NO: 284, SEQ ID NO: 286, SEQ ID NO: 288, SEQ ID  
NO: 290, SEQ ID NO: 292, SEQ ID NO: 294, SEQ ID NO: 296, SEQ ID NO: 298,  
10 SEQ ID NO: 300, SEQ ID NO: 302, SEQ ID NO: 304, SEQ ID NO: 306, SEQ ID  
NO: 308, SEQ ID NO: 310, SEQ ID NO: 312, SEQ ID NO: 314, SEQ ID NO: 316,  
SEQ ID NO: 318, SEQ ID NO: 320, SEQ ID NO: 322, SEQ ID NO: 324, SEQ ID  
NO: 326, SEQ ID NO: 328, SEQ ID NO: 330, SEQ ID NO: 332, SEQ ID NO: 334,  
SEQ ID NO: 336, SEQ ID NO: 338, SEQ ID NO: 340, SEQ ID NO: 342, SEQ ID  
15 NO: 344, SEQ ID NO: 346, SEQ ID NO: 348, SEQ ID NO: 350, SEQ ID NO: 352,  
SEQ ID NO: 354, SEQ ID NO: 356, SEQ ID NO: 358, SEQ ID NO: 360, SEQ ID  
NO: 362, SEQ ID NO: 364, SEQ ID NO: 366, SEQ ID NO: 368, SEQ ID NO: 370,  
SEQ ID NO: 372, SEQ ID NO: 374, SEQ ID NO: 376, SEQ ID NO: 378, SEQ ID  
NO: 380, SEQ ID NO: 382, SEQ ID NO: 384, SEQ ID NO: 386, SEQ ID NO: 388,  
20 SEQ ID NO: 390, SEQ ID NO: 392, SEQ ID NO: 394, SEQ ID NO: 396, SEQ ID  
NO: 398, SEQ ID NO: 400, SEQ ID NO: 402, SEQ ID NO: 404, SEQ ID NO: 406,  
SEQ ID NO: 408, SEQ ID NO: 410, SEQ ID NO: 412, SEQ ID NO: 414, SEQ ID  
NO: 416, SEQ ID NO: 418, SEQ ID NO: 420, SEQ ID NO: 422, SEQ ID NO: 424,  
SEQ ID NO: 426, SEQ ID NO: 428, SEQ ID NO: 430, SEQ ID NO: 432, SEQ ID  
25 NO: 434, SEQ ID NO: 436, SEQ ID NO: 438, SEQ ID NO: 440, SEQ ID NO: 442,  
SEQ ID NO: 444, SEQ ID NO: 446, SEQ ID NO: 448, SEQ ID NO: 450, SEQ ID  
NO: 452, SEQ ID NO: 454, SEQ ID NO: 456, SEQ ID NO: 458, SEQ ID NO: 460,  
SEQ ID NO: 462, SEQ ID NO: 464, SEQ ID NO: 466, SEQ ID NO: 468, SEQ ID  
NO: 470, SEQ ID NO: 472, SEQ ID NO: 474, SEQ ID NO: 476, SEQ ID NO: 478,  
30 SEQ ID NO: 480, SEQ ID NO: 482, SEQ ID NO: 484, SEQ ID NO: 486, SEQ ID  
NO: 488, SEQ ID NO: 490, SEQ ID NO: 492, SEQ ID NO: 494, SEQ ID NO: 496,  
SEQ ID NO: 498, SEQ ID NO: 500, SEQ ID NO: 502, SEQ ID NO: 504, SEQ ID  
NO: 506, SEQ ID NO: 508, SEQ ID NO: 510 and SEQ ID NO: 512 or a nucleic acid

sequence which exhibits at least 50% sequence identity to a fragment comprising at least 100 contiguous nucleotides of said nucleic acid sequence.

15. An isolated nucleic acid sequence which exhibits at least 60% sequence identity with a nucleic acid sequence selected from the group consisting of:
- 5 SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ
- 10 ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID NO: 60, SEQ ID NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID NO: 70, SEQ ID NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 80, SEQ ID NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 90, SEQ
- 15 ID NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID NO: 100, SEQ ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 108, SEQ ID NO: 110, SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 116, SEQ ID NO: 118, SEQ ID NO: 120, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID NO: 128, SEQ ID NO: 130, SEQ ID NO: 132, SEQ ID NO: 134, SEQ ID NO: 136,
- 20 SEQ ID NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, SEQ ID NO: 144, SEQ ID NO: 146, SEQ ID NO: 148, SEQ ID NO: 150, SEQ ID NO: 152, SEQ ID NO: 154, SEQ ID NO: 156, SEQ ID NO: 158, SEQ ID NO: 160, SEQ ID NO: 162, SEQ ID NO: 164, SEQ ID NO: 166, SEQ ID NO: 168, SEQ ID NO: 170, SEQ ID NO: 172, SEQ ID NO: 174, SEQ ID NO: 176, SEQ ID NO: 178, SEQ ID NO: 180, SEQ ID
- 25 NO: 182, SEQ ID NO: 184, SEQ ID NO: 186, SEQ ID NO: 188, SEQ ID NO: 190, SEQ ID NO: 192, SEQ ID NO: 194, SEQ ID NO: 196, SEQ ID NO: 198, SEQ ID NO: 200, SEQ ID NO: 202, SEQ ID NO: 204, SEQ ID NO: 206, SEQ ID NO: 208, SEQ ID NO: 210, SEQ ID NO: 212, SEQ ID NO: 214, SEQ ID NO: 216, SEQ ID NO: 218, SEQ ID NO: 220, SEQ ID NO: 222, SEQ ID NO: 224, SEQ ID NO: 226,
- 30 SEQ ID NO: 228, SEQ ID NO: 230, SEQ ID NO: 232, SEQ ID NO: 234, SEQ ID NO: 236, SEQ ID NO: 238, SEQ ID NO: 240, SEQ ID NO: 242, SEQ ID NO: 244, SEQ ID NO: 246, SEQ ID NO: 248, SEQ ID NO: 250, SEQ ID NO: 252, SEQ ID NO: 254, SEQ ID NO: 256, SEQ ID NO: 258, SEQ ID NO: 260, SEQ ID NO: 262,

SEQ ID NO: 264, SEQ ID NO: 266, SEQ ID NO: 268, SEQ ID NO: 270, SEQ ID NO: 272, SEQ ID NO: 274, SEQ ID NO: 276, SEQ ID NO: 278, SEQ ID NO: 280, SEQ ID NO: 282, SEQ ID NO: 284, SEQ ID NO: 286, SEQ ID NO: 288, SEQ ID NO: 290, SEQ ID NO: 292, SEQ ID NO: 294, SEQ ID NO: 296, SEQ ID NO: 298, 5 SEQ ID NO: 300, SEQ ID NO: 302, SEQ ID NO: 304, SEQ ID NO: 306, SEQ ID NO: 308, SEQ ID NO: 310, SEQ ID NO: 312, SEQ ID NO: 314, SEQ ID NO: 316, SEQ ID NO: 318, SEQ ID NO: 320, SEQ ID NO: 322, SEQ ID NO: 324, SEQ ID NO: 326, SEQ ID NO: 328, SEQ ID NO: 330, SEQ ID NO: 332, SEQ ID NO: 334, SEQ ID NO: 336, SEQ ID NO: 338, SEQ ID NO: 340, SEQ ID NO: 342, SEQ ID NO: 344, SEQ ID NO: 346, SEQ ID NO: 348, SEQ ID NO: 350, SEQ ID NO: 352, 10 SEQ ID NO: 354, SEQ ID NO: 356, SEQ ID NO: 358, SEQ ID NO: 360, SEQ ID NO: 362, SEQ ID NO: 364, SEQ ID NO: 366, SEQ ID NO: 368, SEQ ID NO: 370, SEQ ID NO: 372, SEQ ID NO: 374, SEQ ID NO: 376, SEQ ID NO: 378, SEQ ID NO: 380, SEQ ID NO: 382, SEQ ID NO: 384, SEQ ID NO: 386, SEQ ID NO: 388, 15 SEQ ID NO: 390, SEQ ID NO: 392, SEQ ID NO: 394, SEQ ID NO: 396, SEQ ID NO: 398, SEQ ID NO: 400, SEQ ID NO: 402, SEQ ID NO: 404, SEQ ID NO: 406, SEQ ID NO: 408, SEQ ID NO: 410, SEQ ID NO: 412, SEQ ID NO: 414, SEQ ID NO: 416, SEQ ID NO: 418, SEQ ID NO: 420, SEQ ID NO: 422, SEQ ID NO: 424, SEQ ID NO: 426, SEQ ID NO: 428, SEQ ID NO: 430, SEQ ID NO: 432, SEQ ID NO: 434, SEQ ID NO: 436, SEQ ID NO: 438, SEQ ID NO: 440, SEQ ID NO: 442, 20 SEQ ID NO: 444, SEQ ID NO: 446, SEQ ID NO: 448, SEQ ID NO: 450, SEQ ID NO: 452, SEQ ID NO: 454, SEQ ID NO: 456, SEQ ID NO: 458, SEQ ID NO: 460, SEQ ID NO: 462, SEQ ID NO: 464, SEQ ID NO: 466, SEQ ID NO: 468, SEQ ID NO: 470, SEQ ID NO: 472, SEQ ID NO: 474, SEQ ID NO: 476, SEQ ID NO: 478, 25 SEQ ID NO: 480, SEQ ID NO: 482, SEQ ID NO: 484, SEQ ID NO: 486, SEQ ID NO: 488, SEQ ID NO: 490, SEQ ID NO: 492, SEQ ID NO: 494, SEQ ID NO: 496, SEQ ID NO: 498, SEQ ID NO: 500, SEQ ID NO: 502, SEQ ID NO: 504, SEQ ID NO: 506, SEQ ID NO: 508, SEQ ID NO: 510 and SEQ ID NO: 512 or a nucleic acid sequence which exhibits at least 60% sequence identity to a fragment comprising at 30 least 100 contiguous nucleotides of said nucleic acid sequence.

16. An isolated nucleic acid sequence that exhibits at least 70% sequence identity with a nucleic acid sequence selected from the group consisting of: SEQ ID

NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID  
NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID  
NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID  
NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID  
5 NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID  
NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID NO: 60, SEQ ID  
NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID NO: 70, SEQ ID  
NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 80, SEQ ID  
NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 90, SEQ ID  
10 NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID NO: 100, SEQ  
ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 108, SEQ ID NO: 110,  
SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 116, SEQ ID NO: 118, SEQ ID  
NO: 120, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID NO: 128,  
SEQ ID NO: 130, SEQ ID NO: 132, SEQ ID NO: 134, SEQ ID NO: 136, SEQ ID  
15 NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, SEQ ID NO: 144, SEQ ID NO: 146,  
SEQ ID NO: 148, SEQ ID NO: 150, SEQ ID NO: 152, SEQ ID NO: 154, SEQ ID  
NO: 156, SEQ ID NO: 158, SEQ ID NO: 160, SEQ ID NO: 162, SEQ ID NO: 164,  
SEQ ID NO: 166, SEQ ID NO: 168, SEQ ID NO: 170, SEQ ID NO: 172, SEQ ID  
NO: 174, SEQ ID NO: 176, SEQ ID NO: 178, SEQ ID NO: 180, SEQ ID NO: 182,  
20 SEQ ID NO: 184, SEQ ID NO: 186, SEQ ID NO: 188, SEQ ID NO: 190, SEQ ID  
NO: 192, SEQ ID NO: 194, SEQ ID NO: 196, SEQ ID NO: 198, SEQ ID NO: 200,  
SEQ ID NO: 202, SEQ ID NO: 204, SEQ ID NO: 206, SEQ ID NO: 208, SEQ ID  
NO: 210, SEQ ID NO: 212, SEQ ID NO: 214, SEQ ID NO: 216, SEQ ID NO: 218,  
SEQ ID NO: 220, SEQ ID NO: 222, SEQ ID NO: 224, SEQ ID NO: 226, SEQ ID  
25 NO: 228, SEQ ID NO: 230, SEQ ID NO: 232, SEQ ID NO: 234, SEQ ID NO: 236,  
SEQ ID NO: 238, SEQ ID NO: 240, SEQ ID NO: 242, SEQ ID NO: 244, SEQ ID  
NO: 246, SEQ ID NO: 248, SEQ ID NO: 250, SEQ ID NO: 252, SEQ ID NO: 254,  
SEQ ID NO: 256, SEQ ID NO: 258, SEQ ID NO: 260, SEQ ID NO: 262, SEQ ID  
NO: 264, SEQ ID NO: 266, SEQ ID NO: 268, SEQ ID NO: 270, SEQ ID NO: 272,  
30 SEQ ID NO: 274, SEQ ID NO: 276, SEQ ID NO: 278, SEQ ID NO: 280, SEQ ID  
NO: 282, SEQ ID NO: 284, SEQ ID NO: 286, SEQ ID NO: 288, SEQ ID NO: 290,  
SEQ ID NO: 292, SEQ ID NO: 294, SEQ ID NO: 296, SEQ ID NO: 298, SEQ ID  
NO: 300, SEQ ID NO: 302, SEQ ID NO: 304, SEQ ID NO: 306, SEQ ID NO: 308,

SEQ ID NO: 310, SEQ ID NO: 312, SEQ ID NO: 314, SEQ ID NO: 316, SEQ ID NO: 318, SEQ ID NO: 320, SEQ ID NO: 322, SEQ ID NO: 324, SEQ ID NO: 326, SEQ ID NO: 328, SEQ ID NO: 330, SEQ ID NO: 332, SEQ ID NO: 334, SEQ ID NO: 336, SEQ ID NO: 338, SEQ ID NO: 340, SEQ ID NO: 342, SEQ ID NO: 344, 5 SEQ ID NO: 346, SEQ ID NO: 348, SEQ ID NO: 350, SEQ ID NO: 352, SEQ ID NO: 354, SEQ ID NO: 356, SEQ ID NO: 358, SEQ ID NO: 360, SEQ ID NO: 362, SEQ ID NO: 364, SEQ ID NO: 366, SEQ ID NO: 368, SEQ ID NO: 370, SEQ ID NO: 372, SEQ ID NO: 374, SEQ ID NO: 376, SEQ ID NO: 378, SEQ ID NO: 380, SEQ ID NO: 382, SEQ ID NO: 384, SEQ ID NO: 386, SEQ ID NO: 388, SEQ ID NO: 390, SEQ ID NO: 392, SEQ ID NO: 394, SEQ ID NO: 396, SEQ ID NO: 398, 10 SEQ ID NO: 400, SEQ ID NO: 402, SEQ ID NO: 404, SEQ ID NO: 406, SEQ ID NO: 408, SEQ ID NO: 410, SEQ ID NO: 412, SEQ ID NO: 414, SEQ ID NO: 416, SEQ ID NO: 418, SEQ ID NO: 420, SEQ ID NO: 422, SEQ ID NO: 424, SEQ ID NO: 426, SEQ ID NO: 428, SEQ ID NO: 430, SEQ ID NO: 432, SEQ ID NO: 434, 15 SEQ ID NO: 436, SEQ ID NO: 438, SEQ ID NO: 440, SEQ ID NO: 442, SEQ ID NO: 444, SEQ ID NO: 446, SEQ ID NO: 448, SEQ ID NO: 450, SEQ ID NO: 452, SEQ ID NO: 454, SEQ ID NO: 456, SEQ ID NO: 458, SEQ ID NO: 460, SEQ ID NO: 462, SEQ ID NO: 464, SEQ ID NO: 466, SEQ ID NO: 468, SEQ ID NO: 470, SEQ ID NO: 472, SEQ ID NO: 474, SEQ ID NO: 476, SEQ ID NO: 478, SEQ ID NO: 480, SEQ ID NO: 482, SEQ ID NO: 484, SEQ ID NO: 486, SEQ ID NO: 488, 20 SEQ ID NO: 490, SEQ ID NO: 492, SEQ ID NO: 494, SEQ ID NO: 496, SEQ ID NO: 498, SEQ ID NO: 500, SEQ ID NO: 502, SEQ ID NO: 504, SEQ ID NO: 506, SEQ ID NO: 508, SEQ ID NO: 510 and SEQ ID NO: 512 or a nucleic acid sequence having at least 70% sequence identity with a fragment thereof comprising at least 100 25 contiguous nucleotides thereof.

17. An isolated nucleic acid sequence that exhibits at least 80% sequence identity with a nucleic acid sequence selected from the group consisting of: SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID



NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID NO: 60, SEQ ID  
NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID NO: 70, SEQ ID  
NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 80, SEQ ID  
NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 90, SEQ ID  
5 NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID NO: 100, SEQ  
ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 108, SEQ ID NO: 110,  
SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 116, SEQ ID NO: 118, SEQ ID  
NO: 120, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID NO: 128,  
SEQ ID NO: 130, SEQ ID NO: 132, SEQ ID NO: 134, SEQ ID NO: 136, SEQ ID  
10 NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, SEQ ID NO: 144, SEQ ID NO: 146,  
SEQ ID NO: 148, SEQ ID NO: 150, SEQ ID NO: 152, SEQ ID NO: 154, SEQ ID  
NO: 156, SEQ ID NO: 158, SEQ ID NO: 160, SEQ ID NO: 162, SEQ ID NO: 164,  
SEQ ID NO: 166, SEQ ID NO: 168, SEQ ID NO: 170, SEQ ID NO: 172, SEQ ID  
NO: 174, SEQ ID NO: 176, SEQ ID NO: 178, SEQ ID NO: 180, SEQ ID NO: 182,  
15 SEQ ID NO: 184, SEQ ID NO: 186, SEQ ID NO: 188, SEQ ID NO: 190, SEQ ID  
NO: 192, SEQ ID NO: 194, SEQ ID NO: 196, SEQ ID NO: 198, SEQ ID NO: 200,  
SEQ ID NO: 202, SEQ ID NO: 204, SEQ ID NO: 206, SEQ ID NO: 208, SEQ ID  
NO: 210, SEQ ID NO: 212, SEQ ID NO: 214, SEQ ID NO: 216, SEQ ID NO: 218,  
SEQ ID NO: 220, SEQ ID NO: 222, SEQ ID NO: 224, SEQ ID NO: 226, SEQ ID  
20 NO: 228, SEQ ID NO: 230, SEQ ID NO: 232, SEQ ID NO: 234, SEQ ID NO: 236,  
SEQ ID NO: 238, SEQ ID NO: 240, SEQ ID NO: 242, SEQ ID NO: 244, SEQ ID  
NO: 246, SEQ ID NO: 248, SEQ ID NO: 250, SEQ ID NO: 252, SEQ ID NO: 254,  
SEQ ID NO: 256, SEQ ID NO: 258, SEQ ID NO: 260, SEQ ID NO: 262, SEQ ID  
NO: 264, SEQ ID NO: 266, SEQ ID NO: 268, SEQ ID NO: 270, SEQ ID NO: 272,  
25 SEQ ID NO: 274, SEQ ID NO: 276, SEQ ID NO: 278, SEQ ID NO: 280, SEQ ID  
NO: 282, SEQ ID NO: 284, SEQ ID NO: 286, SEQ ID NO: 288, SEQ ID NO: 290,  
SEQ ID NO: 292, SEQ ID NO: 294, SEQ ID NO: 296, SEQ ID NO: 298, SEQ ID  
NO: 300, SEQ ID NO: 302, SEQ ID NO: 304, SEQ ID NO: 306, SEQ ID NO: 308,  
SEQ ID NO: 310, SEQ ID NO: 312, SEQ ID NO: 314, SEQ ID NO: 316, SEQ ID  
30 NO: 318, SEQ ID NO: 320, SEQ ID NO: 322, SEQ ID NO: 324, SEQ ID NO: 326,  
SEQ ID NO: 328, SEQ ID NO: 330, SEQ ID NO: 332, SEQ ID NO: 334, SEQ ID  
NO: 336, SEQ ID NO: 338, SEQ ID NO: 340, SEQ ID NO: 342, SEQ ID NO: 344,  
SEQ ID NO: 346, SEQ ID NO: 348, SEQ ID NO: 350, SEQ ID NO: 352, SEQ ID

NO: 354, SEQ ID NO: 356, SEQ ID NO: 358, SEQ ID NO: 360, SEQ ID NO: 362,  
 SEQ ID NO: 364, SEQ ID NO: 366, SEQ ID NO: 368, SEQ ID NO: 370, SEQ ID  
 NO: 372, SEQ ID NO: 374, SEQ ID NO: 376, SEQ ID NO: 378, SEQ ID NO: 380,  
 SEQ ID NO: 382, SEQ ID NO: 384, SEQ ID NO: 386, SEQ ID NO: 388, SEQ ID  
 5 NO: 390, SEQ ID NO: 392, SEQ ID NO: 394, SEQ ID NO: 396, SEQ ID NO: 398,  
 SEQ ID NO: 400, SEQ ID NO: 402, SEQ ID NO: 404, SEQ ID NO: 406, SEQ ID  
 NO: 408, SEQ ID NO: 410, SEQ ID NO: 412, SEQ ID NO: 414, SEQ ID NO: 416,  
 SEQ ID NO: 418, SEQ ID NO: 420, SEQ ID NO: 422, SEQ ID NO: 424, SEQ ID  
 NO: 426, SEQ ID NO: 428, SEQ ID NO: 430, SEQ ID NO: 432, SEQ ID NO: 434,  
 10 SEQ ID NO: 436, SEQ ID NO: 438, SEQ ID NO: 440, SEQ ID NO: 442, SEQ ID  
 NO: 444, SEQ ID NO: 446, SEQ ID NO: 448, SEQ ID NO: 450, SEQ ID NO: 452,  
 SEQ ID NO: 454, SEQ ID NO: 456, SEQ ID NO: 458, SEQ ID NO: 460, SEQ ID  
 NO: 462, SEQ ID NO: 464, SEQ ID NO: 466, SEQ ID NO: 468, SEQ ID NO: 470,  
 SEQ ID NO: 472, SEQ ID NO: 474, SEQ ID NO: 476, SEQ ID NO: 478, SEQ ID  
 15 NO: 480, SEQ ID NO: 482, SEQ ID NO: 484, SEQ ID NO: 486, SEQ ID NO: 488,  
 SEQ ID NO: 490, SEQ ID NO: 492, SEQ ID NO: 494, SEQ ID NO: 496, SEQ ID  
 NO: 498, SEQ ID NO: 500, SEQ ID NO: 502, SEQ ID NO: 504, SEQ ID NO: 506,  
 SEQ ID NO: 508, SEQ ID NO: 510 and SEQ ID NO: 512 or a nucleic acid sequence  
 having at least 80% sequence identity with a fragment thereof comprising at least 100  
 20 contiguous nucleotides thereof.

18. An isolated nucleic acid sequence that exhibits at least 85% sequence  
 identity with a nucleic acid sequence selected from the group consisting of: SEQ ID  
 NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID  
 25 NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID  
 NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID  
 NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID  
 NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID  
 NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID NO: 60, SEQ ID  
 30 NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID NO: 70, SEQ ID  
 NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 80, SEQ ID  
 NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 90, SEQ ID  
 NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID NO: 100, SEQ

ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 108, SEQ ID NO: 110,  
SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 116, SEQ ID NO: 118, SEQ ID  
NO: 120, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID NO: 128,  
SEQ ID NO: 130, SEQ ID NO: 132, SEQ ID NO: 134, SEQ ID NO: 136, SEQ ID  
5 NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, SEQ ID NO: 144, SEQ ID NO: 146,  
SEQ ID NO: 148, SEQ ID NO: 150, SEQ ID NO: 152, SEQ ID NO: 154, SEQ ID  
NO: 156, SEQ ID NO: 158, SEQ ID NO: 160, SEQ ID NO: 162, SEQ ID NO: 164,  
SEQ ID NO: 166, SEQ ID NO: 168, SEQ ID NO: 170, SEQ ID NO: 172, SEQ ID  
NO: 174, SEQ ID NO: 176, SEQ ID NO: 178, SEQ ID NO: 180, SEQ ID NO: 182,  
10 SEQ ID NO: 184, SEQ ID NO: 186, SEQ ID NO: 188, SEQ ID NO: 190, SEQ ID  
NO: 192, SEQ ID NO: 194, SEQ ID NO: 196, SEQ ID NO: 198, SEQ ID NO: 200,  
SEQ ID NO: 202, SEQ ID NO: 204, SEQ ID NO: 206, SEQ ID NO: 208, SEQ ID  
NO: 210, SEQ ID NO: 212, SEQ ID NO: 214, SEQ ID NO: 216, SEQ ID NO: 218,  
SEQ ID NO: 220, SEQ ID NO: 222, SEQ ID NO: 224, SEQ ID NO: 226, SEQ ID  
15 NO: 228, SEQ ID NO: 230, SEQ ID NO: 232, SEQ ID NO: 234, SEQ ID NO: 236,  
SEQ ID NO: 238, SEQ ID NO: 240, SEQ ID NO: 242, SEQ ID NO: 244, SEQ ID  
NO: 246, SEQ ID NO: 248, SEQ ID NO: 250, SEQ ID NO: 252, SEQ ID NO: 254,  
SEQ ID NO: 256, SEQ ID NO: 258, SEQ ID NO: 260, SEQ ID NO: 262, SEQ ID  
NO: 264, SEQ ID NO: 266, SEQ ID NO: 268, SEQ ID NO: 270, SEQ ID NO: 272,  
20 SEQ ID NO: 274, SEQ ID NO: 276, SEQ ID NO: 278, SEQ ID NO: 280, SEQ ID  
NO: 282, SEQ ID NO: 284, SEQ ID NO: 286, SEQ ID NO: 288, SEQ ID NO: 290,  
SEQ ID NO: 292, SEQ ID NO: 294, SEQ ID NO: 296, SEQ ID NO: 298, SEQ ID  
NO: 300, SEQ ID NO: 302, SEQ ID NO: 304, SEQ ID NO: 306, SEQ ID NO: 308,  
SEQ ID NO: 310, SEQ ID NO: 312, SEQ ID NO: 314, SEQ ID NO: 316, SEQ ID  
25 NO: 318, SEQ ID NO: 320, SEQ ID NO: 322, SEQ ID NO: 324, SEQ ID NO: 326,  
SEQ ID NO: 328, SEQ ID NO: 330, SEQ ID NO: 332, SEQ ID NO: 334, SEQ ID  
NO: 336, SEQ ID NO: 338, SEQ ID NO: 340, SEQ ID NO: 342, SEQ ID NO: 344,  
SEQ ID NO: 346, SEQ ID NO: 348, SEQ ID NO: 350, SEQ ID NO: 352, SEQ ID  
NO: 354, SEQ ID NO: 356, SEQ ID NO: 358, SEQ ID NO: 360, SEQ ID NO: 362,  
30 SEQ ID NO: 364, SEQ ID NO: 366, SEQ ID NO: 368, SEQ ID NO: 370, SEQ ID  
NO: 372, SEQ ID NO: 374, SEQ ID NO: 376, SEQ ID NO: 378, SEQ ID NO: 380,  
SEQ ID NO: 382, SEQ ID NO: 384, SEQ ID NO: 386, SEQ ID NO: 388, SEQ ID  
NO: 390, SEQ ID NO: 392, SEQ ID NO: 394, SEQ ID NO: 396, SEQ ID NO: 398,

SEQ ID NO: 400, SEQ ID NO: 402, SEQ ID NO: 404, SEQ ID NO: 406, SEQ ID  
NO: 408, SEQ ID NO: 410, SEQ ID NO: 412, SEQ ID NO: 414, SEQ ID NO: 416,  
SEQ ID NO: 418, SEQ ID NO: 420, SEQ ID NO: 422, SEQ ID NO: 424, SEQ ID  
NO: 426, SEQ ID NO: 428, SEQ ID NO: 430, SEQ ID NO: 432, SEQ ID NO: 434,  
5 SEQ ID NO: 436, SEQ ID NO: 438, SEQ ID NO: 440, SEQ ID NO: 442, SEQ ID  
NO: 444, SEQ ID NO: 446, SEQ ID NO: 448, SEQ ID NO: 450, SEQ ID NO: 452,  
SEQ ID NO: 454, SEQ ID NO: 456, SEQ ID NO: 458, SEQ ID NO: 460, SEQ ID  
NO: 462, SEQ ID NO: 464, SEQ ID NO: 466, SEQ ID NO: 468, SEQ ID NO: 470,  
SEQ ID NO: 472, SEQ ID NO: 474, SEQ ID NO: 476, SEQ ID NO: 478, SEQ ID  
10 NO: 480, SEQ ID NO: 482, SEQ ID NO: 484, SEQ ID NO: 486, SEQ ID NO: 488,  
SEQ ID NO: 490, SEQ ID NO: 492, SEQ ID NO: 494, SEQ ID NO: 496, SEQ ID  
NO: 498, SEQ ID NO: 500, SEQ ID NO: 502, SEQ ID NO: 504, SEQ ID NO: 506,  
SEQ ID NO: 508, SEQ ID NO: 510 and SEQ ID NO: 512 or a nucleic acid sequence  
having at least 85% sequence identity with a fragment thereof comprising at least 100  
15 contiguous nucleotides thereof.

19. An isolated nucleic acid sequence that exhibits at least 90% sequence  
identity with a nucleic acid sequence selected from the group consisting of: SEQ ID  
NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID  
20 NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID  
NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID  
NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID  
NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID  
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25 NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID NO: 70, SEQ ID  
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30 SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 116, SEQ ID NO: 118, SEQ ID  
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NO: 336, SEQ ID NO: 338, SEQ ID NO: 340, SEQ ID NO: 342, SEQ ID NO: 344,  
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NO: 354, SEQ ID NO: 356, SEQ ID NO: 358, SEQ ID NO: 360, SEQ ID NO: 362,  
25 SEQ ID NO: 364, SEQ ID NO: 366, SEQ ID NO: 368, SEQ ID NO: 370, SEQ ID  
NO: 372, SEQ ID NO: 374, SEQ ID NO: 376, SEQ ID NO: 378, SEQ ID NO: 380,  
SEQ ID NO: 382, SEQ ID NO: 384, SEQ ID NO: 386, SEQ ID NO: 388, SEQ ID  
NO: 390, SEQ ID NO: 392, SEQ ID NO: 394, SEQ ID NO: 396, SEQ ID NO: 398,  
SEQ ID NO: 400, SEQ ID NO: 402, SEQ ID NO: 404, SEQ ID NO: 406, SEQ ID  
30 NO: 408, SEQ ID NO: 410, SEQ ID NO: 412, SEQ ID NO: 414, SEQ ID NO: 416,  
SEQ ID NO: 418, SEQ ID NO: 420, SEQ ID NO: 422, SEQ ID NO: 424, SEQ ID  
NO: 426, SEQ ID NO: 428, SEQ ID NO: 430, SEQ ID NO: 432, SEQ ID NO: 434,  
SEQ ID NO: 436, SEQ ID NO: 438, SEQ ID NO: 440, SEQ ID NO: 442, SEQ ID

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 SEQ ID NO: 454, SEQ ID NO: 456, SEQ ID NO: 458, SEQ ID NO: 460, SEQ ID  
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 SEQ ID NO: 472, SEQ ID NO: 474, SEQ ID NO: 476, SEQ ID NO: 478, SEQ ID  
 5 NO: 480, SEQ ID NO: 482, SEQ ID NO: 484, SEQ ID NO: 486, SEQ ID NO: 488,  
 SEQ ID NO: 490, SEQ ID NO: 492, SEQ ID NO: 494, SEQ ID NO: 496, SEQ ID  
 NO: 498, SEQ ID NO: 500, SEQ ID NO: 502, SEQ ID NO: 504, SEQ ID NO: 506,  
 SEQ ID NO: 508, SEQ ID NO: 510 and SEQ ID NO: 512 or a nucleic acid sequence  
 having at least 90% sequence identity with a fragment thereof comprising at least 100  
 10 contiguous nucleotides thereof.

20. An isolated nucleic acid sequence that exhibits at least 95% sequence  
 identity with a nucleic acid sequence selected from the group consisting of: SEQ ID  
 NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID  
 15 NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID  
 NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID  
 NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID  
 NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID  
 NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID NO: 60, SEQ ID  
 20 NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID NO: 70, SEQ ID  
 NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 80, SEQ ID  
 NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 90, SEQ ID  
 NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID NO: 100, SEQ  
 ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 108, SEQ ID NO: 110,  
 25 SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 116, SEQ ID NO: 118, SEQ ID  
 NO: 120, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID NO: 128,  
 SEQ ID NO: 130, SEQ ID NO: 132, SEQ ID NO: 134, SEQ ID NO: 136, SEQ ID  
 NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, SEQ ID NO: 144, SEQ ID NO: 146,  
 SEQ ID NO: 148, SEQ ID NO: 150, SEQ ID NO: 152, SEQ ID NO: 154, SEQ ID  
 30 NO: 156, SEQ ID NO: 158, SEQ ID NO: 160, SEQ ID NO: 162, SEQ ID NO: 164,  
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 NO: 174, SEQ ID NO: 176, SEQ ID NO: 178, SEQ ID NO: 180, SEQ ID NO: 182,  
 SEQ ID NO: 184, SEQ ID NO: 186, SEQ ID NO: 188, SEQ ID NO: 190, SEQ ID

NO: 192, SEQ ID NO: 194, SEQ ID NO: 196, SEQ ID NO: 198, SEQ ID NO: 200,  
SEQ ID NO: 202, SEQ ID NO: 204. SEQ ID NO: 206, SEQ ID NO: 208, SEQ ID  
NO: 210, SEQ ID NO: 212, SEQ ID NO: 214, SEQ ID NO: 216, SEQ ID NO: 218,  
SEQ ID NO: 220, SEQ ID NO: 222, SEQ ID NO: 224, SEQ ID NO: 226, SEQ ID  
5 NO: 228, SEQ ID NO: 230, SEQ ID NO: 232, SEQ ID NO: 234, SEQ ID NO: 236,  
SEQ ID NO: 238, SEQ ID NO: 240, SEQ ID NO: 242, SEQ ID NO: 244, SEQ ID  
NO: 246, SEQ ID NO: 248, SEQ ID NO: 250, SEQ ID NO: 252, SEQ ID NO: 254,  
SEQ ID NO: 256, SEQ ID NO: 258, SEQ ID NO: 260, SEQ ID NO: 262, SEQ ID  
NO: 264, SEQ ID NO: 266, SEQ ID NO: 268, SEQ ID NO: 270, SEQ ID NO: 272,  
10 SEQ ID NO: 274, SEQ ID NO: 276, SEQ ID NO: 278, SEQ ID NO: 280, SEQ ID  
NO: 282, SEQ ID NO: 284, SEQ ID NO: 286, SEQ ID NO: 288, SEQ ID NO: 290,  
SEQ ID NO: 292, SEQ ID NO: 294, SEQ ID NO: 296, SEQ ID NO: 298, SEQ ID  
NO: 300, SEQ ID NO: 302, SEQ ID NO: 304, SEQ ID NO: 306, SEQ ID NO: 308,  
SEQ ID NO: 310, SEQ ID NO: 312, SEQ ID NO: 314, SEQ ID NO: 316, SEQ ID  
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20 SEQ ID NO: 364, SEQ ID NO: 366, SEQ ID NO: 368, SEQ ID NO: 370, SEQ ID  
NO: 372, SEQ ID NO: 374, SEQ ID NO: 376, SEQ ID NO: 378, SEQ ID NO: 380,  
SEQ ID NO: 382, SEQ ID NO: 384, SEQ ID NO: 386, SEQ ID NO: 388, SEQ ID  
NO: 390, SEQ ID NO: 392, SEQ ID NO: 394, SEQ ID NO: 396, SEQ ID NO: 398,  
SEQ ID NO: 400, SEQ ID NO: 402, SEQ ID NO: 404, SEQ ID NO: 406, SEQ ID  
25 NO: 408, SEQ ID NO: 410, SEQ ID NO: 412, SEQ ID NO: 414, SEQ ID NO: 416,  
SEQ ID NO: 418, SEQ ID NO: 420, SEQ ID NO: 422, SEQ ID NO: 424, SEQ ID  
NO: 426, SEQ ID NO: 428, SEQ ID NO: 430, SEQ ID NO: 432, SEQ ID NO: 434,  
SEQ ID NO: 436, SEQ ID NO: 438, SEQ ID NO: 440, SEQ ID NO: 442, SEQ ID  
NO: 444, SEQ ID NO: 446, SEQ ID NO: 448, SEQ ID NO: 450, SEQ ID NO: 452,  
30 SEQ ID NO: 454, SEQ ID NO: 456, SEQ ID NO: 458, SEQ ID NO: 460, SEQ ID  
NO: 462, SEQ ID NO: 464, SEQ ID NO: 466, SEQ ID NO: 468, SEQ ID NO: 470,  
SEQ ID NO: 472, SEQ ID NO: 474, SEQ ID NO: 476, SEQ ID NO: 478, SEQ ID  
NO: 480, SEQ ID NO: 482, SEQ ID NO: 484, SEQ ID NO: 486, SEQ ID NO: 488,

SEQ ID NO: 490, SEQ ID NO: 492, SEQ ID NO: 494, SEQ ID NO: 496, SEQ ID NO: 498, SEQ ID NO: 500, SEQ ID NO: 502, SEQ ID NO: 504, SEQ ID NO: 506, SEQ ID NO: 508, SEQ ID NO: 510 and SEQ ID NO: 512 or a nucleic acid sequence having at least 95% sequence identity with a fragment thereof comprising at least 100  
 5 contiguous nucleotides thereof.

21. An isolated nucleic acid sequence that exhibits about 96-99% sequence identity with a nucleic acid sequence encoding an olfactory receptor selected from the group consisting of: SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8,  
 10 SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58,  
 15 SEQ ID NO: 60, SEQ ID NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID NO: 70, SEQ ID NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 80, SEQ ID NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 90, SEQ ID NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID NO: 100, SEQ ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 108, SEQ ID NO: 110, SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 116, SEQ ID NO: 118, SEQ ID NO: 120, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID NO: 128, SEQ ID NO: 130, SEQ ID NO: 132, SEQ ID NO: 134, SEQ ID NO: 136, SEQ ID NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, SEQ ID NO: 144, SEQ ID NO: 146, SEQ ID NO: 148, SEQ ID NO: 150, SEQ ID NO: 152,  
 25 SEQ ID NO: 154, SEQ ID NO: 156, SEQ ID NO: 158, SEQ ID NO: 160, SEQ ID NO: 162, SEQ ID NO: 164, SEQ ID NO: 166, SEQ ID NO: 168, SEQ ID NO: 170, SEQ ID NO: 172, SEQ ID NO: 174, SEQ ID NO: 176, SEQ ID NO: 178, SEQ ID NO: 180, SEQ ID NO: 182, SEQ ID NO: 184, SEQ ID NO: 186, SEQ ID NO: 188, SEQ ID NO: 190, SEQ ID NO: 192, SEQ ID NO: 194, SEQ ID NO: 196, SEQ ID NO: 198, SEQ ID NO: 200, SEQ ID NO: 202, SEQ ID NO: 204, SEQ ID NO: 206, SEQ ID NO: 208, SEQ ID NO: 210, SEQ ID NO: 212, SEQ ID NO: 214, SEQ ID NO: 216, SEQ ID NO: 218, SEQ ID NO: 220, SEQ ID NO: 222, SEQ ID NO: 224, SEQ ID NO: 226, SEQ ID NO: 228, SEQ ID NO: 230, SEQ ID NO: 232, SEQ ID



NO: 234, SEQ ID NO: 236, SEQ ID NO: 238, SEQ. ID NO. 240, SEQ ID NO: 242,  
SEQ ID NO: 244, SEQ ID NO: 246, SEQ ID NO: 248, SEQ ID NO: 250, SEQ ID  
NO: 252, SEQ ID NO: 254, SEQ ID NO: 256, SEQ ID NO: 258, SEQ ID NO: 260,  
SEQ ID NO: 262, SEQ ID NO: 264, SEQ ID NO: 266, SEQ ID NO: 268, SEQ ID  
5 NO: 270, SEQ ID NO: 272, SEQ ID NO: 274, SEQ ID NO: 276, SEQ ID NO: 278,  
SEQ ID NO: 280, SEQ ID NO: 282, SEQ ID NO: 284, SEQ ID NO: 286, SEQ ID  
NO: 288, SEQ ID NO: 290, SEQ ID NO: 292, SEQ ID NO: 294, SEQ ID NO: 296,  
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10 SEQ ID NO: 316, SEQ ID NO: 318, SEQ ID NO: 320, SEQ ID NO: 322, SEQ ID  
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15 NO: 360, SEQ ID NO: 362, SEQ ID NO: 364, SEQ ID NO: 366, SEQ ID NO: 368,  
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20 SEQ ID NO: 406, SEQ ID NO: 408, SEQ ID NO: 410, SEQ ID NO: 412, SEQ ID  
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SEQ ID NO: 442, SEQ ID NO: 444, SEQ ID NO: 446, SEQ ID NO: 448, SEQ ID  
25 NO: 450, SEQ ID NO: 452, SEQ ID NO: 454, SEQ ID NO: 456, SEQ ID NO: 458,  
SEQ ID NO: 460, SEQ ID NO: 462, SEQ ID NO: 464, SEQ ID NO: 466, SEQ ID  
NO: 468, SEQ ID NO: 470, SEQ ID NO: 472, SEQ ID NO: 474, SEQ ID NO: 476,  
SEQ ID NO: 478, SEQ ID NO: 480, SEQ ID NO: 482, SEQ ID NO: 484, SEQ ID  
NO: 486, SEQ ID NO: 488, SEQ ID NO: 490, SEQ ID NO: 492, SEQ ID NO: 494,  
30 SEQ ID NO: 496, SEQ ID NO: 498, SEQ ID NO: 500, SEQ ID NO: 502, SEQ ID  
NO: 504, SEQ ID NO: 506, SEQ ID NO: 508, SEQ ID NO: 510 and SEQ ID NO: 512  
or a fragment having at least 96-99% sequence identity with a fragment thereof  
comprising at least 100 contiguous nucleotides thereof.

22. A nucleic acid sequence which encodes for a functional olfactory receptor polypeptide, wherein said nucleic acid sequence comprises a portion which is at least 100 nucleotides in length and exhibits at least 40% sequence identity with at least 100 contiguous nucleotides of a portion of an olfactory receptor encoding a nucleic acid sequence selected from the group consisting of: SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID NO: 60, SEQ ID NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID NO: 70, SEQ ID NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 80, SEQ ID NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 90, SEQ ID NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID NO: 100, SEQ ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 108, SEQ ID NO: 110, SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 116, SEQ ID NO: 118, SEQ ID NO: 120, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID NO: 128, SEQ ID NO: 130, SEQ ID NO: 132, SEQ ID NO: 134, SEQ ID NO: 136, SEQ ID NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, SEQ ID NO: 144, SEQ ID NO: 146, SEQ ID NO: 148, SEQ ID NO: 150, SEQ ID NO: 152, SEQ ID NO: 154, SEQ ID NO: 156, SEQ ID NO: 158, SEQ ID NO: 160, SEQ ID NO: 162, SEQ ID NO: 164, SEQ ID NO: 166, SEQ ID NO: 168, SEQ ID NO: 170, SEQ ID NO: 172, SEQ ID NO: 174, SEQ ID NO: 176, SEQ ID NO: 178, SEQ ID NO: 180, SEQ ID NO: 182, SEQ ID NO: 184, SEQ ID NO: 186, SEQ ID NO: 188, SEQ ID NO: 190, SEQ ID NO: 192, SEQ ID NO: 194, SEQ ID NO: 196, SEQ ID NO: 198, SEQ ID NO: 200, SEQ ID NO: 202, SEQ ID NO: 204, SEQ ID NO: 206, SEQ ID NO: 208, SEQ ID NO: 210, SEQ ID NO: 212, SEQ ID NO: 214, SEQ ID NO: 216, SEQ ID NO: 218, SEQ ID NO: 220, SEQ ID NO: 222, SEQ ID NO: 224, SEQ ID NO: 226, SEQ ID NO: 228, SEQ ID NO: 230, SEQ ID NO: 232, SEQ ID NO: 234, SEQ ID NO: 236, SEQ ID NO: 238, SEQ ID NO: 240, SEQ ID NO: 242, SEQ ID NO: 244, SEQ ID NO: 246, SEQ ID NO: 248, SEQ ID NO: 250, SEQ ID NO: 252, SEQ ID NO: 254, SEQ ID NO: 256,

SEQ ID NO: 258, SEQ ID NO: 260, SEQ ID NO: 262, SEQ ID NO: 264, SEQ ID NO: 266, SEQ ID NO: 268, SEQ ID NO: 270, SEQ ID NO: 272, SEQ ID NO: 274, SEQ ID NO: 276, SEQ ID NO: 278, SEQ ID NO: 280, SEQ ID NO: 282, SEQ ID NO: 284, SEQ ID NO: 286, SEQ ID NO: 288, SEQ ID NO: 290, SEQ ID NO: 292, SEQ ID NO: 294, SEQ ID NO: 296, SEQ ID NO: 298, SEQ ID NO: 300, SEQ ID NO: 302, SEQ ID NO: 304, SEQ ID NO: 306, SEQ ID NO: 308, SEQ ID NO: 310, SEQ ID NO: 312, SEQ ID NO: 314, SEQ ID NO: 316, SEQ ID NO: 318, SEQ ID NO: 320, SEQ ID NO: 322, SEQ ID NO: 324, SEQ ID NO: 326, SEQ ID NO: 328, SEQ ID NO: 330, SEQ ID NO: 332, SEQ ID NO: 334, SEQ ID NO: 336, SEQ ID NO: 338, SEQ ID NO: 340, SEQ ID NO: 342, SEQ ID NO: 344, SEQ ID NO: 346, SEQ ID NO: 348, SEQ ID NO: 350, SEQ ID NO: 352, SEQ ID NO: 354, SEQ ID NO: 356, SEQ ID NO: 358, SEQ ID NO: 360, SEQ ID NO: 362, SEQ ID NO: 364, SEQ ID NO: 366, SEQ ID NO: 368, SEQ ID NO: 370, SEQ ID NO: 372, SEQ ID NO: 374, SEQ ID NO: 376, SEQ ID NO: 378, SEQ ID NO: 380, SEQ ID NO: 382, SEQ ID NO: 384, SEQ ID NO: 386, SEQ ID NO: 388, SEQ ID NO: 390, SEQ ID NO: 392, SEQ ID NO: 394, SEQ ID NO: 396, SEQ ID NO: 398, SEQ ID NO: 400, SEQ ID NO: 402, SEQ ID NO: 404, SEQ ID NO: 406, SEQ ID NO: 408, SEQ ID NO: 410, SEQ ID NO: 412, SEQ ID NO: 414, SEQ ID NO: 416, SEQ ID NO: 418, SEQ ID NO: 420, SEQ ID NO: 422, SEQ ID NO: 424, SEQ ID NO: 426, SEQ ID NO: 428, SEQ ID NO: 430, SEQ ID NO: 432, SEQ ID NO: 434, SEQ ID NO: 436, SEQ ID NO: 438, SEQ ID NO: 440, SEQ ID NO: 442, SEQ ID NO: 444, SEQ ID NO: 446, SEQ ID NO: 448, SEQ ID NO: 450, SEQ ID NO: 452, SEQ ID NO: 454, SEQ ID NO: 456, SEQ ID NO: 458, SEQ ID NO: 460, SEQ ID NO: 462, SEQ ID NO: 464, SEQ ID NO: 466, SEQ ID NO: 468, SEQ ID NO: 470, SEQ ID NO: 472, SEQ ID NO: 474, SEQ ID NO: 476, SEQ ID NO: 478, SEQ ID NO: 480, SEQ ID NO: 482, SEQ ID NO: 484, SEQ ID NO: 486, SEQ ID NO: 488, SEQ ID NO: 490, SEQ ID NO: 492, SEQ ID NO: 494, SEQ ID NO: 496, SEQ ID NO: 498, SEQ ID NO: 500, SEQ ID NO: 502, SEQ ID NO: 504, SEQ ID NO: 506, SEQ ID NO: 508, SEQ ID NO: 510 and SEQ ID NO: 512.

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23. The nucleic acid sequence of Claim 22 which is a chimeric nucleic acid sequence, wherein said nucleic acid sequence is produced by combining portions of at least two different G protein-coupled receptors.

24. The chimeric nucleic acid sequence of Claim 23 wherein said two different G protein-coupled receptors are olfactory receptors.

5 25. The chimeric nucleic acid sequence of Claim 23 wherein said chimeric sequence contains at least 200 contiguous nucleotides that are at least 40% identical to a portion of one of said olfactory receptor encoding nucleic acid sequences.

10 26. An isolated nucleic acid sequence according to Claim 1, wherein said isolated nucleic acid sequence is directly or indirectly attached to a nucleic acid sequence that encodes a detectable polypeptide.

27. The nucleic acid sequence of Claim 26, wherein said detectable polypeptide is green fluorescent protein, or a fragment or variant thereof.

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28. An isolated nucleic acid sequence which encodes a polypeptide that exhibits at least 40% sequence identity with a polypeptide selected from the group consisting of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID

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29. An isolated nucleic acid sequence which encodes a polypeptide that exhibits at least 50% sequence identity with a polypeptide selected from the group consisting of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, 25 SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID NO: 159, SEQ ID NO: 161, 30 SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID

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NO: 477, SEQ ID NO: 479, SEQ ID NO: 481, SEQ ID NO: 483, SEQ ID NO: 485,

SEQ ID NO: 487, SEQ ID NO: 489, SEQ ID NO: 491, SEQ ID NO: 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511 or a fragment thereof comprising at least 40 contiguous amino acids thereof that optionally is directly or indirectly attached to a sequence that facilitates the expression and/or translocation of said polypeptide on the surface of a cell.

30. An isolated nucleic acid sequence which encodes a polypeptide that exhibits at least 60% sequence identity with a polypeptide selected from the group consisting of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID NO: 191, SEQ ID NO: 193, SEQ ID NO: 195, SEQ ID NO: 197, SEQ ID NO: 199, SEQ ID NO: 201, SEQ ID NO: 203, SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID NO: 213, SEQ ID NO: 215, SEQ ID NO: 217, SEQ ID NO: 219, SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID



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NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID NO: 503,  
SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511 or a  
fragment thereof comprising at least 40 contiguous amino acids thereof that optionally

is directly or indirectly attached to a sequence that facilitates the expression and/or translocation of said polypeptide on the surface of a cell.

31. An isolated nucleic acid sequence which encodes a polypeptide that  
5 exhibits at least 70% sequence identity with a polypeptide selected from the group  
consisting of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID  
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10 NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID  
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SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511 or a  
fragment thereof comprising at least 40 contiguous amino acids thereof that optionally  
30 is directly or indirectly attached to a sequence that facilitates the expression and/or  
translocation of said polypeptide on the surface of a cell.

32. An isolated nucleic acid sequence which encodes a polypeptide that exhibits at least 80% sequence identity with a polypeptide selected from the group consisting of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID NO: 191, SEQ ID NO: 193, SEQ ID NO: 195, SEQ ID NO: 197, SEQ ID NO: 199, SEQ ID NO: 201, SEQ ID NO: 203, SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID NO: 213, SEQ ID NO: 215, SEQ ID NO: 217, SEQ ID NO: 219, SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID NO: 225, SEQ ID NO: 227, SEQ ID NO: 229, SEQ ID NO: 231, SEQ ID NO: 233, SEQ ID NO: 235, SEQ ID NO: 237, SEQ ID NO: 239, SEQ ID NO: 241, SEQ ID NO: 243, SEQ ID NO: 245, SEQ ID NO: 247, SEQ ID NO: 249, SEQ ID NO: 251, SEQ ID NO: 253, SEQ ID NO: 255, SEQ ID NO: 257, SEQ ID NO: 259, SEQ ID NO: 261, SEQ ID NO: 263, SEQ ID NO: 265, SEQ ID NO: 267, SEQ ID NO: 269, SEQ ID NO: 271, SEQ ID NO: 273, SEQ ID NO: 275, SEQ ID NO: 277, SEQ ID NO: 279, SEQ ID NO: 281, SEQ ID NO: 283, SEQ ID NO: 285, SEQ ID NO: 287,

SEQ ID NO: 289, SEQ ID NO: 291, SEQ ID NO: 293, SEQ ID NO: 295, SEQ ID NO: 297, SEQ ID NO: 299, SEQ ID NO: 301, SEQ ID NO: 303, SEQ ID NO: 305, SEQ ID NO: 307, SEQ ID NO: 309, SEQ ID NO: 311, SEQ ID NO: 313, SEQ ID NO: 315, SEQ ID NO: 317, SEQ ID NO: 319, SEQ ID NO: 321, SEQ ID NO: 323, 5 SEQ ID NO: 325, SEQ ID NO: 327, SEQ ID NO: 329, SEQ ID NO: 331, SEQ ID NO: 333, SEQ ID NO: 335, SEQ ID NO: 337, SEQ ID NO: 339, SEQ ID NO: 341, SEQ ID NO: 343, SEQ ID NO: 345, SEQ ID NO: 347, SEQ ID NO: 349, SEQ ID NO: 351, SEQ ID NO: 353, SEQ ID NO: 355, SEQ ID NO: 357, SEQ ID NO: 359, SEQ ID NO: 361, SEQ ID NO: 363, SEQ ID NO: 365, SEQ ID NO: 367, SEQ ID NO: 369, SEQ ID NO: 371, SEQ ID NO: 373, SEQ ID NO: 375, SEQ ID NO: 377, 10 SEQ ID NO: 379, SEQ ID NO: 381, SEQ ID NO: 383, SEQ ID NO: 385, SEQ ID NO: 387, SEQ ID NO: 389, SEQ ID NO: 391, SEQ ID NO: 393, SEQ ID NO: 395, SEQ ID NO: 397, SEQ ID NO: 399, SEQ ID NO: 401, SEQ ID NO: 403, SEQ ID NO: 405, SEQ ID NO: 407, SEQ ID NO: 409, SEQ ID NO: 411, SEQ ID NO: 413, 15 SEQ ID NO: 415, SEQ ID NO: 417, SEQ ID NO: 419, SEQ ID NO: 421, SEQ ID NO: 423, SEQ ID NO: 425, SEQ ID NO: 427, SEQ ID NO: 429, SEQ ID NO: 431, SEQ ID NO: 433, SEQ ID NO: 435, SEQ ID NO: 437, SEQ ID NO: 439, SEQ ID NO: 441, SEQ ID NO: 443, SEQ ID NO: 445, SEQ ID NO: 447, SEQ ID NO: 449, SEQ ID NO: 451, SEQ ID NO: 453, SEQ ID NO: 455, SEQ ID NO: 457, SEQ ID NO: 459, SEQ ID NO: 461, SEQ ID NO: 463, SEQ ID NO: 465, SEQ ID NO: 467, 20 SEQ ID NO: 469, SEQ ID NO: 471, SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID NO: 477, SEQ ID NO: 479, SEQ ID NO: 481, SEQ ID NO: 483, SEQ ID NO: 485, SEQ ID NO: 487, SEQ ID NO: 489, SEQ ID NO: 491, SEQ ID NO: 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID NO: 503, 25 SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511 or a fragment thereof comprising at least 40 contiguous amino acids thereof that optionally is directly or indirectly attached to a sequence that facilitates the expression and/or translocation of said polypeptide on the surface of a cell.

30           33.    An isolated nucleic acid sequence which encodes a polypeptide that exhibits at least 85% sequence identity with a polypeptide selected from the group consisting of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID

NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID  
NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID  
NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID  
NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID  
5 NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID  
NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID  
NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID  
NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID  
NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107,  
10 SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID  
NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125,  
SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID  
NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143,  
SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID  
15 NO: 153, SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID NO: 159, SEQ ID NO: 161,  
SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID  
NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID NO: 177, SEQ ID NO: 179,  
SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID  
NO: 189, SEQ ID NO: 191, SEQ ID NO: 193, SEQ ID NO: 195, SEQ ID NO: 197,  
20 SEQ ID NO: 199, SEQ ID NO: 201, SEQ ID NO: 203, SEQ ID NO: 205, SEQ ID  
NO: 207, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID NO: 213, SEQ ID NO: 215,  
SEQ ID NO: 217, SEQ ID NO: 219, SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID  
NO: 225, SEQ ID NO: 227, SEQ ID NO: 229, SEQ ID NO: 231, SEQ ID NO: 233,  
SEQ ID NO: 235, SEQ ID NO: 237, SEQ ID NO: 239, SEQ ID NO: 241, SEQ ID  
25 NO: 243, SEQ ID NO: 245, SEQ ID NO: 247, SEQ ID NO: 249, SEQ ID NO: 251,  
SEQ ID NO: 253, SEQ ID NO: 255, SEQ ID NO: 257, SEQ ID NO: 259, SEQ ID  
NO: 261, SEQ ID NO: 263, SEQ ID NO: 265, SEQ ID NO: 267, SEQ ID NO: 269,  
SEQ ID NO: 271, SEQ ID NO: 273, SEQ ID NO: 275, SEQ ID NO: 277, SEQ ID  
NO: 279, SEQ ID NO: 281, SEQ ID NO: 283, SEQ ID NO: 285, SEQ ID NO: 287,  
30 SEQ ID NO: 289, SEQ ID NO: 291, SEQ ID NO: 293, SEQ ID NO: 295, SEQ ID  
NO: 297, SEQ ID NO: 299, SEQ ID NO: 301, SEQ ID NO: 303, SEQ ID NO: 305,  
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NO: 315, SEQ ID NO: 317, SEQ ID NO: 319, SEQ ID NO: 321, SEQ ID NO: 323,

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25

34. An isolated nucleic acid sequence which encodes a polypeptide that exhibits at least 90% sequence identity with a polypeptide selected from the group consisting of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID

NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID  
NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID  
NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID  
NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID  
5 NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107,  
SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID  
NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125,  
SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID  
NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143,  
10 SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID  
NO: 153, SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID NO: 159, SEQ ID NO: 161,  
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NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID NO: 177, SEQ ID NO: 179,  
SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID  
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NO: 207, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID NO: 213, SEQ ID NO: 215,  
SEQ ID NO: 217, SEQ ID NO: 219, SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID  
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20 SEQ ID NO: 235, SEQ ID NO: 237, SEQ ID NO: 239, SEQ ID NO: 241, SEQ ID  
NO: 243, SEQ ID NO: 245, SEQ ID NO: 247, SEQ ID NO: 249, SEQ ID NO: 251,  
SEQ ID NO: 253, SEQ ID NO: 255, SEQ ID NO: 257, SEQ ID NO: 259, SEQ ID  
NO: 261, SEQ ID NO: 263, SEQ ID NO: 265, SEQ ID NO: 267, SEQ ID NO: 269,  
SEQ ID NO: 271, SEQ ID NO: 273, SEQ ID NO: 275, SEQ ID NO: 277, SEQ ID  
25 NO: 279, SEQ ID NO: 281, SEQ ID NO: 283, SEQ ID NO: 285, SEQ ID NO: 287,  
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NO: 315, SEQ ID NO: 317, SEQ ID NO: 319, SEQ ID NO: 321, SEQ ID NO: 323,  
30 SEQ ID NO: 325, SEQ ID NO: 327, SEQ ID NO: 329, SEQ ID NO: 331, SEQ ID  
NO: 333, SEQ ID NO: 335, SEQ ID NO: 337, SEQ ID NO: 339, SEQ ID NO: 341,  
SEQ ID NO: 343, SEQ ID NO: 345, SEQ ID NO: 347, SEQ ID NO: 349, SEQ ID  
NO: 351, SEQ ID NO: 353, SEQ ID NO: 355, SEQ ID NO: 357, SEQ ID NO: 359,



SEQ ID NO: 361, SEQ ID NO: 363, SEQ ID NO: 365, SEQ ID NO: 367, SEQ ID NO: 369, SEQ ID NO: 371, SEQ ID NO: 373, SEQ ID NO: 375, SEQ ID NO: 377, SEQ ID NO: 379, SEQ ID NO: 381, SEQ ID NO: 383, SEQ ID NO: 385, SEQ ID NO: 387, SEQ ID NO: 389, SEQ ID NO: 391, SEQ ID NO: 393, SEQ ID NO: 395, 5 SEQ ID NO: 397, SEQ ID NO: 399, SEQ ID NO: 401, SEQ ID NO: 403, SEQ ID NO: 405, SEQ ID NO: 407, SEQ ID NO: 409, SEQ ID NO: 411, SEQ ID NO: 413, SEQ ID NO: 415, SEQ ID NO: 417, SEQ ID NO: 419, SEQ ID NO: 421, SEQ ID NO: 423, SEQ ID NO: 425, SEQ ID NO: 427, SEQ ID NO: 429, SEQ ID NO: 431, SEQ ID NO: 433, SEQ ID NO: 435, SEQ ID NO: 437, SEQ ID NO: 439, SEQ ID NO: 441, SEQ ID NO: 443, SEQ ID NO: 445, SEQ ID NO: 447, SEQ ID NO: 449, SEQ ID NO: 451, SEQ ID NO: 453, SEQ ID NO: 455, SEQ ID NO: 457, SEQ ID NO: 459, SEQ ID NO: 461, SEQ ID NO: 463, SEQ ID NO: 465, SEQ ID NO: 467, SEQ ID NO: 469, SEQ ID NO: 471, SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID NO: 477, SEQ ID NO: 479, SEQ ID NO: 481, SEQ ID NO: 483, SEQ ID NO: 485, 15 SEQ ID NO: 487, SEQ ID NO: 489, SEQ ID NO: 491, SEQ ID NO: 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511 or a fragment thereof comprising at least 40 contiguous amino acids thereof that optionally is directly or indirectly attached to a sequence that facilitates the expression and/or 20 translocation of said polypeptide on the surface of a cell.

35. An isolated nucleic acid sequence which encodes a polypeptide that exhibits about 90-99% sequence identity with a polypeptide selected from the group consisting of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID

NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107,  
SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID  
NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125,  
SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID  
5 NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143,  
SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID  
NO: 153, SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID NO: 159, SEQ ID NO: 161,  
SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID  
NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID NO: 177, SEQ ID NO: 179,  
10 SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID  
NO: 189, SEQ ID NO: 191, SEQ ID NO: 193, SEQ ID NO: 195, SEQ ID NO: 197,  
SEQ ID NO: 199, SEQ ID NO: 201, SEQ ID NO: 203, SEQ ID NO: 205, SEQ ID  
NO: 207, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID NO: 213, SEQ ID NO: 215,  
SEQ ID NO: 217, SEQ ID NO: 219, SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID  
15 NO: 225, SEQ ID NO: 227, SEQ ID NO: 229, SEQ ID NO: 231, SEQ ID NO: 233,  
SEQ ID NO: 235, SEQ ID NO: 237, SEQ ID NO: 239, SEQ ID NO: 241, SEQ ID  
NO: 243, SEQ ID NO: 245, SEQ ID NO: 247, SEQ ID NO: 249, SEQ ID NO: 251,  
SEQ ID NO: 253, SEQ ID NO: 255, SEQ ID NO: 257, SEQ ID NO: 259, SEQ ID  
NO: 261, SEQ ID NO: 263, SEQ ID NO: 265, SEQ ID NO: 267, SEQ ID NO: 269,  
20 SEQ ID NO: 271, SEQ ID NO: 273, SEQ ID NO: 275, SEQ ID NO: 277, SEQ ID  
NO: 279, SEQ ID NO: 281, SEQ ID NO: 283, SEQ ID NO: 285, SEQ ID NO: 287,  
SEQ ID NO: 289, SEQ ID NO: 291, SEQ ID NO: 293, SEQ ID NO: 295, SEQ ID  
NO: 297, SEQ ID NO: 299, SEQ ID NO: 301, SEQ ID NO: 303, SEQ ID NO: 305,  
SEQ ID NO: 307, SEQ ID NO: 309, SEQ ID NO: 311, SEQ ID NO: 313, SEQ ID  
25 NO: 315, SEQ ID NO: 317, SEQ ID NO: 319, SEQ ID NO: 321, SEQ ID NO: 323,  
SEQ ID NO: 325, SEQ ID NO: 327, SEQ ID NO: 329, SEQ ID NO: 331, SEQ ID  
NO: 333, SEQ ID NO: 335, SEQ ID NO: 337, SEQ ID NO: 339, SEQ ID NO: 341,  
SEQ ID NO: 343, SEQ ID NO: 345, SEQ ID NO: 347, SEQ ID NO: 349, SEQ ID  
NO: 351, SEQ ID NO: 353, SEQ ID NO: 355, SEQ ID NO: 357, SEQ ID NO: 359,  
30 SEQ ID NO: 361, SEQ ID NO: 363, SEQ ID NO: 365, SEQ ID NO: 367, SEQ ID  
NO: 369, SEQ ID NO: 371, SEQ ID NO: 373, SEQ ID NO: 375, SEQ ID NO: 377,  
SEQ ID NO: 379, SEQ ID NO: 381, SEQ ID NO: 383, SEQ ID NO: 385, SEQ ID  
NO: 387, SEQ ID NO: 389, SEQ ID NO: 391, SEQ ID NO: 393, SEQ ID NO: 395,

SEQ ID NO: 397, SEQ ID NO: 399, SEQ ID NO: 401, SEQ ID NO: 403, SEQ ID NO: 405, SEQ ID NO: 407, SEQ ID NO: 409, SEQ ID NO: 411, SEQ ID NO: 413, SEQ ID NO: 415, SEQ ID NO: 417, SEQ ID NO: 419, SEQ ID NO: 421, SEQ ID NO: 423, SEQ ID NO: 425, SEQ ID NO: 427, SEQ ID NO: 429, SEQ ID NO: 431, SEQ ID NO: 433, SEQ ID NO: 435, SEQ ID NO: 437, SEQ ID NO: 439, SEQ ID NO: 441, SEQ ID NO: 443, SEQ ID NO: 445, SEQ ID NO: 447, SEQ ID NO: 449, SEQ ID NO: 451, SEQ ID NO: 453, SEQ ID NO: 455, SEQ ID NO: 457, SEQ ID NO: 459, SEQ ID NO: 461, SEQ ID NO: 463, SEQ ID NO: 465, SEQ ID NO: 467, SEQ ID NO: 469, SEQ ID NO: 471, SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID NO: 477, SEQ ID NO: 479, SEQ ID NO: 481, SEQ ID NO: 483, SEQ ID NO: 485, SEQ ID NO: 487, SEQ ID NO: 489, SEQ ID NO: 491, SEQ ID NO: 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511 or a fragment thereof comprising at least 40 contiguous amino acids thereof that optionally is directly or indirectly attached to a sequence that facilitates the expression and/or translocation of said polypeptide on the surface of a cell.

36. The isolated nucleic acid sequence according to Claim 26, wherein said isolated nucleic acid sequence is operably linked to a constitutive promoter.

20

37. The isolated nucleic acid sequence according to Claim 1, wherein said isolated nucleic acid sequence is operably linked to a regulatable promoter.

38. The isolated nucleic acid sequence of Claim 1, wherein said isolated nucleic acid sequence is directly or indirectly attached to a nucleic acid sequence encoding a mammalian rhodopsin polypeptide or a fragment thereof.

39. An isolated nucleic acid molecule comprising a nucleotide sequence that encodes a fragment of at least 60 contiguous amino acids of a polypeptide having an amino acid sequence selected from the group consisting of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID

NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID  
NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID  
NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID  
NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID  
5 NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID  
NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID  
NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ  
ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111,  
SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID  
10 NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129,  
SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID  
NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147,  
SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID NO: 155, SEQ ID  
NO: 157, SEQ ID NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165,  
15 SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID  
NO: 175, SEQ ID NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID NO: 183,  
SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID NO: 191, SEQ ID  
NO: 193, SEQ ID NO: 195, SEQ ID NO: 197, SEQ ID NO: 199, SEQ ID NO: 201,  
SEQ ID NO: 203, SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID NO: 209, SEQ ID  
20 NO: 211, SEQ ID NO: 213, SEQ ID NO: 215, SEQ ID NO: 217, SEQ ID NO: 219,  
SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID NO: 225, SEQ ID NO: 227, SEQ ID  
NO: 229, SEQ ID NO: 231, SEQ ID NO: 233, SEQ ID NO: 235, SEQ ID NO: 237,  
SEQ ID NO: 239, SEQ ID NO: 241, SEQ ID NO: 243, SEQ ID NO: 245, SEQ ID  
NO: 247, SEQ ID NO: 249, SEQ ID NO: 251, SEQ ID NO: 253, SEQ ID NO: 255,  
25 SEQ ID NO: 257, SEQ ID NO: 259, SEQ ID NO: 261, SEQ ID NO: 263, SEQ ID  
NO: 265, SEQ ID NO: 267, SEQ ID NO: 269, SEQ ID NO: 271, SEQ ID NO: 273,  
SEQ ID NO: 275, SEQ ID NO: 277, SEQ ID NO: 279, SEQ ID NO: 281, SEQ ID  
NO: 283, SEQ ID NO: 285, SEQ ID NO: 287, SEQ ID NO: 289, SEQ ID NO: 291,  
SEQ ID NO: 293, SEQ ID NO: 295, SEQ ID NO: 297, SEQ ID NO: 299, SEQ ID  
30 NO: 301, SEQ ID NO: 303, SEQ ID NO: 305, SEQ ID NO: 307, SEQ ID NO: 309,  
SEQ ID NO: 311, SEQ ID NO: 313, SEQ ID NO: 315, SEQ ID NO: 317, SEQ ID  
NO: 319, SEQ ID NO: 321, SEQ ID NO: 323, SEQ ID NO: 325, SEQ ID NO: 327,  
SEQ ID NO: 329, SEQ ID NO: 331, SEQ ID NO: 333, SEQ ID NO: 335, SEQ ID

NO: 337, SEQ ID NO: 339, SEQ ID NO: 341, SEQ ID NO: 343, SEQ ID NO: 345,  
SEQ ID NO: 347, SEQ ID NO: 349, SEQ ID NO: 351, SEQ ID NO: 353, SEQ ID  
NO: 355, SEQ ID NO: 357, SEQ ID NO: 359, SEQ ID NO: 361, SEQ ID NO: 363,  
SEQ ID NO: 365, SEQ ID NO: 367, SEQ ID NO: 369, SEQ ID NO: 371, SEQ ID  
5 NO: 373, SEQ ID NO: 375, SEQ ID NO: 377, SEQ ID NO: 379, SEQ ID NO: 381,  
SEQ ID NO: 383, SEQ ID NO: 385, SEQ ID NO: 387, SEQ ID NO: 389, SEQ ID  
NO: 391, SEQ ID NO: 393, SEQ ID NO: 395, SEQ ID NO: 397, SEQ ID NO: 399,  
SEQ ID NO: 401, SEQ ID NO: 403, SEQ ID NO: 405, SEQ ID NO: 407, SEQ ID  
NO: 409, SEQ ID NO: 411, SEQ ID NO: 413, SEQ ID NO: 415, SEQ ID NO: 417,  
10 SEQ ID NO: 419, SEQ ID NO: 421, SEQ ID NO: 423, SEQ ID NO: 425, SEQ ID  
NO: 427, SEQ ID NO: 429, SEQ ID NO: 431, SEQ ID NO: 433, SEQ ID NO: 435,  
SEQ ID NO: 437, SEQ ID NO: 439, SEQ ID NO: 441, SEQ ID NO: 443, SEQ ID  
NO: 445, SEQ ID NO: 447, SEQ ID NO: 449, SEQ ID NO: 451, SEQ ID NO: 453,  
SEQ ID NO: 455, SEQ ID NO: 457, SEQ ID NO: 459, SEQ ID NO: 461, SEQ ID  
15 NO: 463, SEQ ID NO: 465, SEQ ID NO: 467, SEQ ID NO: 469, SEQ ID NO: 471,  
SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID NO: 477, SEQ ID NO: 479, SEQ ID  
NO: 481, SEQ ID NO: 483, SEQ ID NO: 485, SEQ ID NO: 487, SEQ ID NO: 489,  
SEQ ID NO: 491, SEQ ID NO: 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID  
NO: 499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507,  
20 SEQ ID NO: 509, and SEQ ID NO: 511.

40. The isolated nucleic acid molecule of Claim 39, wherein the nucleotide  
sequence encodes at least 100 amino acids.

25 41. The isolated nucleic acid molecule of Claim 39, wherein the nucleotide  
sequence encodes at least 150 amino acids.

42. The isolated nucleic acid molecule of Claim 39, wherein the nucleotide  
sequence encodes at least 200 amino acids.

30

43. The isolated nucleic acid molecule of Claim 39, wherein the nucleotide  
sequence encodes at least 250 amino acids.

44. The isolated nucleic acid molecule of Claim 39, wherein the polypeptide is an olfactory G protein-coupled receptor.

45. The isolated nucleic acid molecule of Claim 39, wherein the expression  
5 product binds an odorant.

46. The isolated nucleic acid molecule of Claim 1 comprising a nucleotide sequence selected from the group consisting of: SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID NO: 52, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 58, SEQ ID NO: 60, SEQ ID NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID NO: 70, SEQ ID NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 80, SEQ ID NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 90, SEQ ID NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID NO: 100, SEQ ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 108, SEQ ID NO: 110, SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 116, SEQ ID NO: 118, SEQ ID NO: 120, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID NO: 128, SEQ ID NO: 130, SEQ ID NO: 132, SEQ ID NO: 134, SEQ ID NO: 136, SEQ ID NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, SEQ ID NO: 144, SEQ ID NO: 146, SEQ ID NO: 148, SEQ ID NO: 150, SEQ ID NO: 152, SEQ ID NO: 154, SEQ ID NO: 156, SEQ ID NO: 158, SEQ ID NO: 160, SEQ ID NO: 162, SEQ ID NO: 164, SEQ ID NO: 166, SEQ ID NO: 168, SEQ ID NO: 170, SEQ ID NO: 172, SEQ ID NO: 174, SEQ ID NO: 176, SEQ ID NO: 178, SEQ ID NO: 180, SEQ ID NO: 182, SEQ ID NO: 184, SEQ ID NO: 186, SEQ ID NO: 188, SEQ ID NO: 190, SEQ ID NO: 192, SEQ ID NO: 194, SEQ ID NO: 196, SEQ ID NO: 198, SEQ ID NO: 200, SEQ ID NO: 202, SEQ ID NO: 204, SEQ ID NO: 206, SEQ ID NO: 208, SEQ ID NO: 210, SEQ ID NO: 212, SEQ ID NO: 214, SEQ ID NO: 216, SEQ ID NO: 218, SEQ ID NO: 220, SEQ ID NO: 222, SEQ ID NO: 224, SEQ ID NO: 226, SEQ ID NO: 228, SEQ ID NO: 230, SEQ ID NO: 232, SEQ ID NO: 234, SEQ ID NO: 236, SEQ ID NO: 238, SEQ ID NO: 240,

SEQ ID NO: 242, SEQ ID NO: 244, SEQ ID NO: 246, SEQ ID NO: 248, SEQ ID  
NO: 250, SEQ ID NO: 252, SEQ ID NO: 254, SEQ ID NO: 256, SEQ ID NO: 258,  
SEQ ID NO: 260, SEQ ID NO: 262, SEQ ID NO: 264, SEQ ID NO: 266, SEQ ID  
NO: 268, SEQ ID NO: 270, SEQ ID NO: 272, SEQ ID NO: 274, SEQ ID NO: 276,  
5 SEQ ID NO: 278, SEQ ID NO: 280, SEQ ID NO: 282, SEQ ID NO: 284, SEQ ID  
NO: 286, SEQ ID NO: 288, SEQ ID NO: 290, SEQ ID NO: 292, SEQ ID NO: 294,  
SEQ ID NO: 296, SEQ ID NO: 298, SEQ ID NO: 300, SEQ ID NO: 302, SEQ ID  
NO: 304, SEQ ID NO: 306, SEQ ID NO: 308, SEQ ID NO: 310, SEQ ID NO: 312,  
SEQ ID NO: 314, SEQ ID NO: 316, SEQ ID NO: 318, SEQ ID NO: 320, SEQ ID  
10 NO: 322, SEQ ID NO: 324, SEQ ID NO: 326, SEQ ID NO: 328, SEQ ID NO: 330,  
SEQ ID NO: 332, SEQ ID NO: 334, SEQ ID NO: 336, SEQ ID NO: 338, SEQ ID  
NO: 340, SEQ ID NO: 342, SEQ ID NO: 344, SEQ ID NO: 346, SEQ ID NO: 348,  
SEQ ID NO: 350, SEQ ID NO: 352, SEQ ID NO: 354, SEQ ID NO: 356, SEQ ID  
NO: 358, SEQ ID NO: 360, SEQ ID NO: 362, SEQ ID NO: 364, SEQ ID NO: 366,  
15 SEQ ID NO: 368, SEQ ID NO: 370, SEQ ID NO: 372, SEQ ID NO: 374, SEQ ID  
NO: 376, SEQ ID NO: 378, SEQ ID NO: 380, SEQ ID NO: 382, SEQ ID NO: 384,  
SEQ ID NO: 386, SEQ ID NO: 388, SEQ ID NO: 390, SEQ ID NO: 392, SEQ ID  
NO: 394, SEQ ID NO: 396, SEQ ID NO: 398, SEQ ID NO: 400, SEQ ID NO: 402,  
SEQ ID NO: 404, SEQ ID NO: 406, SEQ ID NO: 408, SEQ ID NO: 410, SEQ ID  
20 NO: 412, SEQ ID NO: 414, SEQ ID NO: 416, SEQ ID NO: 418, SEQ ID NO: 420,  
SEQ ID NO: 422, SEQ ID NO: 424, SEQ ID NO: 426, SEQ ID NO: 428, SEQ ID  
NO: 430, SEQ ID NO: 432, SEQ ID NO: 434, SEQ ID NO: 436, SEQ ID NO: 438,  
SEQ ID NO: 440, SEQ ID NO: 442, SEQ ID NO: 444, SEQ ID NO: 446, SEQ ID  
NO: 448, SEQ ID NO: 450, SEQ ID NO: 452, SEQ ID NO: 454, SEQ ID NO: 456,  
25 SEQ ID NO: 458, SEQ ID NO: 460, SEQ ID NO: 462, SEQ ID NO: 464, SEQ ID  
NO: 466, SEQ ID NO: 468, SEQ ID NO: 470, SEQ ID NO: 472, SEQ ID NO: 474,  
SEQ ID NO: 476, SEQ ID NO: 478, SEQ ID NO: 480, SEQ ID NO: 482, SEQ ID  
NO: 484, SEQ ID NO: 486, SEQ ID NO: 488, SEQ ID NO: 490, SEQ ID NO: 492,  
SEQ ID NO: 494, SEQ ID NO: 496, SEQ ID NO: 498, SEQ ID NO: 500, SEQ ID  
30 NO: 502, SEQ ID NO: 504, SEQ ID NO: 506, SEQ ID NO: 508, SEQ ID NO: 510  
and SEQ ID NO: 512.

47. An expression vector that comprises a nucleic acid sequence according to Claim 1.

48. The expression vector of Claim 47, wherein said vector is a  
5 mammalian, yeast, bacterial or insect expression vector.

49. A cell which is transfected or transformed with at least one nucleic acid sequence according to Claim 1.

10 50. A mammalian cell according to Claim 49.

51. A human cell according to Claim 50.

52. A yeast or insect cell according to Claim 49.

15

53. The mammalian cell according to Claim 49 which is selected from the group consisting of: an olfactory cell, Chinese hamster ovary cell, baby hamster kidney cell, and a myeloma cell.

20 54. A solid phase comprising at least one isolated nucleic acid sequence according to Claim 1.

55. A solid phase comprising at least one isolated nucleic acid sequence according to Claim 1, wherein the solid phase is attached to an array comprising at  
25 least one additional nucleic acid sequence.

56. The solid phase according to Claim 55 which comprises an array of at least 4 different nucleic acid sequences that encode olfactory receptors or fragments or variants thereof.

30

57. The solid phase according to Claim 55 which comprises at least 10 different nucleic acid sequences that encode olfactory receptors or fragments or variants thereof.



58. The solid phase according to Claim 55 which comprises at least 50 different nucleic acid sequences that encode olfactory receptors or fragments or variants thereof.

5

59. The solid phase according to Claim 55 which comprises at least 100 different sequences that encode olfactory receptors or fragments or variants thereof.

60. An isolated polypeptide that is selected from the group consisting of:

- 10 (i) a polypeptide comprising an amino acid sequence selected from the group consisting of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID NO: 191, SEQ ID NO: 193, SEQ ID NO: 195, SEQ ID NO: 197, SEQ ID NO: 199, SEQ ID NO: 201, SEQ ID NO: 203, SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID NO: 213, SEQ ID NO: 215,
- 15  
20  
25  
30

SEQ ID NO: 217, SEQ ID NO: 219, SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID  
NO: 225, SEQ ID NO: 227, SEQ ID NO: 229, SEQ ID NO: 231, SEQ ID NO: 233,  
SEQ ID NO: 235, SEQ ID NO: 237, SEQ ID NO: 239, SEQ ID NO: 241, SEQ ID  
NO: 243, SEQ ID NO: 245, SEQ ID NO: 247, SEQ ID NO: 249, SEQ ID NO: 251,  
5 SEQ ID NO: 253, SEQ ID NO: 255, SEQ ID NO: 257, SEQ ID NO: 259, SEQ ID  
NO: 261, SEQ ID NO: 263, SEQ ID NO: 265, SEQ ID NO: 267, SEQ ID NO: 269,  
SEQ ID NO: 271, SEQ ID NO: 273, SEQ ID NO: 275, SEQ ID NO: 277, SEQ ID  
NO: 279, SEQ ID NO: 281, SEQ ID NO: 283, SEQ ID NO: 285, SEQ ID NO: 287,  
SEQ ID NO: 289, SEQ ID NO: 291, SEQ ID NO: 293, SEQ ID NO: 295, SEQ ID  
10 NO: 297, SEQ ID NO: 299, SEQ ID NO: 301, SEQ ID NO: 303, SEQ ID NO: 305,  
SEQ ID NO: 307, SEQ ID NO: 309, SEQ ID NO: 311, SEQ ID NO: 313, SEQ ID  
NO: 315, SEQ ID NO: 317, SEQ ID NO: 319, SEQ ID NO: 321, SEQ ID NO: 323,  
SEQ ID NO: 325, SEQ ID NO: 327, SEQ ID NO: 329, SEQ ID NO: 331, SEQ ID  
NO: 333, SEQ ID NO: 335, SEQ ID NO: 337, SEQ ID NO: 339, SEQ ID NO: 341,  
15 SEQ ID NO: 343, SEQ ID NO: 345, SEQ ID NO: 347, SEQ ID NO: 349, SEQ ID  
NO: 351, SEQ ID NO: 353, SEQ ID NO: 355, SEQ ID NO: 357, SEQ ID NO: 359,  
SEQ ID NO: 361, SEQ ID NO: 363, SEQ ID NO: 365, SEQ ID NO: 367, SEQ ID  
NO: 369, SEQ ID NO: 371, SEQ ID NO: 373, SEQ ID NO: 375, SEQ ID NO: 377,  
SEQ ID NO: 379, SEQ ID NO: 381, SEQ ID NO: 383, SEQ ID NO: 385, SEQ ID  
20 NO: 387, SEQ ID NO: 389, SEQ ID NO: 391, SEQ ID NO: 393, SEQ ID NO: 395,  
SEQ ID NO: 397, SEQ ID NO: 399, SEQ ID NO: 401, SEQ ID NO: 403, SEQ ID  
NO: 405, SEQ ID NO: 407, SEQ ID NO: 409, SEQ ID NO: 411, SEQ ID NO: 413,  
SEQ ID NO: 415, SEQ ID NO: 417, SEQ ID NO: 419, SEQ ID NO: 421, SEQ ID  
NO: 423, SEQ ID NO: 425, SEQ ID NO: 427, SEQ ID NO: 429, SEQ ID NO: 431,  
25 SEQ ID NO: 433, SEQ ID NO: 435, SEQ ID NO: 437, SEQ ID NO: 439, SEQ ID  
NO: 441, SEQ ID NO: 443, SEQ ID NO: 445, SEQ ID NO: 447, SEQ ID NO: 449,  
SEQ ID NO: 451, SEQ ID NO: 453, SEQ ID NO: 455, SEQ ID NO: 457, SEQ ID  
NO: 459, SEQ ID NO: 461, SEQ ID NO: 463, SEQ ID NO: 465, SEQ ID NO: 467,  
SEQ ID NO: 469, SEQ ID NO: 471, SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID  
30 NO: 477, SEQ ID NO: 479, SEQ ID NO: 481, SEQ ID NO: 483, SEQ ID NO: 485,  
SEQ ID NO: 487, SEQ ID NO: 489, SEQ ID NO: 491, SEQ ID NO: 493, SEQ ID  
NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID NO: 503,  
SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511;

- (ii) a polypeptide comprising an amino acid sequence that exhibits at least 40% sequence identity with an amino acid sequence selected from the group consisting of:
- SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID NO: 191, SEQ ID NO: 193, SEQ ID NO: 195, SEQ ID NO: 197, SEQ ID NO: 199, SEQ ID NO: 201, SEQ ID NO: 203, SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID NO: 213, SEQ ID NO: 215, SEQ ID NO: 217, SEQ ID NO: 219, SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID NO: 225, SEQ ID NO: 227, SEQ ID NO: 229, SEQ ID NO: 231, SEQ ID NO: 233, SEQ ID NO: 235, SEQ ID NO: 237, SEQ ID NO: 239, SEQ ID NO: 241, SEQ ID NO: 243, SEQ ID NO: 245, SEQ ID NO: 247, SEQ ID NO: 249, SEQ ID NO: 251, SEQ ID NO: 253, SEQ ID NO: 255, SEQ ID NO: 257, SEQ ID NO: 259, SEQ ID NO: 261, SEQ ID NO: 263, SEQ ID NO: 265, SEQ ID NO: 267, SEQ ID NO: 269, SEQ ID NO: 271, SEQ ID NO: 273, SEQ ID NO: 275, SEQ ID NO: 277, SEQ ID NO: 279, SEQ ID NO: 281, SEQ ID NO: 283, SEQ ID NO: 285, SEQ ID NO: 287, SEQ ID NO: 289,

- SEQ ID NO: 291, SEQ ID NO: 293, SEQ ID NO: 295, SEQ ID NO: 297, SEQ ID NO: 299, SEQ ID NO: 301, SEQ ID NO: 303, SEQ ID NO: 305, SEQ ID NO: 307, SEQ ID NO: 309, SEQ ID NO: 311, SEQ ID NO: 313, SEQ ID NO: 315, SEQ ID NO: 317, SEQ ID NO: 319, SEQ ID NO: 321, SEQ ID NO: 323, SEQ ID NO: 325, SEQ ID NO: 327, SEQ ID NO: 329, SEQ ID NO: 331, SEQ ID NO: 333, SEQ ID NO: 335, SEQ ID NO: 337, SEQ ID NO: 339, SEQ ID NO: 341, SEQ ID NO: 343, SEQ ID NO: 345, SEQ ID NO: 347, SEQ ID NO: 349, SEQ ID NO: 351, SEQ ID NO: 353, SEQ ID NO: 355, SEQ ID NO: 357, SEQ ID NO: 359, SEQ ID NO: 361, SEQ ID NO: 363, SEQ ID NO: 365, SEQ ID NO: 367, SEQ ID NO: 369, SEQ ID NO: 371, SEQ ID NO: 373, SEQ ID NO: 375, SEQ ID NO: 377, SEQ ID NO: 379, SEQ ID NO: 381, SEQ ID NO: 383, SEQ ID NO: 385, SEQ ID NO: 387, SEQ ID NO: 389, SEQ ID NO: 391, SEQ ID NO: 393, SEQ ID NO: 395, SEQ ID NO: 397, SEQ ID NO: 399, SEQ ID NO: 401, SEQ ID NO: 403, SEQ ID NO: 405, SEQ ID NO: 407, SEQ ID NO: 409, SEQ ID NO: 411, SEQ ID NO: 413, SEQ ID NO: 415, SEQ ID NO: 417, SEQ ID NO: 419, SEQ ID NO: 421, SEQ ID NO: 423, SEQ ID NO: 425, SEQ ID NO: 427, SEQ ID NO: 429, SEQ ID NO: 431, SEQ ID NO: 433, SEQ ID NO: 435, SEQ ID NO: 437, SEQ ID NO: 439, SEQ ID NO: 441, SEQ ID NO: 443, SEQ ID NO: 445, SEQ ID NO: 447, SEQ ID NO: 449, SEQ ID NO: 451, SEQ ID NO: 453, SEQ ID NO: 455, SEQ ID NO: 457, SEQ ID NO: 459, SEQ ID NO: 461, SEQ ID NO: 463, SEQ ID NO: 465, SEQ ID NO: 467, SEQ ID NO: 469, SEQ ID NO: 471, SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID NO: 477, SEQ ID NO: 479, SEQ ID NO: 481, SEQ ID NO: 483, SEQ ID NO: 485, SEQ ID NO: 487, SEQ ID NO: 489, SEQ ID NO: 491, SEQ ID NO: 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511;
- (iii) a polypeptide comprising an amino acid sequence that exhibits at least 60% sequence identity with a fragment of a polypeptide according to (i) which fragment is at least 40 amino acids in length;
- (iv) a chimeric polypeptide that comprises a portion of a polypeptide according to (i) or (ii) that is at least 40 amino acids in length and a portion of at least one other G protein-coupled receptor; and
- (v) a variant of a polypeptide according to (i) which differs by said polypeptide by at least one substitution, addition or deletion modification.

61. An isolated polypeptide according to Claim 60 wherein such polypeptide exhibits at least 70% sequence identity with a polypeptide having a sequence selected from the group consisting of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID NO: 191, SEQ ID NO: 193, SEQ ID NO: 195, SEQ ID NO: 197, SEQ ID NO: 199, SEQ ID NO: 201, SEQ ID NO: 203, SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID NO: 213, SEQ ID NO: 215, SEQ ID NO: 217, SEQ ID NO: 219, SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID NO: 225, SEQ ID NO: 227, SEQ ID NO: 229, SEQ ID NO: 231, SEQ ID NO: 233, SEQ ID NO: 235, SEQ ID NO: 237, SEQ ID NO: 239, SEQ ID NO: 241, SEQ ID NO: 243, SEQ ID NO: 245, SEQ ID NO: 247, SEQ ID NO: 249, SEQ ID NO: 251, SEQ ID NO: 253, SEQ ID NO: 255, SEQ ID NO: 257, SEQ ID NO: 259, SEQ ID NO: 261, SEQ ID NO: 263, SEQ ID NO: 265, SEQ ID NO: 267, SEQ ID NO: 269, SEQ ID NO: 271, SEQ ID NO: 273, SEQ ID NO: 275,

SEQ ID NO: 277, SEQ ID NO: 279, SEQ ID NO: 281, SEQ ID NO: 283, SEQ ID  
NO: 285, SEQ ID NO: 287, SEQ ID NO: 289, SEQ ID NO: 291, SEQ ID NO: 293,  
SEQ ID NO: 295, SEQ ID NO: 297, SEQ ID NO: 299, SEQ ID NO: 301, SEQ ID  
NO: 303, SEQ ID NO: 305, SEQ ID NO: 307, SEQ ID NO: 309, SEQ ID NO: 311,  
5 SEQ ID NO: 313, SEQ ID NO: 315, SEQ ID NO: 317, SEQ ID NO: 319, SEQ ID  
NO: 321, SEQ ID NO: 323, SEQ ID NO: 325, SEQ ID NO: 327, SEQ ID NO: 329,  
SEQ ID NO: 331, SEQ ID NO: 333, SEQ ID NO: 335, SEQ ID NO: 337, SEQ ID  
NO: 339, SEQ ID NO: 341, SEQ ID NO: 343, SEQ ID NO: 345, SEQ ID NO: 347,  
SEQ ID NO: 349, SEQ ID NO: 351, SEQ ID NO: 353, SEQ ID NO: 355, SEQ ID  
10 NO: 357, SEQ ID NO: 359, SEQ ID NO: 361, SEQ ID NO: 363, SEQ ID NO: 365,  
SEQ ID NO: 367, SEQ ID NO: 369, SEQ ID NO: 371, SEQ ID NO: 373, SEQ ID  
NO: 375, SEQ ID NO: 377, SEQ ID NO: 379, SEQ ID NO: 381, SEQ ID NO: 383,  
SEQ ID NO: 385, SEQ ID NO: 387, SEQ ID NO: 389, SEQ ID NO: 391, SEQ ID  
NO: 393, SEQ ID NO: 395, SEQ ID NO: 397, SEQ ID NO: 399, SEQ ID NO: 401,  
15 SEQ ID NO: 403, SEQ ID NO: 405, SEQ ID NO: 407, SEQ ID NO: 409, SEQ ID  
NO: 411, SEQ ID NO: 413, SEQ ID NO: 415, SEQ ID NO: 417, SEQ ID NO: 419,  
SEQ ID NO: 421, SEQ ID NO: 423, SEQ ID NO: 425, SEQ ID NO: 427, SEQ ID  
NO: 429, SEQ ID NO: 431, SEQ ID NO: 433, SEQ ID NO: 435, SEQ ID NO: 437,  
SEQ ID NO: 439, SEQ ID NO: 441, SEQ ID NO: 443, SEQ ID NO: 445, SEQ ID  
20 NO: 447, SEQ ID NO: 449, SEQ ID NO: 451, SEQ ID NO: 453, SEQ ID NO: 455,  
SEQ ID NO: 457, SEQ ID NO: 459, SEQ ID NO: 461, SEQ ID NO: 463, SEQ ID  
NO: 465, SEQ ID NO: 467, SEQ ID NO: 469, SEQ ID NO: 471, SEQ ID NO: 473,  
SEQ ID NO: 475, SEQ ID NO: 477, SEQ ID NO: 479, SEQ ID NO: 481, SEQ ID  
NO: 483, SEQ ID NO: 485, SEQ ID NO: 487, SEQ ID NO: 489, SEQ ID NO: 491,  
25 SEQ ID NO: 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID  
NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509  
and SEQ ID NO: 511 or a fragment thereof which is at least 50 amino acids.

62. An isolated polypeptide according to Claim 60 wherein said  
30 polypeptide exhibits at least 80% sequence identity with a polypeptide having a  
sequence selected from the group consisting of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ  
ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID  
NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID

NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID  
NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID  
NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID  
NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID  
5 NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID  
NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID  
NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID  
NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ  
ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113,  
10 SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID  
NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131,  
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NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149,  
SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID  
15 NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167,  
SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID  
NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185,  
SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID NO: 191, SEQ ID NO: 193, SEQ ID  
NO: 195, SEQ ID NO: 197, SEQ ID NO: 199, SEQ ID NO: 201, SEQ ID NO: 203,  
20 SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID  
NO: 213, SEQ ID NO: 215, SEQ ID NO: 217, SEQ ID NO: 219, SEQ ID NO: 221,  
SEQ ID NO: 223, SEQ ID NO: 225, SEQ ID NO: 227, SEQ ID NO: 229, SEQ ID  
NO: 231, SEQ ID NO: 233, SEQ ID NO: 235, SEQ ID NO: 237, SEQ ID NO: 239,  
SEQ ID NO: 241, SEQ ID NO: 243, SEQ ID NO: 245, SEQ ID NO: 247, SEQ ID  
25 NO: 249, SEQ ID NO: 251, SEQ ID NO: 253, SEQ ID NO: 255, SEQ ID NO: 257,  
SEQ ID NO: 259, SEQ ID NO: 261, SEQ ID NO: 263, SEQ ID NO: 265, SEQ ID  
NO: 267, SEQ ID NO: 269, SEQ ID NO: 271, SEQ ID NO: 273, SEQ ID NO: 275,  
SEQ ID NO: 277, SEQ ID NO: 279, SEQ ID NO: 281, SEQ ID NO: 283, SEQ ID  
NO: 285, SEQ ID NO: 287, SEQ ID NO: 289, SEQ ID NO: 291, SEQ ID NO: 293,  
30 SEQ ID NO: 295, SEQ ID NO: 297, SEQ ID NO: 299, SEQ ID NO: 301, SEQ ID  
NO: 303, SEQ ID NO: 305, SEQ ID NO: 307, SEQ ID NO: 309, SEQ ID NO: 311,  
SEQ ID NO: 313, SEQ ID NO: 315, SEQ ID NO: 317, SEQ ID NO: 319, SEQ ID  
NO: 321, SEQ ID NO: 323, SEQ ID NO: 325, SEQ ID NO: 327, SEQ ID NO: 329,

SEQ ID NO: 331, SEQ ID NO: 333, SEQ ID NO: 335, SEQ ID NO: 337, SEQ ID  
NO: 339, SEQ ID NO: 341, SEQ ID NO: 343, SEQ ID NO: 345, SEQ ID NO: 347,  
SEQ ID NO: 349, SEQ ID NO: 351, SEQ ID NO: 353, SEQ ID NO: 355, SEQ ID  
NO: 357, SEQ ID NO: 359, SEQ ID NO: 361, SEQ ID NO: 363, SEQ ID NO: 365,  
5 SEQ ID NO: 367, SEQ ID NO: 369, SEQ ID NO: 371, SEQ ID NO: 373, SEQ ID  
NO: 375, SEQ ID NO: 377, SEQ ID NO: 379, SEQ ID NO: 381, SEQ ID NO: 383,  
SEQ ID NO: 385, SEQ ID NO: 387, SEQ ID NO: 389, SEQ ID NO: 391, SEQ ID  
NO: 393, SEQ ID NO: 395, SEQ ID NO: 397, SEQ ID NO: 399, SEQ ID NO: 401,  
SEQ ID NO: 403, SEQ ID NO: 405, SEQ ID NO: 407, SEQ ID NO: 409, SEQ ID  
10 NO: 411, SEQ ID NO: 413, SEQ ID NO: 415, SEQ ID NO: 417, SEQ ID NO: 419,  
SEQ ID NO: 421, SEQ ID NO: 423, SEQ ID NO: 425, SEQ ID NO: 427, SEQ ID  
NO: 429, SEQ ID NO: 431, SEQ ID NO: 433, SEQ ID NO: 435, SEQ ID NO: 437,  
SEQ ID NO: 439, SEQ ID NO: 441, SEQ ID NO: 443, SEQ ID NO: 445, SEQ ID  
NO: 447, SEQ ID NO: 449, SEQ ID NO: 451, SEQ ID NO: 453, SEQ ID NO: 455,  
15 SEQ ID NO: 457, SEQ ID NO: 459, SEQ ID NO: 461, SEQ ID NO: 463, SEQ ID  
NO: 465, SEQ ID NO: 467, SEQ ID NO: 469, SEQ ID NO: 471, SEQ ID NO: 473,  
SEQ ID NO: 475, SEQ ID NO: 477, SEQ ID NO: 479, SEQ ID NO: 481, SEQ ID  
NO: 483, SEQ ID NO: 485, SEQ ID NO: 487, SEQ ID NO: 489, SEQ ID NO: 491,  
SEQ ID NO: 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID  
20 NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509  
and SEQ ID NO: 511 or a fragment thereof which is at least 50 amino acids.

63. An isolated polypeptide according to Claim 60 wherein said  
polypeptide exhibits at least 90% sequence identity with a polypeptide having a  
25 sequence selected from the group consisting of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ  
ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID  
NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID  
NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID  
NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID  
30 NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID  
NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID  
NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID  
NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID



NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID  
NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ  
ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113,  
SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID  
5 NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131,  
SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID  
NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149,  
SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID  
NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167,  
10 SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID  
NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185,  
SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID NO: 191, SEQ ID NO: 193, SEQ ID  
NO: 195, SEQ ID NO: 197, SEQ ID NO: 199, SEQ ID NO: 201, SEQ ID NO: 203,  
SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID  
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NO: 249, SEQ ID NO: 251, SEQ ID NO: 253, SEQ ID NO: 255, SEQ ID NO: 257,  
20 SEQ ID NO: 259, SEQ ID NO: 261, SEQ ID NO: 263, SEQ ID NO: 265, SEQ ID  
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NO: 285, SEQ ID NO: 287, SEQ ID NO: 289, SEQ ID NO: 291, SEQ ID NO: 293,  
SEQ ID NO: 295, SEQ ID NO: 297, SEQ ID NO: 299, SEQ ID NO: 301, SEQ ID  
25 NO: 303, SEQ ID NO: 305, SEQ ID NO: 307, SEQ ID NO: 309, SEQ ID NO: 311,  
SEQ ID NO: 313, SEQ ID NO: 315, SEQ ID NO: 317, SEQ ID NO: 319, SEQ ID  
NO: 321, SEQ ID NO: 323, SEQ ID NO: 325, SEQ ID NO: 327, SEQ ID NO: 329,  
SEQ ID NO: 331, SEQ ID NO: 333, SEQ ID NO: 335, SEQ ID NO: 337, SEQ ID  
NO: 339, SEQ ID NO: 341, SEQ ID NO: 343, SEQ ID NO: 345, SEQ ID NO: 347,  
30 SEQ ID NO: 349, SEQ ID NO: 351, SEQ ID NO: 353, SEQ ID NO: 355, SEQ ID  
NO: 357, SEQ ID NO: 359, SEQ ID NO: 361, SEQ ID NO: 363, SEQ ID NO: 365,  
SEQ ID NO: 367, SEQ ID NO: 369, SEQ ID NO: 371, SEQ ID NO: 373, SEQ ID  
NO: 375, SEQ ID NO: 377, SEQ ID NO: 379, SEQ ID NO: 381, SEQ ID NO: 383,

SEQ ID NO: 385, SEQ ID NO: 387, SEQ ID NO: 389, SEQ ID NO: 391, SEQ ID NO: 393, SEQ ID NO: 395, SEQ ID NO: 397, SEQ ID NO: 399, SEQ ID NO: 401, SEQ ID NO: 403, SEQ ID NO: 405, SEQ ID NO: 407, SEQ ID NO: 409, SEQ ID NO: 411, SEQ ID NO: 413, SEQ ID NO: 415, SEQ ID NO: 417, SEQ ID NO: 419, SEQ ID NO: 421, SEQ ID NO: 423, SEQ ID NO: 425, SEQ ID NO: 427, SEQ ID NO: 429, SEQ ID NO: 431, SEQ ID NO: 433, SEQ ID NO: 435, SEQ ID NO: 437, SEQ ID NO: 439, SEQ ID NO: 441, SEQ ID NO: 443, SEQ ID NO: 445, SEQ ID NO: 447, SEQ ID NO: 449, SEQ ID NO: 451, SEQ ID NO: 453, SEQ ID NO: 455, SEQ ID NO: 457, SEQ ID NO: 459, SEQ ID NO: 461, SEQ ID NO: 463, SEQ ID NO: 465, SEQ ID NO: 467, SEQ ID NO: 469, SEQ ID NO: 471, SEQ ID NO: 473, SEQ ID NO: 475, SEQ ID NO: 477, SEQ ID NO: 479, SEQ ID NO: 481, SEQ ID NO: 483, SEQ ID NO: 485, SEQ ID NO: 487, SEQ ID NO: 489, SEQ ID NO: 491, SEQ ID NO: 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511 or a fragment thereof which is at least 50 amino acids.

64. An isolated polypeptide according to Claim 60 wherein said polypeptide exhibits about 80-90% sequence identity with a polypeptide having a sequence selected from the group consisting of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID

NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149,  
SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID  
NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167,  
SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID  
5 NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185,  
SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID NO: 191, SEQ ID NO: 193, SEQ ID  
NO: 195, SEQ ID NO: 197, SEQ ID NO: 199, SEQ ID NO: 201, SEQ ID NO: 203,  
SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID  
NO: 213, SEQ ID NO: 215, SEQ ID NO: 217, SEQ ID NO: 219, SEQ ID NO: 221,  
10 SEQ ID NO: 223, SEQ ID NO: 225, SEQ ID NO: 227, SEQ ID NO: 229, SEQ ID  
NO: 231, SEQ ID NO: 233, SEQ ID NO: 235, SEQ ID NO: 237, SEQ ID NO: 239,  
SEQ ID NO: 241, SEQ ID NO: 243, SEQ ID NO: 245, SEQ ID NO: 247, SEQ ID  
NO: 249, SEQ ID NO: 251, SEQ ID NO: 253, SEQ ID NO: 255, SEQ ID NO: 257,  
SEQ ID NO: 259, SEQ ID NO: 261, SEQ ID NO: 263, SEQ ID NO: 265, SEQ ID  
15 NO: 267, SEQ ID NO: 269, SEQ ID NO: 271, SEQ ID NO: 273, SEQ ID NO: 275,  
SEQ ID NO: 277, SEQ ID NO: 279, SEQ ID NO: 281, SEQ ID NO: 283, SEQ ID  
NO: 285, SEQ ID NO: 287, SEQ ID NO: 289, SEQ ID NO: 291, SEQ ID NO: 293,  
SEQ ID NO: 295, SEQ ID NO: 297, SEQ ID NO: 299, SEQ ID NO: 301, SEQ ID  
NO: 303, SEQ ID NO: 305, SEQ ID NO: 307, SEQ ID NO: 309, SEQ ID NO: 311,  
20 SEQ ID NO: 313, SEQ ID NO: 315, SEQ ID NO: 317, SEQ ID NO: 319, SEQ ID  
NO: 321, SEQ ID NO: 323, SEQ ID NO: 325, SEQ ID NO: 327, SEQ ID NO: 329,  
SEQ ID NO: 331, SEQ ID NO: 333, SEQ ID NO: 335, SEQ ID NO: 337, SEQ ID  
NO: 339, SEQ ID NO: 341, SEQ ID NO: 343, SEQ ID NO: 345, SEQ ID NO: 347,  
SEQ ID NO: 349, SEQ ID NO: 351, SEQ ID NO: 353, SEQ ID NO: 355, SEQ ID  
25 NO: 357, SEQ ID NO: 359, SEQ ID NO: 361, SEQ ID NO: 363, SEQ ID NO: 365,  
SEQ ID NO: 367, SEQ ID NO: 369, SEQ ID NO: 371, SEQ ID NO: 373, SEQ ID  
NO: 375, SEQ ID NO: 377, SEQ ID NO: 379, SEQ ID NO: 381, SEQ ID NO: 383,  
SEQ ID NO: 385, SEQ ID NO: 387, SEQ ID NO: 389, SEQ ID NO: 391, SEQ ID  
NO: 393, SEQ ID NO: 395, SEQ ID NO: 397, SEQ ID NO: 399, SEQ ID NO: 401,  
30 SEQ ID NO: 403, SEQ ID NO: 405, SEQ ID NO: 407, SEQ ID NO: 409, SEQ ID  
NO: 411, SEQ ID NO: 413, SEQ ID NO: 415, SEQ ID NO: 417, SEQ ID NO: 419,  
SEQ ID NO: 421, SEQ ID NO: 423, SEQ ID NO: 425, SEQ ID NO: 427, SEQ ID  
NO: 429, SEQ ID NO: 431, SEQ ID NO: 433, SEQ ID NO: 435, SEQ ID NO: 437,

SEQ ID NO: 439, SEQ ID NO: 441, SEQ ID NO: 443, SEQ ID NO: 445, SEQ ID NO: 447, SEQ ID NO: 449, SEQ ID NO: 451, SEQ ID NO: 453, SEQ ID NO: 455, SEQ ID NO: 457, SEQ ID NO: 459, SEQ ID NO: 461, SEQ ID NO: 463, SEQ ID NO: 465, SEQ ID NO: 467, SEQ ID NO: 469, SEQ ID NO: 471, SEQ ID NO: 473, 5 SEQ ID NO: 475, SEQ ID NO: 477, SEQ ID NO: 479, SEQ ID NO: 481, SEQ ID NO: 483, SEQ ID NO: 485, SEQ ID NO: 487, SEQ ID NO: 489, SEQ ID NO: 491, SEQ ID NO: 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511 or a fragment thereof which is at least 50 amino acids.

10

65. An isolated polypeptide according to Claim 60 wherein said polypeptide exhibits at least 90-95% sequence identity with a polypeptide having a sequence selected from the group consisting of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113, 25 SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167, 30 SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID NO: 191, SEQ ID NO: 193, SEQ ID

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30 SEQ ID NO: 457, SEQ ID NO: 459, SEQ ID NO: 461, SEQ ID NO: 463, SEQ ID  
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SEQ ID NO: 475, SEQ ID NO: 477, SEQ ID NO: 479, SEQ ID NO: 481, SEQ ID  
NO: 483, SEQ ID NO: 485, SEQ ID NO: 487, SEQ ID NO: 489, SEQ ID NO: 491,

SEQ ID NO: 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511 or a fragment thereof which is at least 50 amino acids.

5           66. An isolated polypeptide according to Claim 60 wherein said polypeptide exhibits about 95-99% sequence identity with a polypeptide having a sequence selected from the group consisting of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID NO: 191, SEQ ID NO: 193, SEQ ID NO: 195, SEQ ID NO: 197, SEQ ID NO: 199, SEQ ID NO: 201, SEQ ID NO: 203, SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID NO: 213, SEQ ID NO: 215, SEQ ID NO: 217, SEQ ID NO: 219, SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID NO: 225, SEQ ID NO: 227, SEQ ID NO: 229, SEQ ID NO: 231, SEQ ID NO: 233, SEQ ID NO: 235, SEQ ID NO: 237, SEQ ID NO: 239, SEQ ID NO: 241, SEQ ID NO: 243, SEQ ID NO: 245, SEQ ID NO: 247, SEQ ID

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 15 NO: 375, SEQ ID NO: 377, SEQ ID NO: 379, SEQ ID NO: 381, SEQ ID NO: 383,  
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 20 SEQ ID NO: 421, SEQ ID NO: 423, SEQ ID NO: 425, SEQ ID NO: 427, SEQ ID  
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 SEQ ID NO: 457, SEQ ID NO: 459, SEQ ID NO: 461, SEQ ID NO: 463, SEQ ID  
 25 NO: 465, SEQ ID NO: 467, SEQ ID NO: 469, SEQ ID NO: 471, SEQ ID NO: 473,  
 SEQ ID NO: 475, SEQ ID NO: 477, SEQ ID NO: 479, SEQ ID NO: 481, SEQ ID  
 NO: 483, SEQ ID NO: 485, SEQ ID NO: 487, SEQ ID NO: 489, SEQ ID NO: 491,  
 SEQ ID NO: 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID  
 NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509  
 30 and SEQ ID NO: 511 or a fragment thereof which is at least 50 amino acids.

67. A variant according to Claim 60(v) which comprises at least 5 conservative amino acid substitutions.

68. A variant according to Claim 60(v) which comprises at most 5 conservative amino acid substitutions.

5 69. A variant according to Claim 60(v) which comprises 5 to 7 conservative substitution modifications.

70. A variant according to Claim 60(v) which comprises 3 to 4 conservative substitution modifications.

10

71. A variant according to Claim 60(v) which comprises 1 or 2 conservative substitution modifications.

72. A solid phase comprising at least one directly or indirectly  
15 immobilized isolated polypeptide according to Claim 60, or a cell which expresses said polypeptide on the surface thereof.

73. The solid phase of Claim 72 comprising at least 4 different immobilized polypeptides according to Claim 60, or a cell which expresses said  
20 polypeptide on the surface thereof.

74. The solid phase of Claim 72 comprising at least 16 different immobilized polypeptides according to Claim 60, or a cell which expresses said polypeptide on the surface thereof.

25

75. The solid phase of Claim 72 comprising at least 25 different immobilized polypeptides according to Claim 60 or a cell which expresses said polypeptide on the surface thereof.

30 76. A method of detecting expression of an olfactory receptor gene comprising (a) hybridizing at least one sample with a nucleic acid according to Claim 1 and (b) detecting expression of the olfactory receptor gene by a positive hybridization signal.



77. A method of screening a library comprising (a) hybridizing the library with a nucleic acid according to Claim 1 and (b) detecting one or more olfactory receptor clones in the library by a positive hybridization signal.

5

78. A recombinant polynucleotide comprising a nucleic acid according to Claim 1 attached directly or indirectly to a heterologous nucleic acid.

79. An expression vector comprising the nucleic acid of Claim 1 and an operably linked heterologous nucleic acid that drives expression thereof.

10

80. A transfected or transformed cell comprising the recombinant polynucleotide of Claim 78 introduced into a host cell, or a progeny thereof.

81. A transgenic non-human organism comprising the recombinant polynucleotide of Claim 78 introduced into a cell of a host non-human organism, or a progeny thereof.

15

82. A method of making a recombinant polynucleotide comprising ligating the nucleic acid of Claim 1 to a heterologous nucleic acid.

20

83. The method of Claim 82 wherein the heterologous nucleic acid comprises a translational and/or transcriptional regulatory region.

84. A method of making a transfected cell comprising introducing the recombinant polynucleotide of Claim 79 into a host cell, and propagating the host cell in which the recombinant polynucleotide has been introduced.

25

85. A method of detecting specific binding of a putative ligand to an olfactory receptor comprising (a) contacting the putative ligand with a cell in which the expression vector of Claim 79 has been introduced, wherein the olfactory receptor is expressed by the cell thereby, and (b) directly or indirectly detecting specific binding between the putative ligand and the olfactory receptor.

30

86. A method of making transgenic non-human organism comprising introducing the recombinant polynucleotide of Claim 78 into a cell of a host non-human organism, or propagating the host non-human organism in which the  
5 recombinant polynucleotide has been introduced.

87. An isolated protein molecule comprising a fragment of at least 60 contiguous amino acids of a polypeptide having an amino acid sequence selected from the group consisting of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID  
10 NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID  
15 NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ  
20 ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149, SEQ ID NO: 151,  
25 SEQ ID NO: 153, SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID NO: 191, SEQ ID NO: 193, SEQ ID NO: 195, SEQ ID  
30 NO: 197, SEQ ID NO: 199, SEQ ID NO: 201, SEQ ID NO: 203, SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID NO: 213, SEQ ID NO: 215, SEQ ID NO: 217, SEQ ID NO: 219, SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID NO: 225, SEQ ID NO: 227, SEQ ID NO: 229, SEQ ID NO: 231, SEQ ID

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10 SEQ ID NO: 315, SEQ ID NO: 317, SEQ ID NO: 319, SEQ ID NO: 321, SEQ ID  
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SEQ ID NO: 477, SEQ ID NO: 479, SEQ ID NO: 481, SEQ ID NO: 483, SEQ ID  
NO: 485, SEQ ID NO: 487, SEQ ID NO: 489, SEQ ID NO: 491, SEQ ID NO: 493,  
30 SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID  
NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO:  
511.

88. The isolated protein molecule of Claim 87, wherein the fragment contains at least 100 amino acids.

89. The isolated protein molecule of Claim 87, wherein the fragment  
5 contains at least 150 amino acids.

90. The isolated protein molecule of Claim 87, wherein the fragment contains at least 200 amino acids.

10 91. The isolated protein molecule of Claim 87, wherein the fragment contains at least 250 amino acids.

92. The isolated protein molecule of Claim 87, which is a functional olfactory receptor polypeptide.

15 93. The isolated protein molecule of Claim 87, wherein the fragment specifically binds an odorant molecule.

94. A recombinant polypeptide comprising the protein molecule of Claim  
20 87 and a heterologous peptide domain.

95. The recombinant polypeptide of Claim 94, wherein the heterologous peptide domain comprises a G protein-coupled receptor transmembrane domain.

25 96. The recombinant polypeptide of Claim 94 comprising a seven-transmembrane receptor with an olfactory receptor ligand-binding domain, wherein the olfactory receptor ligand-binding domain is a chimera of at least two different olfactory receptors.

30 97. A method of detecting specific binding of a ligand to an olfactory receptor comprising (a) contacting the ligand with the protein of Claim 86, and (b) directly or indirectly detecting specific binding between the ligand and the olfactory receptor.

98. An antibody or antibody fragment that specifically binds a polypeptide having an amino acid sequence selected from the group consisting of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID NO: 191, SEQ ID NO: 193, SEQ ID NO: 195, SEQ ID NO: 197, SEQ ID NO: 199, SEQ ID NO: 201, SEQ ID NO: 203, SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID NO: 213, SEQ ID NO: 215, SEQ ID NO: 217, SEQ ID NO: 219, SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID NO: 225, SEQ ID NO: 227, SEQ ID NO: 229, SEQ ID NO: 231, SEQ ID NO: 233, SEQ ID NO: 235, SEQ ID NO: 237, SEQ ID NO: 239, SEQ ID NO: 241, SEQ ID NO: 243, SEQ ID NO: 245, SEQ ID NO: 247, SEQ ID NO: 249, SEQ ID NO: 251, SEQ ID NO: 253, SEQ ID NO: 255, SEQ ID NO: 257, SEQ ID NO: 259, SEQ ID NO: 261, SEQ ID NO: 263, SEQ ID NO: 265, SEQ ID NO: 267, SEQ ID NO: 269, SEQ ID NO: 271, SEQ ID NO: 273, SEQ ID NO: 275, SEQ ID NO: 277, SEQ ID NO: 279, SEQ ID NO: 281,

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NO: 291, SEQ ID NO: 293, SEQ ID NO: 295, SEQ ID NO: 297, SEQ ID NO: 299,  
SEQ ID NO: 301, SEQ ID NO: 303, SEQ ID NO: 305, SEQ ID NO: 307, SEQ ID  
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5 SEQ ID NO: 319, SEQ ID NO: 321, SEQ ID NO: 323, SEQ ID NO: 325, SEQ ID  
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SEQ ID NO: 337, SEQ ID NO: 339, SEQ ID NO: 341, SEQ ID NO: 343, SEQ ID  
NO: 345, SEQ ID NO: 347, SEQ ID NO: 349, SEQ ID NO: 351, SEQ ID NO: 353,  
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25 SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID  
NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511.

99. A method of detecting specific binding of the antibody of Claim 98 to  
an olfactory receptor comprising (a) contacting the antibody with a sample comprising  
30 the olfactory receptor and (b) detecting specific binding therebetween.

100. The method of Claim 99, wherein specific binding of the antibody to a  
cell in the sample identifies the cell as an olfactory cell.

101. A method of screening a library of chemical compounds for compounds that are involved in olfactory sensation comprising contacting compounds in said library with at least one polypeptide according to Claim 87 and identifying  
5 compounds that specifically bind to at least one of said polypeptides.

102. The method of Claim 101 wherein said library is a combinatorial chemical library.

10 103. The method of Claim 101 wherein said library is a peptide library.

104. The method of Claim 101 wherein said library is a peptide, encoded peptide, benzodiazepine, diversomer, vinylogous polypeptide, nonpeptidal peptidomimetic, or small molecule organic compound library.

15

105. The method of Claim 101 wherein said library is a random combination of compounds.

106. The method of Claim 101 wherein said compounds are screened by  
20 high turning point screening.

107. The method of Claim 101 wherein said screening is effected using animal cells or tissues that express at least one of said polypeptides.

25 108. A cell-based assay for identifying molecules that interact with an olfactory receptor comprising:

obtaining a cell that expresses at least one polypeptide according to Claim 60 or a chimeric protein comprising a portion of said protein and that of another G protein-coupled receptor, and which optionally expresses at least one functional G protein;  
30 contacting said cell with a molecule to be screened for its ability to modulate an olfactory receptor; and  
detecting whether modulation occurs.

109. The method of Claim 108 wherein modulation is detected based on changes in intracellular calcium.

110. The method of Claim 108 wherein modulation is detected by measuring the transfer of  $^{32}\text{P}$  from gamma-labeled GTP to the olfactory receptor polypeptide.

111. The method of Claim 108 wherein modulation is determined based on a comparison to a control compound known to modulate the particular olfactory receptor protein.

112. The method of Claim 108 wherein the G protein is  $\text{G}\alpha 15$  or  $\text{G}\alpha 16$  or another promiscuous G protein.

113. The method of Claim 108 wherein modulation is determined by detecting whether a change in the level of intracellular cyclic nucleotides occurs.

114. The method of Claim 108 wherein modulation is determined based on the level of transcription of said olfactory polypeptide after contacting the cell with the screened compound.

115. The method of Claim 108 when said screened compounds are synthesized by computer assisted drug devices based on the predicted or actual three-dimensional structure of the amino acid sequence of the olfactory protein or a fragment thereof.

116. The method of Claim 108 wherein compounds that modulate olfactory receptor are identified based on whether they specifically bind to a olfactory receptor polypeptide.

117. The method of Claim 108 wherein modulation refers to the inhibition of olfactory receptor function.



118. The method of Claim 108 wherein modulation refers to the enhancement of olfactory receptor function.

119. A method for representing the olfactory perception of one or more  
5 odors in one or more mammals, comprising:  
providing values  $X_1$  to  $X_n$  representative of the quantitative stimulation of each of n  
odor receptors of said mammals; and  
generating from said values a quantitative representation of odor perception, wherein  
at least one of said odor receptors is an odor receptor polypeptide having a sequence  
10 that is at least about 40% identical to a sequence selected from the group consisting  
of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9,  
SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19,  
SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29,  
SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39,  
15 SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49,  
SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59,  
SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69,  
SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79,  
SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89,  
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SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID  
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25 SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID  
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30 SEQ ID NO: 479, SEQ ID NO: 481, SEQ ID NO: 483, SEQ ID NO: 485, SEQ ID  
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SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID NO: 501, SEQ ID NO: 503, SEQ ID  
NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID NO: 511.

120. The method of claim 119, wherein said representation constitutes a point or a volume in n-dimensional space.

5 121. The method of claim 119, wherein said representation constitutes a graph or a spectrum.

122. The method of claim 119, wherein said representation constitutes a matrix of quantitative representations.

10

123. The method of claim 119, wherein said providing step comprises contacting a plurality of recombinantly produced olfactory receptors with a test composition, and quantitatively measuring the interaction of said composition with said receptors.

15

124. A method for predicting the odor perception in a mammal generated by one or more molecules or combinations of molecules comprising:

providing values  $X_1$  to  $X_n$  representative of the quantitative stimulation of each of n odor receptors of said mammal, for one or more molecules or combinations of

20

molecules yielding known odor perception in a mammal,

generating from said values a quantitative representation of odor perception in a mammal for the one or more molecules or combinations of molecules yielding known odor perception in a mammal;

providing values  $X_1$  to  $X_n$  representative of the quantitative stimulation of each of n

25

odor receptors of said mammal, for one or more molecules or combinations of molecules yielding unknown odor perception in a mammal;

generating from said values a quantitative representation of odor perception in a mammal for the one or more molecules or combinations of molecules yielding unknown odor perception in a mammal; and

30

predicting the olfactory perception in a mammal generated by one or more molecules or combinations of molecules yielding unknown odor perception in a mammal by comparing the quantitative representation of odor perception in a mammal generated by one or more molecules or combinations of molecules yielding unknown odor

perception in a mammal to the quantitative representation of odor perception in a mammal for the one or more molecules or combinations of molecules yielding known odor perception in a mammal, wherein at least one of said odor receptors is a odor receptor polypeptide having a sequence that is at least about 40% identical to a

5 sequence selected from the group consisting of: SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 87, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 105, SEQ ID NO: 107, SEQ ID NO: 109, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 123, SEQ ID NO: 125, SEQ ID NO: 127, SEQ ID NO: 129, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 139, SEQ ID NO: 141, SEQ ID NO: 143, SEQ ID NO: 145, SEQ ID NO: 147, SEQ ID NO: 149, SEQ ID NO: 151, SEQ ID NO: 153, SEQ ID NO: 155, SEQ ID NO: 157, SEQ ID NO: 159, SEQ ID NO: 161, SEQ ID NO: 163, SEQ ID NO: 165, SEQ ID NO: 167, SEQ ID NO: 169, SEQ ID NO: 171, SEQ ID NO: 173, SEQ ID NO: 175, SEQ ID NO: 177, SEQ ID NO: 179, SEQ ID NO: 181, SEQ ID NO: 183, SEQ ID NO: 185, SEQ ID NO: 187, SEQ ID NO: 189, SEQ ID NO: 191, SEQ ID NO: 193, SEQ ID NO: 195, SEQ ID NO: 197, SEQ ID NO: 199, SEQ ID NO: 201, SEQ ID NO: 203, SEQ ID NO: 205, SEQ ID NO: 207, SEQ ID NO: 209, SEQ ID NO: 211, SEQ ID NO: 213, SEQ ID NO: 215, SEQ ID NO: 217, SEQ ID NO: 219, SEQ ID NO: 221, SEQ ID NO: 223, SEQ ID NO: 225, SEQ ID NO: 227, SEQ ID NO: 229, SEQ ID NO: 231, SEQ ID NO: 233, SEQ ID NO: 235, SEQ ID NO: 237, SEQ ID NO: 239, SEQ ID NO: 241, SEQ ID NO: 243, SEQ ID NO: 245, SEQ ID NO: 247, SEQ ID NO: 249, SEQ ID NO: 251, SEQ ID NO: 253, SEQ ID NO: 255, SEQ ID NO: 257, SEQ ID NO: 259, SEQ ID NO: 261, SEQ ID NO: 263, SEQ ID NO: 265, SEQ ID NO:

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15 SEQ ID NO: 395, SEQ ID NO: 397, SEQ ID NO: 399, SEQ ID NO: 401, SEQ ID  
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NO: 475, SEQ ID NO: 477, SEQ ID NO: 479, SEQ ID NO: 481, SEQ ID NO: 483,  
25 SEQ ID NO: 485, SEQ ID NO: 487, SEQ ID NO: 489, SEQ ID NO: 491, SEQ ID  
NO: 493, SEQ ID NO: 495, SEQ ID NO: 497, SEQ ID NO: 499, SEQ ID NO: 501,  
SEQ ID NO: 503, SEQ ID NO: 505, SEQ ID NO: 507, SEQ ID NO: 509 and SEQ ID  
NO: 511.

AOLFR01.pr : 20 \* \* 40 \* 60 \* 80 \* 100  
AOLFR02.pr : KT-----MMVLR-----FSSFIQIGRMHQGNQTTI-----TETIRGFFKODE-HQNLZVETIRG : 46  
AOLFR03.pr : -----LLTDR-----NLSMEPTTALGCEFDYPK-IQIPTELZVL : 35  
AOLFR04.pr : -----GKE-----ENQNN-----VTEPIRGEMENLEWKIPSA-WNIV : 34  
AOLFR05.pr : -----MASER-----NCTTVARITIGSDVPE-LRVCEITLIL : 31  
AOLFR06.pr : -----SYFRLKLMKEAVLKLPT-----NQSSTPEITIGSEYPE-IQVPEITLIL : 33  
AOLFR07.pr : -----ATSNHSSGAEITIGSESNPK-LQKPHAEITIG : 35  
AOLFR08.pr : -----LARNNSLVETITIGADRDPE-FWQPNFETIRG : 70  
AOLFR09.pr : -----LARNNSLVETITIGADRDPE-FWQPNFETIRG : 33  
AOLFR10.pr : -----LARNNSLVETITIGADRDPE-FWQPNFETIRG : 33  
AOLFR11.pr : -----LARNNSLVETITIGADRDPE-FWQPNFETIRG : 33  
AOLFR12.pr : -----LARNNSLVETITIGADRDPE-FWQPNFETIRG : 33  
AOLFR13.pr : -----LARNNSLVETITIGADRDPE-FWQPNFETIRG : 33  
AOLFR14.pr : -----LARNNSLVETITIGADRDPE-FWQPNFETIRG : 33  
AOLFR15.pr : -----LARNNSLVETITIGADRDPE-FWQPNFETIRG : 33  
AOLFR16.pr : -----LARNNSLVETITIGADRDPE-FWQPNFETIRG : 33  
AOLFR17.pr : -----LARNNSLVETITIGADRDPE-FWQPNFETIRG : 33  
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AOLFR20.pr : -----LARNNSLVETITIGADRDPE-FWQPNFETIRG : 33  
AOLFR21.pr : -----LARNNSLVETITIGADRDPE-FWQPNFETIRG : 33  
AOLFR22.pr : -----LARNNSLVETITIGADRDPE-FWQPNFETIRG : 33  
AOLFR23.pr : -----LARNNSLVETITIGADRDPE-FWQPNFETIRG : 33  
AOLFR24.pr : -----LARNNSLVETITIGADRDPE-FWQPNFETIRG : 33  
AOLFR25.pr : -----LARNNSLVETITIGADRDPE-FWQPNFETIRG : 33  
AOLFR26.pr : -----LARNNSLVETITIGADRDPE-FWQPNFETIRG : 33  
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AOLFR28.pr : -----LARNNSLVETITIGADRDPE-FWQPNFETIRG : 33  
AOLFR29.pr : -----LARNNSLVETITIGADRDPE-FWQPNFETIRG : 33  
AOLFR30.pr : -----LARNNSLVETITIGADRDPE-FWQPNFETIRG : 33  
AOLFR31.pr : -----LARNNSLVETITIGADRDPE-FWQPNFETIRG : 33  
AOLFR32.pr : -----LARNNSLVETITIGADRDPE-FWQPNFETIRG : 33  
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AOLFR34.pr : -----LARNNSLVETITIGADRDPE-FWQPNFETIRG : 33  
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AOLFR50.pr : -----LARNNSLVETITIGADRDPE-FWQPNFETIRG : 33  
AOLFR51.pr : -----LARNNSLVETITIGADRDPE-FWQPNFETIRG : 33  
AOLFR52.pr : -----LARNNSLVETITIGADRDPE-FWQPNFETIRG : 33

Figure 1

AOLF01.pr : 120 \* 140 \* 160 \* 180 \* 200 \*  
 AOLF02.pr : 120 \* 140 \* 160 \* 180 \* 200 \*  
 AOLF03.pr : 120 \* 140 \* 160 \* 180 \* 200 \*  
 AOLF04.pr : 120 \* 140 \* 160 \* 180 \* 200 \*  
 AOLF05.pr : 120 \* 140 \* 160 \* 180 \* 200 \*  
 AOLF06.pr : 120 \* 140 \* 160 \* 180 \* 200 \*  
 AOLF07.pr : 120 \* 140 \* 160 \* 180 \* 200 \*  
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 AOLF09.pr : 120 \* 140 \* 160 \* 180 \* 200 \*  
 AOLF10.pr : 120 \* 140 \* 160 \* 180 \* 200 \*  
 AOLF11.pr : 120 \* 140 \* 160 \* 180 \* 200 \*  
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 AOLF25.pr : 120 \* 140 \* 160 \* 180 \* 200 \*  
 AOLF26.pr : 120 \* 140 \* 160 \* 180 \* 200 \*  
 AOLF27.pr : 120 \* 140 \* 160 \* 180 \* 200 \*  
 AOLF28.pr : 120 \* 140 \* 160 \* 180 \* 200 \*  
 AOLF29.pr : 120 \* 140 \* 160 \* 180 \* 200 \*  
 AOLF30.pr : 120 \* 140 \* 160 \* 180 \* 200 \*  
 AOLF31.pr : 120 \* 140 \* 160 \* 180 \* 200 \*  
 AOLF32.pr : 120 \* 140 \* 160 \* 180 \* 200 \*  
 AOLF33.pr : 120 \* 140 \* 160 \* 180 \* 200 \*  
 AOLF34.pr : 120 \* 140 \* 160 \* 180 \* 200 \*  
 AOLF35.pr : 120 \* 140 \* 160 \* 180 \* 200 \*  
 AOLF36.pr : 120 \* 140 \* 160 \* 180 \* 200 \*  
 AOLF37.pr : 120 \* 140 \* 160 \* 180 \* 200 \*  
 AOLF38.pr : 120 \* 140 \* 160 \* 180 \* 200 \*  
 AOLF39.pr : 120 \* 140 \* 160 \* 180 \* 200 \*  
 AOLF40.pr : 120 \* 140 \* 160 \* 180 \* 200 \*  
 AOLF41.pr : 120 \* 140 \* 160 \* 180 \* 200 \*  
 AOLF42.pr : 120 \* 140 \* 160 \* 180 \* 200 \*  
 AOLF43.pr : 120 \* 140 \* 160 \* 180 \* 200 \*  
 AOLF44.pr : 120 \* 140 \* 160 \* 180 \* 200 \*  
 AOLF45.pr : 120 \* 140 \* 160 \* 180 \* 200 \*  
 AOLF46.pr : 120 \* 140 \* 160 \* 180 \* 200 \*  
 AOLF47.pr : 120 \* 140 \* 160 \* 180 \* 200 \*  
 AOLF48.pr : 120 \* 140 \* 160 \* 180 \* 200 \*  
 AOLF49.pr : 120 \* 140 \* 160 \* 180 \* 200 \*  
 AOLF50.pr : 120 \* 140 \* 160 \* 180 \* 200 \*  
 AOLF51.pr : 120 \* 140 \* 160 \* 180 \* 200 \*  
 AOLF52.pr : 120 \* 140 \* 160 \* 180 \* 200 \*

Figure 1

Figure 1



Figure 1

440

AOLFR01.pr	:	-----	:	-
AOLFR02.pr	:	-----	:	-
AOLFR03.pr	:	-----	:	-
AOLFR04.pr	:	-----	:	-
AOLFR05.pr	:	-----	:	-
AOLFR06.pr	:	-----	:	-
AOLFR07.pr	:	-----	:	-
AOLFR08.pr	:	-----	:	-
AOLFR09.pr	:	-----	:	-
AOLFR10.pr	:	-----	:	-
AOLFR11.pr	:	-----	:	-
AOLFR12.pr	:	-----	:	-
AOLFR13.pr	:	-----	:	-
AOLFR14.pr	:	-----	:	-
AOLFR15.pr	:	-----	:	-
AOLFR16.pr	:	-----	:	-
AOLFR17.pr	:	-----	:	-
AOLFR18.pr	:	-----	:	-
AOLFR19.pr	:	-----	:	-
AOLFR20.pr	:	-----	:	-
AOLFR21.pr	:	-----	:	-
AOLFR22.pr	:	-----	:	-
AOLFR23.pr	:	-----	:	-
AOLFR25.pr	:	-----	:	-
AOLFR26.pr	:	-----	:	-
AOLFR27.pr	:	-----	:	-
AOLFR28.pr	:	-----	:	-
AOLFR29.pr	:	-----	:	-
AOLFR30.pr	:	-----	:	-
AOLFR31.pr	:	-----	:	-
AOLFR32.pr	:	-----	:	-
AOLFR34.pr	:	-----	:	-
AOLFR35.pr	:	-----	:	-
AOLFR36.pr	:	HBIFTSANBAP	:	305
AOLFR37.pr	:	-----	:	-
AOLFR38.pr	:	EKGQPH	:	300
AOLFR39.pr	:	-----	:	-
AOLFR40.pr	:	-----	:	-
AOLFR41.pr	:	-----	:	-
AOLFR42.pr	:	-----	:	-
AOLFR43.pr	:	-----	:	-
AOLFR44.pr	:	-----	:	-
AOLFR45.pr	:	-----	:	-
AOLFR46.pr	:	-----	:	-
AOLFR47.pr	:	-----	:	-
AOLFR48.pr	:	-----	:	-
AOLFR49.pr	:	-----	:	-
AOLFR50.pr	:	-----	:	-
AOLFR51.pr	:	-----	:	-
AOLFR52.pr	:	-----	:	-

Figure 1

AOLFR54.pr	---	SDSNLSNHL	---	POVFTLIGIPOL	---	BAAHFWLAMP	---	CHAEVALY	---	50
AOLFR57.pr	---	---	---	---	---	---	---	---	---	59
AOLFR58.pr	---	---	---	---	---	---	---	---	---	99
AOLFR59.pr	---	---	---	---	---	---	---	---	---	49
AOLFR60.pr	---	---	---	---	---	---	---	---	---	49
AOLFR61.pr	---	---	---	---	---	---	---	---	---	49
AOLFR62.pr	---	---	---	---	---	---	---	---	---	49
AOLFR63.pr	---	---	---	---	---	---	---	---	---	49
AOLFR64.pr	---	---	---	---	---	---	---	---	---	49
AOLFR65.pr	---	---	---	---	---	---	---	---	---	53
AOLFR66.pr	---	---	---	---	---	---	---	---	---	49
AOLFR67.pr	---	---	---	---	---	---	---	---	---	49
AOLFR68.pr	---	---	---	---	---	---	---	---	---	51
AOLFR69.pr	---	---	---	---	---	---	---	---	---	86
AOLFR70.pr	---	---	---	---	---	---	---	---	---	77
AOLFR71.pr	---	---	---	---	---	---	---	---	---	47
AOLFR72.pr	---	---	---	---	---	---	---	---	---	47
AOLFR74.pr	---	---	---	---	---	---	---	---	---	47
AOLFR75.pr	---	---	---	---	---	---	---	---	---	45
AOLFR76.pr	---	---	---	---	---	---	---	---	---	47
AOLFR77.pr	---	---	---	---	---	---	---	---	---	49
AOLFR78.pr	---	---	---	---	---	---	---	---	---	54
AOLFR79.pr	---	---	---	---	---	---	---	---	---	47
AOLFR80.pr	---	---	---	---	---	---	---	---	---	65
AOLFR81.pr	---	---	---	---	---	---	---	---	---	45
AOLFR82.pr	---	---	---	---	---	---	---	---	---	46
AOLFR83.pr	---	---	---	---	---	---	---	---	---	45
AOLFR85.pr	---	---	---	---	---	---	---	---	---	72
AOLFR86.pr	---	---	---	---	---	---	---	---	---	101
AOLFR87.pr	---	---	---	---	---	---	---	---	---	47
AOLFR88.pr	---	---	---	---	---	---	---	---	---	72
AOLFR89.pr	---	---	---	---	---	---	---	---	---	99
AOLFR90.pr	---	---	---	---	---	---	---	---	---	45
AOLFR91.pr	---	---	---	---	---	---	---	---	---	45
AOLFR92.pr	---	---	---	---	---	---	---	---	---	46
AOLFR93.pr	---	---	---	---	---	---	---	---	---	48
AOLFR94.pr	---	---	---	---	---	---	---	---	---	72
AOLFR95.pr	---	---	---	---	---	---	---	---	---	47
AOLFR96.pr	---	---	---	---	---	---	---	---	---	98
AOLFR97.pr	---	---	---	---	---	---	---	---	---	48
AOLFR98.pr	---	---	---	---	---	---	---	---	---	47
AOLFR99.pr	---	---	---	---	---	---	---	---	---	51
AOLFR101.pr	---	---	---	---	---	---	---	---	---	47
AOLFR102.pr	---	---	---	---	---	---	---	---	---	47
AOLFR103.pr	---	---	---	---	---	---	---	---	---	47
AOLFR105.pr	---	---	---	---	---	---	---	---	---	47
AOLFR106.pr	---	---	---	---	---	---	---	---	---	47
AOLFR107.pr	---	---	---	---	---	---	---	---	---	47
AOLFR108.pr	---	---	---	---	---	---	---	---	---	63
AOLFR109.pr	---	---	---	---	---	---	---	---	---	47

Figure 2

AOLFR54.pr	120	* 140	* 160	* 180	* 200	153
AOLFR57.pr	120	* 140	* 160	* 180	* 200	153
AOLFR58.pr	120	* 140	* 160	* 180	* 200	153
AOLFR59.pr	120	* 140	* 160	* 180	* 200	153
AOLFR60.pr	120	* 140	* 160	* 180	* 200	153
AOLFR61.pr	120	* 140	* 160	* 180	* 200	153
AOLFR62.pr	120	* 140	* 160	* 180	* 200	153
AOLFR63.pr	120	* 140	* 160	* 180	* 200	153
AOLFR64.pr	120	* 140	* 160	* 180	* 200	153
AOLFR65.pr	120	* 140	* 160	* 180	* 200	153
AOLFR66.pr	120	* 140	* 160	* 180	* 200	153
AOLFR67.pr	120	* 140	* 160	* 180	* 200	153
AOLFR68.pr	120	* 140	* 160	* 180	* 200	153
AOLFR69.pr	120	* 140	* 160	* 180	* 200	153
AOLFR70.pr	120	* 140	* 160	* 180	* 200	153
AOLFR71.pr	120	* 140	* 160	* 180	* 200	153
AOLFR72.pr	120	* 140	* 160	* 180	* 200	153
AOLFR73.pr	120	* 140	* 160	* 180	* 200	153
AOLFR74.pr	120	* 140	* 160	* 180	* 200	153
AOLFR75.pr	120	* 140	* 160	* 180	* 200	153
AOLFR76.pr	120	* 140	* 160	* 180	* 200	153
AOLFR77.pr	120	* 140	* 160	* 180	* 200	153
AOLFR78.pr	120	* 140	* 160	* 180	* 200	153
AOLFR79.pr	120	* 140	* 160	* 180	* 200	153
AOLFR80.pr	120	* 140	* 160	* 180	* 200	153
AOLFR81.pr	120	* 140	* 160	* 180	* 200	153
AOLFR82.pr	120	* 140	* 160	* 180	* 200	153
AOLFR83.pr	120	* 140	* 160	* 180	* 200	153
AOLFR84.pr	120	* 140	* 160	* 180	* 200	153
AOLFR85.pr	120	* 140	* 160	* 180	* 200	153
AOLFR86.pr	120	* 140	* 160	* 180	* 200	153
AOLFR87.pr	120	* 140	* 160	* 180	* 200	153
AOLFR88.pr	120	* 140	* 160	* 180	* 200	153
AOLFR89.pr	120	* 140	* 160	* 180	* 200	153
AOLFR90.pr	120	* 140	* 160	* 180	* 200	153
AOLFR91.pr	120	* 140	* 160	* 180	* 200	153
AOLFR92.pr	120	* 140	* 160	* 180	* 200	153
AOLFR93.pr	120	* 140	* 160	* 180	* 200	153
AOLFR94.pr	120	* 140	* 160	* 180	* 200	153
AOLFR95.pr	120	* 140	* 160	* 180	* 200	153
AOLFR96.pr	120	* 140	* 160	* 180	* 200	153
AOLFR97.pr	120	* 140	* 160	* 180	* 200	153
AOLFR98.pr	120	* 140	* 160	* 180	* 200	153
AOLFR99.pr	120	* 140	* 160	* 180	* 200	153
AOLFR100.pr	120	* 140	* 160	* 180	* 200	153
AOLFR101.pr	120	* 140	* 160	* 180	* 200	153
AOLFR102.pr	120	* 140	* 160	* 180	* 200	153
AOLFR103.pr	120	* 140	* 160	* 180	* 200	153
AOLFR104.pr	120	* 140	* 160	* 180	* 200	153
AOLFR105.pr	120	* 140	* 160	* 180	* 200	153
AOLFR106.pr	120	* 140	* 160	* 180	* 200	153
AOLFR107.pr	120	* 140	* 160	* 180	* 200	153
AOLFR108.pr	120	* 140	* 160	* 180	* 200	153
AOLFR109.pr	120	* 140	* 160	* 180	* 200	153

Figure 2

AOLFR54.pr : RSVAVSPFIRRRPFCGHRV- WHTYVCHMGDARACQNTITNVI-IGUTVALLAGLDSE- STSOFTHKAFHP-SHDAOAKEL-ETCASHI-CHITIP-PA : 258  
 AOLFR57.pr : CQTHSASOFLMTIRPFCGPNR- IDHRCVYRMLACSNIRH- IGLVANSGLUAVTIRP- EHSVFIYTR- -AYSERRSALATCSHSHV-VM-EP-PA : 266  
 AOLFR58.pr : CGLSHSGOILFQFCGPNV- IMZG- DLYR-IEACDHE- FQWVINSGL- JINF- INSVAILSR- -THSEGBWALETCSSHIA-VM-EPVC : 307  
 AOLFR59.pr : RSLGVHPPFIRRHVCHGNA- LSAFQCHDWRISCHDARNS- SGLCVIATVSDSE- EHS- VILNTDHA- SREOL- ZALA-TCASHI-CAVLE-EPV : 257  
 AOLFR60.pr : RALFVPSIL-ELRLEFCGCHV- IPTHYCHMGFAHSCASIKENI- EYGLCAICN- FDIYTHSVHICAFIRIP- THEPPL-LSH-TCSSHICVILA-EP : 256  
 AOLFR61.pr : KSMVUPPPFIRH-ICKKQ- LSHSCLOD-VM-ACSNR- V- YGFGALC- KNDV- LSH-IC-LS-VM-TH-RA-PRP- SDAOL-AL-EG-CAV-EP : 256  
 AOLFR62.pr : RPLVHPPFIRH-ICKQ- LSHSCLOD-VM-ACSNR- V- YGFGALC- KNDV- LSH-IC-LS-VM-TH-RA-PRP- SDAOL-AL-EG-CAV-EP : 256  
 AOLFR63.pr : KSMVUPPPFIRH-ICKKQ- LSHSCLOD-VM-ACSNR- V- YGFGALC- KNDV- LSH-IC-LS-VM-TH-RA-PRP- SDAOL-AL-EG-CAV-EP : 256  
 AOLFR64.pr : RSLVHPPFIRH-ICKKQ- LSHSCLOD-VM-ACSNR- V- YGFGALC- KNDV- LSH-IC-LS-VM-TH-RA-PRP- SDAOL-AL-EG-CAV-EP : 256  
 AOLFR65.pr : RSLVHPPFIRH-ICKKQ- LSHSCLOD-VM-ACSNR- V- YGFGALC- KNDV- LSH-IC-LS-VM-TH-RA-PRP- SDAOL-AL-EG-CAV-EP : 256  
 AOLFR66.pr : RSLVHPPFIRH-ICKKQ- LSHSCLOD-VM-ACSNR- V- YGFGALC- KNDV- LSH-IC-LS-VM-TH-RA-PRP- SDAOL-AL-EG-CAV-EP : 256  
 AOLFR67.pr : RSLVHPPFIRH-ICKKQ- LSHSCLOD-VM-ACSNR- V- YGFGALC- KNDV- LSH-IC-LS-VM-TH-RA-PRP- SDAOL-AL-EG-CAV-EP : 256  
 AOLFR68.pr : RSLVHPPFIRH-ICKKQ- LSHSCLOD-VM-ACSNR- V- YGFGALC- KNDV- LSH-IC-LS-VM-TH-RA-PRP- SDAOL-AL-EG-CAV-EP : 256  
 AOLFR69.pr : RSLVHPPFIRH-ICKKQ- LSHSCLOD-VM-ACSNR- V- YGFGALC- KNDV- LSH-IC-LS-VM-TH-RA-PRP- SDAOL-AL-EG-CAV-EP : 256  
 AOLFR70.pr : RSLVHPPFIRH-ICKKQ- LSHSCLOD-VM-ACSNR- V- YGFGALC- KNDV- LSH-IC-LS-VM-TH-RA-PRP- SDAOL-AL-EG-CAV-EP : 256  
 AOLFR71.pr : RSLVHPPFIRH-ICKKQ- LSHSCLOD-VM-ACSNR- V- YGFGALC- KNDV- LSH-IC-LS-VM-TH-RA-PRP- SDAOL-AL-EG-CAV-EP : 256  
 AOLFR72.pr : RSLVHPPFIRH-ICKKQ- LSHSCLOD-VM-ACSNR- V- YGFGALC- KNDV- LSH-IC-LS-VM-TH-RA-PRP- SDAOL-AL-EG-CAV-EP : 256  
 AOLFR73.pr : RSLVHPPFIRH-ICKKQ- LSHSCLOD-VM-ACSNR- V- YGFGALC- KNDV- LSH-IC-LS-VM-TH-RA-PRP- SDAOL-AL-EG-CAV-EP : 256  
 AOLFR74.pr : RSLVHPPFIRH-ICKKQ- LSHSCLOD-VM-ACSNR- V- YGFGALC- KNDV- LSH-IC-LS-VM-TH-RA-PRP- SDAOL-AL-EG-CAV-EP : 256  
 AOLFR75.pr : RSLVHPPFIRH-ICKKQ- LSHSCLOD-VM-ACSNR- V- YGFGALC- KNDV- LSH-IC-LS-VM-TH-RA-PRP- SDAOL-AL-EG-CAV-EP : 256  
 AOLFR76.pr : RSLVHPPFIRH-ICKKQ- LSHSCLOD-VM-ACSNR- V- YGFGALC- KNDV- LSH-IC-LS-VM-TH-RA-PRP- SDAOL-AL-EG-CAV-EP : 256  
 AOLFR77.pr : RSLVHPPFIRH-ICKKQ- LSHSCLOD-VM-ACSNR- V- YGFGALC- KNDV- LSH-IC-LS-VM-TH-RA-PRP- SDAOL-AL-EG-CAV-EP : 256  
 AOLFR78.pr : RSLVHPPFIRH-ICKKQ- LSHSCLOD-VM-ACSNR- V- YGFGALC- KNDV- LSH-IC-LS-VM-TH-RA-PRP- SDAOL-AL-EG-CAV-EP : 256  
 AOLFR79.pr : RSLVHPPFIRH-ICKKQ- LSHSCLOD-VM-ACSNR- V- YGFGALC- KNDV- LSH-IC-LS-VM-TH-RA-PRP- SDAOL-AL-EG-CAV-EP : 256  
 AOLFR80.pr : RSLVHPPFIRH-ICKKQ- LSHSCLOD-VM-ACSNR- V- YGFGALC- KNDV- LSH-IC-LS-VM-TH-RA-PRP- SDAOL-AL-EG-CAV-EP : 256  
 AOLFR81.pr : RSLVHPPFIRH-ICKKQ- LSHSCLOD-VM-ACSNR- V- YGFGALC- KNDV- LSH-IC-LS-VM-TH-RA-PRP- SDAOL-AL-EG-CAV-EP : 256  
 AOLFR82.pr : RSLVHPPFIRH-ICKKQ- LSHSCLOD-VM-ACSNR- V- YGFGALC- KNDV- LSH-IC-LS-VM-TH-RA-PRP- SDAOL-AL-EG-CAV-EP : 256  
 AOLFR83.pr : RSLVHPPFIRH-ICKKQ- LSHSCLOD-VM-ACSNR- V- YGFGALC- KNDV- LSH-IC-LS-VM-TH-RA-PRP- SDAOL-AL-EG-CAV-EP : 256  
 AOLFR84.pr : RSLVHPPFIRH-ICKKQ- LSHSCLOD-VM-ACSNR- V- YGFGALC- KNDV- LSH-IC-LS-VM-TH-RA-PRP- SDAOL-AL-EG-CAV-EP : 256  
 AOLFR85.pr : RSLVHPPFIRH-ICKKQ- LSHSCLOD-VM-ACSNR- V- YGFGALC- KNDV- LSH-IC-LS-VM-TH-RA-PRP- SDAOL-AL-EG-CAV-EP : 256  
 AOLFR86.pr : RSLVHPPFIRH-ICKKQ- LSHSCLOD-VM-ACSNR- V- YGFGALC- KNDV- LSH-IC-LS-VM-TH-RA-PRP- SDAOL-AL-EG-CAV-EP : 256  
 AOLFR87.pr : RSLVHPPFIRH-ICKKQ- LSHSCLOD-VM-ACSNR- V- YGFGALC- KNDV- LSH-IC-LS-VM-TH-RA-PRP- SDAOL-AL-EG-CAV-EP : 256  
 AOLFR88.pr : RSLVHPPFIRH-ICKKQ- LSHSCLOD-VM-ACSNR- V- YGFGALC- KNDV- LSH-IC-LS-VM-TH-RA-PRP- SDAOL-AL-EG-CAV-EP : 256  
 AOLFR89.pr : RSLVHPPFIRH-ICKKQ- LSHSCLOD-VM-ACSNR- V- YGFGALC- KNDV- LSH-IC-LS-VM-TH-RA-PRP- SDAOL-AL-EG-CAV-EP : 256  
 AOLFR90.pr : RSLVHPPFIRH-ICKKQ- LSHSCLOD-VM-ACSNR- V- YGFGALC- KNDV- LSH-IC-LS-VM-TH-RA-PRP- SDAOL-AL-EG-CAV-EP : 256  
 AOLFR91.pr : RSLVHPPFIRH-ICKKQ- LSHSCLOD-VM-ACSNR- V- YGFGALC- KNDV- LSH-IC-LS-VM-TH-RA-PRP- SDAOL-AL-EG-CAV-EP : 256  
 AOLFR92.pr : RSLVHPPFIRH-ICKKQ- LSHSCLOD-VM-ACSNR- V- YGFGALC- KNDV- LSH-IC-LS-VM-TH-RA-PRP- SDAOL-AL-EG-CAV-EP : 256  
 AOLFR93.pr : RSLVHPPFIRH-ICKKQ- LSHSCLOD-VM-ACSNR- V- YGFGALC- KNDV- LSH-IC-LS-VM-TH-RA-PRP- SDAOL-AL-EG-CAV-EP : 256  
 AOLFR94.pr : RSLVHPPFIRH-ICKKQ- LSHSCLOD-VM-ACSNR- V- YGFGALC- KNDV- LSH-IC-LS-VM-TH-RA-PRP- SDAOL-AL-EG-CAV-EP : 256  
 AOLFR95.pr : RSLVHPPFIRH-ICKKQ- LSHSCLOD-VM-ACSNR- V- YGFGALC- KNDV- LSH-IC-LS-VM-TH-RA-PRP- SDAOL-AL-EG-CAV-EP : 256  
 AOLFR96.pr : RSLVHPPFIRH-ICKKQ- LSHSCLOD-VM-ACSNR- V- YGFGALC- KNDV- LSH-IC-LS-VM-TH-RA-PRP- SDAOL-AL-EG-CAV-EP : 256  
 AOLFR97.pr : RSLVHPPFIRH-ICKKQ- LSHSCLOD-VM-ACSNR- V- YGFGALC- KNDV- LSH-IC-LS-VM-TH-RA-PRP- SDAOL-AL-EG-CAV-EP : 256  
 AOLFR98.pr : RSLVHPPFIRH-ICKKQ- LSHSCLOD-VM-ACSNR- V- YGFGALC- KNDV- LSH-IC-LS-VM-TH-RA-PRP- SDAOL-AL-EG-CAV-EP : 256  
 AOLFR99.pr : RSLVHPPFIRH-ICKKQ- LSHSCLOD-VM-ACSNR- V- YGFGALC- KNDV- LSH-IC-LS-VM-TH-RA-PRP- SDAOL-AL-EG-CAV-EP : 256  
 AOLFR100.pr : RSLVHPPFIRH-ICKKQ- LSHSCLOD-VM-ACSNR- V- YGFGALC- KNDV- LSH-IC-LS-VM-TH-RA-PRP- SDAOL-AL-EG-CAV-EP : 256  
 AOLFR101.pr : RSLVHPPFIRH-ICKKQ- LSHSCLOD-VM-ACSNR- V- YGFGALC- KNDV- LSH-IC-LS-VM-TH-RA-PRP- SDAOL-AL-EG-CAV-EP : 256  
 AOLFR102.pr : RSLVHPPFIRH-ICKKQ- LSHSCLOD-VM-ACSNR- V- YGFGALC- KNDV- LSH-IC-LS-VM-TH-RA-PRP- SDAOL-AL-EG-CAV-EP : 256  
 AOLFR103.pr : RSLVHPPFIRH-ICKKQ- LSHSCLOD-VM-ACSNR- V- YGFGALC- KNDV- LSH-IC-LS-VM-TH-RA-PRP- SDAOL-AL-EG-CAV-EP : 256  
 AOLFR104.pr : RSLVHPPFIRH-ICKKQ- LSHSCLOD-VM-ACSNR- V- YGFGALC- KNDV- LSH-IC-LS-VM-TH-RA-PRP- SDAOL-AL-EG-CAV-EP : 256  
 AOLFR105.pr : RSLVHPPFIRH-ICKKQ- LSHSCLOD-VM-ACSNR- V- YGFGALC- KNDV- LSH-IC-LS-VM-TH-RA-PRP- SDAOL-AL-EG-CAV-EP : 256  
 AOLFR106.pr : RSLVHPPFIRH-ICKKQ- LSHSCLOD-VM-ACSNR- V- YGFGALC- KNDV- LSH-IC-LS-VM-TH-RA-PRP- SDAOL-AL-EG-CAV-EP : 256  
 AOLFR107.pr : RSLVHPPFIRH-ICKKQ- LSHSCLOD-VM-ACSNR- V- YGFGALC- KNDV- LSH-IC-LS-VM-TH-RA-PRP- SDAOL-AL-EG-CAV-EP : 256  
 AOLFR108.pr : RSLVHPPFIRH-ICKKQ- LSHSCLOD-VM-ACSNR- V- YGFGALC- KNDV- LSH-IC-LS-VM-TH-RA-PRP- SDAOL-AL-EG-CAV-EP : 256  
 AOLFR109.pr : RSLVHPPFIRH-ICKKQ- LSHSCLOD-VM-ACSNR- V- YGFGALC- KNDV- LSH-IC-LS-VM-TH-RA-PRP- SDAOL-AL-EG-CAV-EP : 256

Figure 2

BNSDOCID: <WO 0168805A2 | >



Figure 3

[illegible]

Figure 3



AOLFR110.P	220	REPCCGPRC	240	260	280	300	320
AOLFR111.P		SHSCGSMV					
AOLFR112.P		QIPCCGPRC					
AOLFR113.P		QIPCCGPRC					
AOLFR114.P		QIPCCGPRC					
AOLFR115.P		QIPCCGPRC					
AOLFR116.P		QIPCCGPRC					
AOLFR117.P		QIPCCGPRC					
AOLFR118.P		QIPCCGPRC					
AOLFR119.P		QIPCCGPRC					
AOLFR120.P		QIPCCGPRC					
AOLFR121.P		QIPCCGPRC					
AOLFR122.P		QIPCCGPRC					
AOLFR123.P		QIPCCGPRC					
AOLFR124.P		QIPCCGPRC					
AOLFR125.P		QIPCCGPRC					
AOLFR126.P		QIPCCGPRC					
AOLFR127.P		QIPCCGPRC					
AOLFR128.P		QIPCCGPRC					
AOLFR129.P		QIPCCGPRC					
AOLFR130.P		QIPCCGPRC					
AOLFR131.P		QIPCCGPRC					
AOLFR132.P		QIPCCGPRC					
AOLFR133.P		QIPCCGPRC					
AOLFR134.P		QIPCCGPRC					
AOLFR135.P		QIPCCGPRC					
AOLFR136.P		QIPCCGPRC					
AOLFR137.P		QIPCCGPRC					
AOLFR138.P		QIPCCGPRC					
AOLFR139.P		QIPCCGPRC					
AOLFR140.P		QIPCCGPRC					
AOLFR141.P		QIPCCGPRC					
AOLFR142.P		QIPCCGPRC					
AOLFR143.P		QIPCCGPRC					
AOLFR144.P		QIPCCGPRC					
AOLFR145.P		QIPCCGPRC					
AOLFR146.P		QIPCCGPRC					
AOLFR147.P		QIPCCGPRC					
AOLFR148.P		QIPCCGPRC					
AOLFR149.P		QIPCCGPRC					
AOLFR150.P		QIPCCGPRC					
AOLFR151.P		QIPCCGPRC					
AOLFR152.P		QIPCCGPRC					
AOLFR153.P		QIPCCGPRC					
AOLFR154.P		QIPCCGPRC					
AOLFR155.P		QIPCCGPRC					
AOLFR156.P		QIPCCGPRC					
AOLFR157.P		QIPCCGPRC					
AOLFR158.P		QIPCCGPRC					
AOLFR159.P		QIPCCGPRC					
AOLFR160.P		QIPCCGPRC					
AOLFR161.P		QIPCCGPRC					
AOLFR162.P		QIPCCGPRC					
AOLFR163.P		QIPCCGPRC					

Figure 3

AOLFR110.P : A-----DKWSPHSHYFFPDPNMYAIRMQNTSTSTSESRHVVCQVDFFIRN----- : 316  
 AOLFR111.P : A-----SILDATSPHSHYFFPDPNMYAIRMQNTSTSTSESRHVVCQVDFFIRN----- : 317  
 AOLFR112.P : A-----SILDATSPHSHYFFPDPNMYAIRMQNTSTSTSESRHVVCQVDFFIRN----- : 318  
 AOLFR113.P : L-----TIDRTANVYSMTTWMNPEIYSRNKEIKHRTTPOKGDKASLAHL----- : 342  
 AOLFR114.P : V-KDH-----VATNVTWSSMNEPITZSRNKEIKHRTTPOKGDKASLAHL----- : 309  
 AOLFR115.P : TERES-----RAAMLVMTIPALNPEIISRNNDSEACLFVSGKTFFL----- : 330  
 AOLFR116.P : L-----DKHATDANITPVNENITERNKEMAVARERCQFVNYKIF----- : 312  
 AOLFR117.P : QENM-----KATNFCNITBMBEYSPRNKEIKHRTTPOKGDKASLAHL----- : 357  
 AOLFR118.P : A-----TLIPV-----HMLHNPESLNPVVALOTKEBFAFOFALTYKEIRS----- : 324  
 AOLFR119.P : TIPPSLHI-----EVANILMLAPPANBYGKIKRSMIYFFQDQKAG----- : 324  
 AOLFR120.P : IN-----FNKYSNPSVWTEMLNPEIISRNNDSEACLFVSGKTFFL----- : 317  
 AOLFR121.P : IE-----KOLATSTMTTTPALNPEIYSRNKEIKHRTTPOKGDKASLAHL----- : 309  
 AOLFR122.P : LNSDDIDATDQVSNKQMBEYSPRNKEIKHRTTPOKGDKASLAHL----- : 318  
 AOLFR123.P : PER-----DKWAALVMTIPALNPEIISRNNDSEACLFVSGKTFFL----- : 346  
 AOLFR124.P : A-----TLIPV-----HMLHNPESLNPVVALOTKEBFAFOFALTYKEIRS----- : 324  
 AOLFR125.P : A-----TLIPV-----HMLHNPESLNPVVALOTKEBFAFOFALTYKEIRS----- : 324  
 AOLFR126.P : DDQD-----MESHFVTVTPALNPEIYSRNKEIKHRTTPOKGDKASLAHL----- : 315  
 AOLFR127.P : DDQD-----MESHFVTVTPALNPEIYSRNKEIKHRTTPOKGDKASLAHL----- : 315  
 AOLFR128.P : A-----DKWSPHSHYFFPDPNMYAIRMQNTSTSTSESRHVVCQVDFFIRN----- : 308  
 AOLFR129.P : V-----DKWSPHSHYFFPDPNMYAIRMQNTSTSTSESRHVVCQVDFFIRN----- : 324  
 AOLFR130.P : A-----TLIPV-----HMLHNPESLNPVVALOTKEBFAFOFALTYKEIRS----- : 324  
 AOLFR131.P : E-----DKWSPHSHYFFPDPNMYAIRMQNTSTSTSESRHVVCQVDFFIRN----- : 309  
 AOLFR132.P : A-----TLIPV-----HMLHNPESLNPVVALOTKEBFAFOFALTYKEIRS----- : 305  
 AOLFR133.P : I-----DKWSPHSHYFFPDPNMYAIRMQNTSTSTSESRHVVCQVDFFIRN----- : 303  
 AOLFR134.P : YN-----SNKWSMLTAVLTPALNPEIYSRNKEIKHRTTPOKGDKASLAHL----- : 325  
 AOLFR135.P : LERD-----KZALNPEIISRNNDSEACLFVSGKTFFL----- : 327  
 AOLFR136.P : LDQE-----KWSWFTVTVTPALNPEIYSRNKEIKHRTTPOKGDKASLAHL----- : 308  
 AOLFR137.P : NDKNI-----HSMITVTPALNPEIYSRNKEIKHRTTPOKGDKASLAHL----- : 322  
 AOLFR138.P : VEQG-----KVAFFTVTVTPALNPEIYSRNKEIKHRTTPOKGDKASLAHL----- : 307  
 AOLFR139.P : V-----PLIPV-----HMLHNPESLNPVVALOTKEBFAFOFALTYKEIRS----- : 299  
 AOLFR140.P : IIPPSCHI-----EVANILMLAPPANBYGKIKRSMIYFFQDQKAG----- : 321  
 AOLFR141.P : -VPVTHI-----LUNVVDTPALNPEIYSRNKEIKHRTTPOKGDKASLAHL----- : 329  
 AOLFR142.P : A-PPVHV-----MNSVLEPDPALNPEIYSRNKEIKHRTTPOKGDKASLAHL----- : 314  
 AOLFR143.P : V-PCYHV-----MNSVLEPDPALNPEIYSRNKEIKHRTTPOKGDKASLAHL----- : 312  
 AOLFR144.P : A-PPAHL-----LUNVVDTPALNPEIYSRNKEIKHRTTPOKGDKASLAHL----- : 326  
 AOLFR145.P : A-SPLHV-----EVANILMLAPPANBYGKIKRSMIYFFQDQKAG----- : 317  
 AOLFR146.P : -VSRTHI-----MNSVLEPDPALNPEIYSRNKEIKHRTTPOKGDKASLAHL----- : 320  
 AOLFR147.P : -IPPCIHI-----EVANILMLAPPANBYGKIKRSMIYFFQDQKAG----- : 318  
 AOLFR148.P : AV-----DKWSPHSHYFFPDPNMYAIRMQNTSTSTSESRHVVCQVDFFIRN----- : 311  
 AOLFR149.P : L-----CHCHPSAEPDTHSERPCNENSHKTEKTRAF----- : 308  
 AOLFR150.P : L-----CHCHPSAEPDTHSERPCNENSHKTEKTRAF----- : 308  
 AOLFR151.P : VEES-----KUTAFVTVTPALNPEIYSRNKEIKHRTTPOKGDKASLAHL----- : 315  
 AOLFR152.P : M-----DYTRHNNVTPALNPEIYSRNKEIKHRTTPOKGDKASLAHL----- : 314  
 AOLFR153.P : VV-----DGVAIEYVTLTPALNPEIYSRNKEIKHRTTPOKGDKASLAHL----- : 311  
 AOLFR154.P : P-----VLDTAELMGLVAFENETYSRNKEIKHRTTPOKGDKASLAHL----- : 331  
 AOLFR155.P : PDQ-----DKTISNFGALAMNPEIYSRNKEIKHRTTPOKGDKASLAHL----- : 308  
 AOLFR156.P : SRGA-----BASVMTVTVTPALNPEIYSRNKEIKHRTTPOKGDKASLAHL----- : 312  
 AOLFR157.P : SRGA-----BASVMTVTVTPALNPEIYSRNKEIKHRTTPOKGDKASLAHL----- : 312  
 AOLFR158.P : SRGA-----BASVMTVTVTPALNPEIYSRNKEIKHRTTPOKGDKASLAHL----- : 312  
 AOLFR159.P : SRGA-----BASVMTVTVTPALNPEIYSRNKEIKHRTTPOKGDKASLAHL----- : 312  
 AOLFR160.P : PRKTA-----VASTWNSFPOWNEPITZSRNKEIKHRTTPOKGDKASLAHL----- : 345  
 AOLFR161.P : TVKEK-----ASAMVTVTVTPALNPEIYSRNKEIKHRTTPOKGDKASLAHL----- : 313  
 AOLFR162.P : MEQD-----KWSWFTVTVTPALNPEIYSRNKEIKHRTTPOKGDKASLAHL----- : 317  
 AOLFR163.P : FDMD-----KWSWFTVTVTPALNPEIYSRNKEIKHRTTPOKGDKASLAHL----- : 305

Figure 3



AOLFR165.P	120	140	150	180	200	128
AOLFR166.P	120	140	150	180	200	127
AOLFR167.P	120	140	150	180	200	130
AOLFR168.P	120	140	150	180	200	125
AOLFR169.P	120	140	150	180	200	123
AOLFR170.P	120	140	150	180	200	211
AOLFR171.P	120	140	150	180	200	89
AOLFR172.P	120	140	150	180	200	132
AOLFR173.P	120	140	150	180	200	129
AOLFR175.P	120	140	150	180	200	165
AOLFR176.P	120	140	150	180	200	145
AOLFR177.P	120	140	150	180	200	137
AOLFR178.P	120	140	150	180	200	127
AOLFR179.P	120	140	150	180	200	156
AOLFR180.P	120	140	150	180	200	127
AOLFR182.P	120	140	150	180	200	132
AOLFR183.P	120	140	150	180	200	129
AOLFR184.P	120	140	150	180	200	135
AOLFR185.P	120	140	150	180	200	209
AOLFR186.P	120	140	150	180	200	126
AOLFR187.P	120	140	150	180	200	146
AOLFR188.P	120	140	150	180	200	125
AOLFR189.P	120	140	150	180	200	125
AOLFR218.P	120	140	150	180	200	127
AOLFR191.P	120	140	150	180	200	128
AOLFR192.P	120	140	150	180	200	125
AOLFR193.P	120	140	150	180	200	125
AOLFR194.P	120	140	150	180	200	127
AOLFR195.P	120	140	150	180	200	157
AOLFR196.P	120	140	150	180	200	127
AOLFR197.P	120	140	150	180	200	147
AOLFR199.P	120	140	150	180	200	125
AOLFR200.P	120	140	150	180	200	127
AOLFR201.P	120	140	150	180	200	127
AOLFR202.P	120	140	150	180	200	127
AOLFR203.P	120	140	150	180	200	127
AOLFR204.P	120	140	150	180	200	125
AOLFR205.P	120	140	150	180	200	127
AOLFR206.P	120	140	150	180	200	125
AOLFR209.P	120	140	150	180	200	127
AOLFR208.P	120	140	150	180	200	127
AOLFR209.P	120	140	150	180	200	127
AOLFR211.P	120	140	150	180	200	127
AOLFR212.P	120	140	150	180	200	127
AOLFR213.P	120	140	150	180	200	168
AOLFR214.P	120	140	150	180	200	127
AOLFR215.P	120	140	150	180	200	127
AOLFR216.P	120	140	150	180	200	127
AOLFR217.P	120	140	150	180	200	137

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Figure 4

AOLFR328.P : \*ALGNH-----SUTFRFGLSADNRIRALLFVLCGVLFTTINENLAVIRA : 51

AOLFR24B.P	: S	120	* 140	* 160	* 180	* 200	
AOLFR33B.P	: S	120	* 140	* 160	* 180	* 200	
AOLFR130B.	: H	120	* 140	* 160	* 180	* 200	
AOLFR142B.	: S	120	* 140	* 160	* 180	* 200	
AOLFR171C.	: R	120	* 140	* 160	* 180	* 200	
AOLFR218.P	: H	120	* 140	* 160	* 180	* 200	
AOLFR219.P	: A	120	* 140	* 160	* 180	* 200	
AOLFR220.P	: A	120	* 140	* 160	* 180	* 200	
AOLFR221.P	: S	120	* 140	* 160	* 180	* 200	
AOLFR222.P	: H	120	* 140	* 160	* 180	* 200	
AOLFR223.P	: A	120	* 140	* 160	* 180	* 200	
AOLFR224.P	: H	120	* 140	* 160	* 180	* 200	
AOLFR225B.	: H	120	* 140	* 160	* 180	* 200	
AOLFR226.P	: T	120	* 140	* 160	* 180	* 200	
AOLFR227.P	: R	120	* 140	* 160	* 180	* 200	
AOLFR228.P	: R	120	* 140	* 160	* 180	* 200	
AOLFR229.P	: R	120	* 140	* 160	* 180	* 200	
AOLFR230.P	: R	120	* 140	* 160	* 180	* 200	
AOLFR231.P	: L	120	* 140	* 160	* 180	* 200	
AOLFR232.P	: R	120	* 140	* 160	* 180	* 200	
AOLFR233.P	: R	120	* 140	* 160	* 180	* 200	
AOLFR234.P	: S	120	* 140	* 160	* 180	* 200	
AOLFR235.P	: H	120	* 140	* 160	* 180	* 200	
AOLFR236.P	: H	120	* 140	* 160	* 180	* 200	
AOLFR237.P	: R	120	* 140	* 160	* 180	* 200	
AOLFR238.P	: R	120	* 140	* 160	* 180	* 200	
AOLFR239.P	: C	120	* 140	* 160	* 180	* 200	
AOLFR240.P	: A	120	* 140	* 160	* 180	* 200	
AOLFR241.P	: S	120	* 140	* 160	* 180	* 200	
AOLFR242.P	: S	120	* 140	* 160	* 180	* 200	
AOLFR243.P	: A	120	* 140	* 160	* 180	* 200	
AOLFR244.P	: R	120	* 140	* 160	* 180	* 200	
AOLFR245.P	: T	120	* 140	* 160	* 180	* 200	
AOLFR246.P	: H	120	* 140	* 160	* 180	* 200	
AOLFR247.P	: H	120	* 140	* 160	* 180	* 200	
AOLFR248.P	: P	120	* 140	* 160	* 180	* 200	
AOLFR249.P	: R	120	* 140	* 160	* 180	* 200	
AOLFR250.P	: H	120	* 140	* 160	* 180	* 200	
AOLFR251.P	: K	120	* 140	* 160	* 180	* 200	
AOLFR252.P	: S	120	* 140	* 160	* 180	* 200	
AOLFR253.P	: R	120	* 140	* 160	* 180	* 200	
AOLFR254.P	: R	120	* 140	* 160	* 180	* 200	
AOLFR255.P	: R	120	* 140	* 160	* 180	* 200	
AOLFR256.P	: K	120	* 140	* 160	* 180	* 200	
AOLFR257.P	: R	120	* 140	* 160	* 180	* 200	
AOLFR258.P	: R	120	* 140	* 160	* 180	* 200	
AOLFR259.P	: R	120	* 140	* 160	* 180	* 200	
AOLFR260.P	: C	120	* 140	* 160	* 180	* 200	
AOLFR261.P	: S	120	* 140	* 160	* 180	* 200	
AOLFR262.P	: S	120	* 140	* 160	* 180	* 200	
AOLFR263.P	: S	120	* 140	* 160	* 180	* 200	
AOLFR264.P	: S	120	* 140	* 160	* 180	* 200	
AOLFR265.P	: S	120	* 140	* 160	* 180	* 200	
AOLFR266.P	: S	120	* 140	* 160	* 180	* 200	
AOLFR267.P	: S	120	* 140	* 160	* 180	* 200	
AOLFR268.P	: S	120	* 140	* 160	* 180	* 200	
AOLFR269.P	: S	120	* 140	* 160	* 180	* 200	
AOLFR270.P	: S	120	* 140	* 160	* 180	* 200	
AOLFR271.P	: S	120	* 140	* 160	* 180	* 200	
AOLFR272.P	: S	120	* 140	* 160	* 180	* 200	
AOLFR273.P	: S	120	* 140	* 160	* 180	* 200	
AOLFR274.P	: S	120	* 140	* 160	* 180	* 200	
AOLFR275.P	: S	120	* 140	* 160	* 180	* 200	
AOLFR276.P	: S	120	* 140	* 160	* 180	* 200	
AOLFR277.P	: S	120	* 140	* 160	* 180	* 200	
AOLFR278.P	: S	120	* 140	* 160	* 180	* 200	
AOLFR279.P	: S	120	* 140	* 160	* 180	* 200	
AOLFR280.P	: S	120	* 140	* 160	* 180	* 200	
AOLFR281.P	: S	120	* 140	* 160	* 180	* 200	
AOLFR282.P	: S	120	* 140	* 160	* 180	* 200	
AOLFR283.P	: S	120	* 140	* 160	* 180	* 200	
AOLFR284.P	: S	120	* 140	* 160	* 180	* 200	
AOLFR285.P	: S	120	* 140	* 160	* 180	* 200	
AOLFR286.P	: S	120	* 140	* 160	* 180	* 200	
AOLFR287.P	: S	120	* 140	* 160	* 180	* 200	
AOLFR288.P	: S	120	* 140	* 160	* 180	* 200	
AOLFR289.P	: S	120	* 140	* 160	* 180	* 200	
AOLFR290.P	: S	120	* 140	* 160	* 180	* 200	
AOLFR291.P	: S	120	* 140	* 160	* 180	* 200	
AOLFR292.P	: S	120	* 140	* 160	* 180	* 200	
AOLFR293.P	: S	120	* 140	* 160	* 180	* 200	
AOLFR294.P	: S	120	* 140	* 160	* 180	* 200	
AOLFR295.P	: S	120	* 140	* 160	* 180	* 200	
AOLFR296.P	: S	120	* 140	* 160	* 180	* 200	
AOLFR297.P	: S	120	* 140	* 160	* 180	* 200	
AOLFR298.P	: S	120	* 140	* 160	* 180	* 200	
AOLFR299.P	: S	120	* 140	* 160	* 180	* 200	
AOLFR300.P	: S	120	* 140	* 160	* 180	* 200	

Figure 5  
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Figure 4



[illegible]
$$\frac{J}{I}$$

Figure 4

[illegible]

Figure 5<sup>1/5</sup>



Figure 5  
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261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300	301	302	303	304	305	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320	321	322	323	324	325	326	327	328	329	330	331	332	333	334	335	336	337	338	339	340	341	342	343	344	345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360	361	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380	381	382	383	384	385	386	387	388	389	390	391	392	393	394	395	396	397	398	399	400	401	402	403	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420	421	422	423	424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460	461	462	463	464	465	466	467	468	469	470	471	472	473	474	475	476	477	478	479	480	481	482	483	484	485	486	487	488	489	490	491	492	493	494	495	496	497	498	499	500	501	502	503	504	505	506	507	508	509	510	511	512	513	514	515	516	517	518	519	520	521	522	523	524	525	526	527	528	529	530	531	532	533	534	535	536	537	538	539	540	541	542	543	544	545	546	547	548	549	550	551	552	553	554	555	556	557	558	559	560	561	562	563	564	565	566	567	568	569	570	571	572	573	574	575	576	577	578	579	580	581	582	583	584	585	586	587	588	589	590	591	592	593	594	595	596	597	598	599	600	601	602	603	604	605	606	607	608	609	610	611	612	613	614	615	616	617	618	619	620	621	622	623	624	625	626	627	628	629	630	631	632	633	634	635	636	637	638	639	640	641	642	643	644	645	646	647	648	649	650	651	652	653	654	655	656	657	658	659	660	661	662	663	664	665	666	667	668	669	670	671	672	673	674	675	676	677	678	679	680	681	682	683	684	685	686	687	688	689	690	691	692	693	694	695	696	697	698	699	700	701	702	703	704	705	706	707	708	709	710	711	712	713	714	715	716	717	718	719	720	721	722	723	724	725	726	727	728	729	730	731	732	733	734	735	736	737	738	739	740	741	742	743	744	745	746	747	748	749	750	751	752	753	754	755	756	757	758	759	760	761	762	763	764	765	766	767	768	769	770	771
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